

(19) World Intellectual Property Organization
International Bureau(43) International Publication Date
22 November 2001 (22.11.2001)

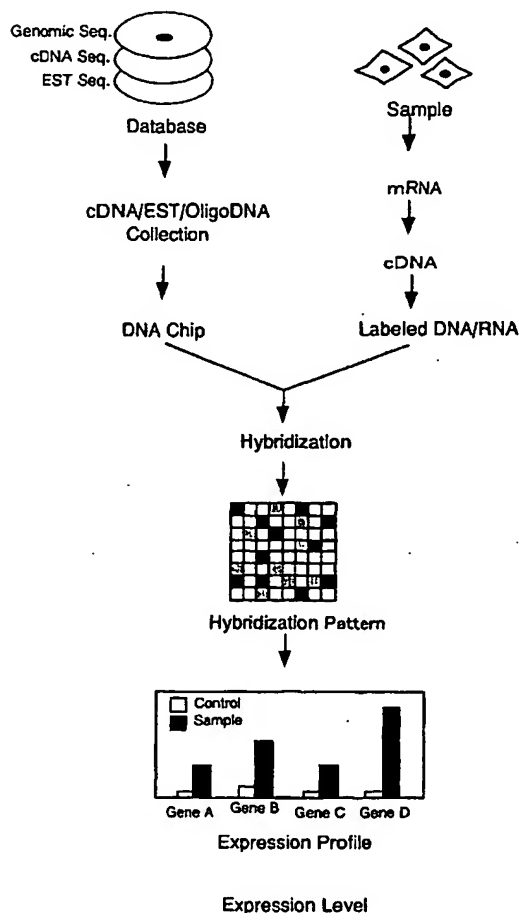
PCT

(10) International Publication Number
WO 01/88188 A2

- (51) International Patent Classification⁷: C12Q 1/68, G06F 19/00
- (21) International Application Number: PCT/JP01/04192
- (22) International Filing Date: 18 May 2001 (18.05.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
2000-145977 18 May 2000 (18.05.2000) JP
- (71) Applicant (for all designated States except US): NIHON UNIVERSITY, SCHOOL JURIDICAL PERSON [JP/JP]; 8-24, Kudan-minami 4-chome, Chiyoda-ku, Tokyo 102-8275 (JP).
- (72) Inventors; and
- (75) Inventors/Applicants (for US only): ISHIKAWA, Koichi
- [JP/JP]; 28-32-1304, Hongo 1-chome, Bunkyo-ku, Tokyo 113-0033 (JP). ASAI, Satoshi [JP/JP]; 36-10-1106, Higashi-ohizumi 1-chome, Nerima-ku, Tokyo 178-0063 (JP). TAKAHASHI, Yasuo [JP/JP]; 3-8-405, Mukaihara 2-chome, Itabashi-ku, Tokyo 173-0036 (JP). NAGATA, Toshihito [JP/JP]; 52-2-205, Ohayaguchi-kamicho, Itabashi-ku, Tokyo 173-0032 (JP). ISHII, Yukimoto [JP/JP]; 22-10, Sekibara 2-chome, Adachi-ku, Tokyo 123-0852 (JP).
- (74) Agents: HIRAKI, Yusuke et al.; Toranomon No.5 Mori Building Third Floor, 17-1, Toranomon 1-chome, Minato-ku, Tokyo 105-0001 (JP).
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK,

[Continued on next page]

(54) Title: METHOD FOR EXAMINING ISCHEMIC CONDITIONS



(57) Abstract: The present invention provides a method for examining ischemic conditions, comprising measuring the expression levels of particular genes in a test sample or determining the expression profile of a gene group in the sample comprising a plurality of genes selected from said particular genes.



SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

Published:

— without international search report and to be republished upon receipt of that report

(84) **Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

DESCRIPTION

METHOD FOR EXAMINING ISCHEMIC CONDITIONS

TEHCHNICAL FIELD

The present invention relates to a method for examining ischemic conditions by measuring the expression levels of particular genes in a test sample or by determining the expression profile of a gene group in the sample comprising a plurality of genes selected from the particular genes.

BACKGROUND ART

Cancer, cerebral apoplexy and heart diseases are called three major adult diseases and they occupy about 60% of the causes of death in the Japanese. Of these, cerebral apoplexy and heart diseases are often caused by ischemia. Thus, early detection of ischemic conditions makes it possible to prevent these diseases from occurring. Ischemia is local anemia and may be classified into groups such as compressive ischemia caused by constriction or occlusion in arterial walls due to external pressure from tumor or the like; occlusive ischemia caused by changes inside the blood vessels or in the blood vessels themselves such as thrombosis or arterial sclerosis; and vasospastic ischemia caused by vasospasms such as cerebral anemia or angina, from the viewpoint of the mechanism of its occurrence. Ischemia in the brain triggers ischemic cerebral apoplexy such as cerebral infarction, and ischemia in the heart triggers ischemic heart diseases such as myocardial infarction. Thus, for the prevention of these diseases, it is important, first of all, to find ischemic conditions as early as possible and to receive appropriate treatment.

As a method for examining ischemic conditions, a method in which abnormality in the cardiac wall movement is used as an indicator (e.g., quantitative analysis of ventricular forms/ultrasonic images, or detection of decrease in tissue systole speed); a method in which abnormality in hemodynamics is used as an indicator (e.g., analysis of the pattern of blood flow rate into the left ventricle, or nuclear medicine examination) and the like have been known to date. Among all, nuclear medicine examination is a method which can

examine ischemic conditions accurately. However, this method is disadvantageous to subjects because it involves exposure to radiation, requires a long time for examination, and is expensive. Under circumstances, a simple examination method for ischemic conditions has been desired which imposes less burden to subjects and can be carried out routinely as a part of health examination.

DISCLOSURE OF THE INVENTION

It is an object of the present invention to provide a method for examining ischemic conditions simply by measuring the expression levels of particular genes in a test sample or by determining the expression profile of a gene group in the sample comprising a plurality of genes selected from the particular genes.

As a result of intensive and extensive researches toward the solution of the above problems, the present inventors have succeeded in identifying those genes expressed under ischemic conditions and in elucidating the expression profile of the genes. Thus, the present invention has been achieved.

The present invention relates to a method for examining ischemic conditions, comprising measuring the expression levels of particular genes in a test sample or determining the expression profile of a gene group in the sample comprising a plurality of genes selected from the particular genes. Specific examples of the particular genes include (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or (b) genes functionally equal to the genes having any of the above-described nucleotide sequences or genes functionally equal to the genes encoding any of the above-described amino acid sequences. The measurement of expression levels and the determination of expression profile may be carried out using a DNA chip (e.g., a synthetic-type DNA chip). Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

Further, the present invention relates to a DNA chip for examining ischemic conditions, which carries a part or all of the following genes (a) or (b) immobilized on its surface: (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through

SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or (b) genes functionally equal to the genes having any of the above-described nucleotide sequences or genes functionally equal to the genes encoding any of the above-described amino acid sequences. Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

Further, the present invention relates to a method of screening for ischemic condition-improving drugs or therapeutics for ischemic diseases. This method is characterized by selecting candidate drugs using as an indicator whether or not:

- (a) the expression levels of particular genes of which expression levels change under ischemic conditions return to a normal expression levels; or
- (b) the expression profile of a gene group comprising a plurality of the particular genes returns to a normal expression profile;

by the administration of a drug to a test animal or test cell, wherein the returning to the normal expression levels or normal expression profile indicates that the drug is a candidate drug. Specific examples of the particular genes include (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or (b) genes functionally equal to the genes having any of the above-described nucleotide sequences or genes functionally equal to the genes encoding any of the above-described amino acid sequences. Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

Further, the present invention relates to a computer-readable record medium in which the following data (i) or (ii) have been recorded: (i) expression level data of particular genes of which expression levels change under ischemic conditions, or (ii) expression profile data of a gene group comprising a plurality of genes selected from the particular genes. Specific examples of the particular genes include (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or (b) genes functionally equal to the genes having any of the above-described

nucleotide sequences or genes functionally equal to the genes encoding any of the above-described amino acid sequences. Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

Further, the present invention relates to a computer-readable record medium in which a program that directs a computer to execute the following procedures has been recorded:

- (a) procedures to input expression level data or expression profile data of particular genes in a test sample;
- (b) procedures to record the input data;
- (c) procedures to check the recorded data with already recorded expression level data or expression profile data of the particular genes under ischemic conditions;
- (d) procedures to determine whether the test sample is under ischemic conditions or not based on the checking results obtained in (c); and
- (e) if the test sample has been determined as being under ischemic conditions, procedures to identify the clinical stage of the ischemic conditions of the test sample based on the checking results obtained in (c). Specific examples of the particular genes include (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or (b) genes functionally equal to the genes having any of the above-described nucleotide sequences or genes functionally equal to the genes encoding any of the above-described amino acid sequences. Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

Hereinbelow, the present invention will be described in detail.

The present specification encompasses the contents of the specification and drawings of Japanese Patent Application No. 2000-145977 based on which the present application claims priority.

The present invention relates to a unique method for examining ischemic conditions using, as an indicator, expression levels of particular genes or an expression profile of a particular gene group. The term "expression level" used herein refers to an absolute or

relative amount of the transcript (i.e., mRNA) of a particular gene; or an absolute or relative amount of the translation product (i.e., protein) of a particular gene. The term "expression profile" used herein refers to expression levels of a plurality of genes collected and arranged in tables, graphs, or the like.

1. Identification of Genes of which Expression Levels Change under Ischemic Conditions

Genes of which expression levels change under ischemic conditions may be identified by, for example, the differential RNA display method [Liang, P. et al., Science 257:967-971 (1992)], the hybrid subtraction method, or a method using a DNA chip. For example, a method of identifying the above genes using a DNA chip may be carried out as illustrated in Fig. 1. Briefly, a plurality of pieces of DNA information (cDNA/EST/oligoDNA collection) are obtained from a DNA database where genomic sequences, cDNA sequences or EST sequences have been recorded. Then, a wide variety of genes of known sequences are immobilized on a DNA chip. Subsequently, labeled DNA or RNA which has been prepared from mRNA derived from biosamples under ischemic conditions is hybridized with the DNA chip. The hybridization strength at each spot of the resultant hybridization pattern is then measured to thereby measure the expression level of each gene. Thus, an expression profile is obtained. Hereinbelow, a method using a DNA chip will be described in more detail.

(1) Preparation of Poly(A)+mRNA from Test Samples

First, poly(A)+mRNA must be prepared from test samples such as tissue or cell to examine expression levels of particular genes in the samples using a DNA chip. Specific examples of test samples useful for the preparation of poly(A)+mRNA to be used in the identification of genes of which expression levels change under ischemic conditions include biotissues (e.g., blood tissue, brain tissue, heart tissue or renal tissue) derived from experiment animals (e.g., mice, rats, guinea pigs, rabbits, dogs, cats, pigs or cows) in which ischemic conditions have been induced artificially or derived from humans under ischemic conditions. It is said that about 80% of genes which may be expressed in a living body are being expressed in the brain. Thus, by examining those genes of which expression levels

change in the brain under ischemic conditions, it is possible to comprehensively identify those genes of which expression levels change under ischemic conditions in tissues other than the brain. More specifically, the hippocampus derived from the above-described mice may be used as a test sample for preparing poly(A)+mRNA. Since cerebral capillaries exist in the hippocampus, blood cells such as erythrocytes, leukocytes and platelets are present there in a mixed state. Therefore, mRNAs from various blood cells may be contained in mixture in poly(A)+mRNA extracted from a hippocampus tissue.

Poly(A)+mRNA may be prepared by obtaining total RNA from test samples by such methods as the guanidine thiocyanate-cesium chloride method [J. Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York (1989)], the guanidine thiocyanate-cesium trifluoroacetate method [H. Okayama et al., *Methods in Enzymology*, 154:3, Academic Press, New York (1987)], the guanidine thiocyanate-phenol-chloroform method [P. Chomczynski et al., *Anal. Biochem.*, 162:156 (1987)] or the phenol-SDS method [R.D. Palmiter, *Biochemistry*, 13:3606 (1974)], loading the resultant total RNA to an oligo-dT cellulose or poly U Sepharose column for specific adsorption of poly(A)+mRNA, and then eluting the poly(A)+mRNA from the column. In particular, when the test sample is a tissue, it is important to perform purification processes accurately because the state of purification of the total RNA or poly(A)+mRNA greatly influences the yield of cDNA, etc.

For example, when poly(A)+mRNA is prepared by the guanidine thiocyanate-cesium chloride method, first, an appropriate amount (e.g., 5 volumes) of guanidine thiocyanate solution is added to a tissue sample. Then, the tissue sample is disrupted using, e.g., a Polytron homogenizer. Sodium N-lauroyl sarcosinate is added to the disrupted tissue to give a desired concentration (e.g., 0.5%) and agitated. The resultant sample is centrifuged (e.g., at 5000 xg for 10 min). The resultant supernatant is layered over a cushion of cesium chloride-EDTA contained in a centrifuge tube and subjected to ultracentrifugation (e.g., at 100,000 xg for 12 hr). The resultant precipitate is rinsed with 70% ethanol and then dissolved in TE buffer to thereby obtain total RNA. The resultant total RNA is applied to an oligo-dT cellulose column to thereby obtain poly(A)+mRNA.

Alternatively, the preparation of poly(A)+mRNA may be performed using

commercial kits. Specific examples of kits for preparing total RNA include RNeasy Total RNA Isolation kit (Qiagen) and TRIzol Reagent (Gibco BRL Life Technologies). Specific examples of kits for isolating poly(A)+mRNA from total RNA include Oligotex Direct mRNA kit (Qiagen) and Oligotex mRNA kit (Quiagen).

(2) Synthesis of cDNA with Reverse Transcriptase

Subsequently, cDNA is synthesized using the poly(A)+mRNA obtained in (1) above as a template. The synthesis of cDNA may be carried out according to the method of Gubler et al. [U. Gubler et al., *Gene* 25:263 (1987)]. Briefly, oligo(dT)₁₂₋₁₈ is added to a solution of poly(A)+mRNA, which is heated and then cooled quickly. To this solution, a single-stranded cDNA synthesis buffer, a dNTP solution (containing mixture of dATP, dGTP, dCTP and dTTP), a ribonuclease inhibitor solution, a dithiothreitol solution, etc. are added and mixed. Then, a reverse transcriptase (e.g., Superscript RT; BRL) is added to the mixture, which is then incubated for a specific period to thereby yield single-stranded cDNA. If necessary, double-stranded cDNA may be synthesized further using the single-stranded cDNA as a template. Briefly, a cDNA synthesis buffer, a dNTP solution (containing mixture of dATP, dGTP, dCTP and dTTP), a dithiothreitol solution, etc. are added to a solution of the single-stranded cDNA and mixed. Then, a DNA polymerase (e.g., T4 DNA polymerase) is added to the mixture, which is then incubated for a specific period to thereby yield double-stranded cDNA. Labeled cDNA may be obtained by using a labeled dNTP (e.g., biotin-labeled dNTP) in the synthesis of single- or double-stranded cDNA.

(3) Preparation of Labeled cRNA Fragments

When a DNA chip on which oligonucleotides are immobilized as DNA probes is used in the method of the invention, labeled cRNA is prepared, if necessary, by *in vitro* transcription using the cDNA obtained in (2) above as a template. The preparation of labeled cRNA by *in vitro* transcription may be carried out according to the method of Kreig et al. [Kreig, P.A. et al., *Methods in Enzymology* 155:397-415 (1987)]. The resultant labeled cRNA molecules must be fragmented before use. The fragmentation of these molecules may be performed by heating in the presence of Mg²⁺ (e.g., at 94°C for 3 min) or by treatment with DNase.

The *in vitro* transcription described above may also be performed using a commercial kit. As an example of *in vitro* transcription kit, MEGAscript™ *In Vitro* Transcription Kit (Ambion) may be given.

(4) Hybridization on a DNA Chip

Subsequently, the labeled nucleotide sample obtained in (2) or (3) above is added to a DNA chip to carry out a hybridization reaction. Specific examples of DNA chips useful in the method of the invention include oligoDNA microarray (also called "synthetic-type DNA chip") which is prepared by synthesizing oligoDNAs on a substrate directly, and DNA microarray (also called "paste-type DNA chip") which is prepared by immobilizing pre-synthesized DNAs on a substrate. In the present invention, it is preferable to use a synthetic-type DNA chip that can provide high detection sensitivity, accuracy and reproducibility (e.g., oligoDNA microarray GeneChip™ manufactured by Affymetrix) for identifying genes of which expression levels change under ischemic conditions.

In the examination of gene expression, it is important to carry out hybridization under high stringency conditions to inhibit non-specific bonding. The term "high stringency conditions" refers to those conditions under which hybridization only occurs between two nucleotide strands having 90% or more homology to each other. Stringency may be raised or lowered by changing salt concentrations (e.g., concentrations of NaCl, trisodium citrate) and/or the reaction temperature. The lower the salt concentrations are and the higher the temperatures is, the higher the stringency becomes. Depending on the type of DNA chip used and other factors, a specific temperature and specific salt conditions may be high stringency conditions or low stringency conditions. Thus, high stringency conditions and low stringency conditions should be decided for each chip to be used. With respect to GeneChip™ Mu6500 used in the present invention, high stringency conditions refer to reaction temperatures ranging from 43 to 65°C, preferably 45°C, and Na⁺ concentrations ranging from 500 to 1000 mM, preferably 1000 mM.

(5) Detection and Data Analysis

The double-strands formed on the microarray as a result of the hybridization are analyzed with a fluorescence image scanner or the like. The fluorescence intensities may be measured automatically with a system integrating a fluorescent laser microscope, a CCD

camera and a computer. Preferably, a scanner is used which is capable of quantitatively discriminating spots having a size of several ten micrometers and having a distance of approx. 10 μ m between every two spots. Further, it is preferable that the scanner be capable of handling a plurality of labels and scanning over a wide range at a high speed, and that the scanner be equipped with an automatic focusing function which allows the scanner to manage microscopic distortion in the substrate. As a specific example of a scanner equipped with such a function, GMS 418 Array Reader (Genetic MicroSystems) may be given. The software to be used for the analysis of the above data is, preferably, capable of performing complicated analysis of a large number of oligonucleotides with partially overlapped sequences, such as analysis of mutation or polymorphism.

Alternatively, a commercial system may be used in the present invention which is integrating a set of components necessary for gene analysis using a DNA chip. These components include (i) a DNA chip, (ii) a device for automatically washing and staining the DNA chip after hybridization, (iii) a scanner which reads fluorescence emission, and (iv) a work station which processes and analyzes the information read. As a specific example of such a system, the GeneChipTM analysis system created by Affimetrix may be given. This system is provided with GeneChipTM Laboratory Information Management System (LIMSTM) and GeneChipTM Expression Data Mining Tool (EDMTTM) as bioinformatics tools for efficient utilization of obtained genetic data. These tools make it possible to output obtained data to SQL compliant databases of GATC (Genetic Analysis Technology Consortium) format to thereby link the system to public genetic information databases on the web. By using this analysis system, more efficient and more extensive data analysis can be made.

The nucleotide sequences of those genes which have been found by the present invention to show altered expression levels under ischemic conditions in mouse, and the amino acid sequences encoded by those genes are shown in SEQ ID NO: 1 through SEQ ID NO: 1066. Since both mouse and human belong to mammals, they are highly similar to each other genetically. Thus, genes which are functionally equivalent to the genes having the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or the genes encoding the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066

may exist in human cells. Accordingly, by measuring expression levels of such human genes, it is possible to perform examination of ischemic conditions on human-derived samples. The term "functionally equivalent genes" used herein includes, in addition to the genes consisting of any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 themselves or the genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 themselves, those genes which have homology to the above genes and play roles identical or similar to the roles of the above genes in the living body. Nucleotide sequence information, amino acid sequence information, etc. on those genes in human cells which are functionally equivalent to mouse-derived genes can be obtained from known databases such as GenBank by searching with keywords such as a part of nucleotide sequence of interest, a part of amino acid sequence of interest, or a gene product name.

It is possible to identify ischemia marker genes of which expression levels change specifically under ischemic conditions. This identification can be performed by further examining the expression levels under other diseases of the above-described genes which were found to show altered expression levels under ischemic conditions.

2. DNA Chips for Examining Ischemic Conditions

DNA chips carrying as DNA probes a part or all of the genes identified in Section 1. above (which show altered expression levels under ischemic conditions) immobilized on their substrates can be used as a DNA chip for examining ischemic conditions. In particular, a DNA chip as shown in Fig. 2 on which three groups of genes (i.e., genes showing high expression levels under ischemic conditions; genes showing moderate expression levels under ischemic conditions; and genes showing low expression levels under ischemic conditions) are located separately may be used as a DNA chip that is capable of evaluating the extent of progress of ischemic conditions. There are two types of DNA chips. One is paste-type chips prepared by immobilizing pre-synthesized DNA probes on their substrates; and the other is synthetic-type chips prepared by synthesizing DNA probes on their substrates directly. The term "DNA probes" used herein refers to DNA strands which are immobilized on the substrate of a DNA chip in order to detect those

genes having DNA strands with specific nucleotide sequences. Hereinbelow, processes for preparing both types of DNA chips will be described specifically.

(1) Method of Preparing Paste-Type DNA Chips

First, as DNA probes, a part or all of the genes identified in Section 1. above which show altered expression levels under ischemic conditions are prepared by PCR or chemical synthesis. DNA probes must be present on the substrate of a DNA chip as single-stranded DNAs so that they can hybridize with target nucleotide strands having sequences complementary to the sequences of the DNA probes when the target strands access to the DNA probes. Thus, in designing DNA probes, it is desirable to select sequences so that formation of secondary structures that would inhibit the hybridization with target nucleotide strands will occur as little as possible. The term "secondary structures" used herein refers to the stem-loop structure, hairpin structure or the like which is formed by hybridization of a part of a probe with another part of the same probe when the probe has been folded back. Whether sequences of interest would form secondary structures or not can be analyzed using a commercial gene analysis software (e.g., DNASIS; Hitachi Software Engineering).

The preparation of DNA probes by PCR may be carried out by conventional methods [see, for example, Sambrook, J. et al., *Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press (1989)] using, as a template, genomic DNA, total RNA, mRNA or cDNA derived from an organism to be tested. For example, the gene consisting of the nucleotide sequence shown in SEQ ID NO: 1006 can be used as a marker for examining ischemic conditions since its expression increases remarkably under ischemic conditions. A DNA probe to detect this gene may be obtained by PCR using sense primer 5'-atgctcttccgagctgtgct-3' (SEQ ID NO: 1067), anti-sense primer 5'-cagctcagttgaacgccttt-3' (SEQ ID NO: 1068) and, as a template, cDNA prepared from mRNA derived from mouse hippocampus under ischemic conditions. Whether the amplified fragment by PCR is the fragment of interest or not may be determined by subcloning the amplified fragment into an appropriate vector such as pBlueScriptSK(+) (Stratagene) or pCR2.1 (Invitrogen) and then determining the nucleotide sequence thereof. The nucleotide sequence may be determined by conventional methods such as the chemical modification method by Maxam-Gilbert or

the dideoxynucleotide chain termination method using M13 phage. Usually, the nucleotide sequence may be determined using an automated DNA sequencer (e.g., 373A DNA sequencer; Perkin-Elmer).

On the other hand, the preparation of DNA probes by chemical synthesis may be carried out according to conventional DNA synthesis methods used in the art, e.g., the phosphoramidite method, or the phosphonate method. For example, when DNA probes are synthesized by the phosphoramidite method, a nucleoside derivative obtained by introducing a trivalent phosphoramidite residue into the hydroxyl group at 3'-position of the sugar moiety is used as a synthesis unit. First, this amidite unit is activated with 1H-tetrazol and reacted with the 5'-hydroxyl of a DNA strand on a solid phase (step 1), to thereby yield a trivalent phosphite ester. Subsequently, the trivalent phosphite ester is led to a pentavalent phosphate triester through oxidation (step 2), capping (step 3) and hydrogenation (step 4). Then, steps 1 to 4 are repeated. Finally, an oligomer block having the desired nucleotide sequence is cleaved from the solid phase and deprotected to thereby yield the DNA strand of interest.

Subsequently, the thus obtained DNA probe is immobilized on the substrate of a DNA chip. Specific examples of substrates useful for this purpose include glass sheets, quartz sheets and silicone wafers. As a size of the substrate, 3.5 mm x 5.5 mm, 18 mm x 18 mm or 22 mm x 75 mm may be used, for example. This size may be varied appropriately depending on, for example, the number and size of spots of DNA probes on the substrate. As to a method for immobilizing DNA, DNA may be electrostatically bound to a solid support that has been surface-treated with a polycation such as polylysine, polyethyleneimine or polyalkylamine, utilizing the electric charge of the DNA; or DNA probes into which a functional group such as amino group, aldehyde group, SH-group or biotin has been introduced may be covalently bound to the surface of a solid support into which a functional group such as amino group, aldehyde group or epoxy group has been introduced.

The spotting of DNA probes on the substrate may be performed using an arrayer which is capable of quantitatively spotting DNA probes in sizes ranging from several ten micrometers to several hundred micrometers and at pre-determined locations. As to the

technology of spotting, pin technology utilizing the mechanical contact of pin tips with a solid support; inkjet technology utilizing the principle of inkjet printer; or capillary technology utilizing a capillary device may be enumerated.

(2) Method for Preparing Synthetic-Type DNA Chips

As a method for synthesizing DNA probes on a substrate directly, the method of Fodor et al. may be used in which photolithographic fabrication techniques are combined with solid phase DNA synthesis techniques [Fodor, S.P.A. et al, Science 251:767-773 (1991)]. Briefly, a synthetic linker having a protective group removable by a photochemical reaction is bound onto a substrate. Then, the substrate is illuminated by light through a blocking material called mask to thereby remove only those protective groups in specific areas. Subsequently, the substrate is reacted with nucleotides having protected hydroxyl groups. As a result, polymerization occurs only in those areas where protective groups have been removed. Then, the substrate is illuminated by light through another mask, and polymerization of nucleotides is repeated. Thus, coupling reactions with different nucleotide precursors are repeated using various masks. As a result, DNA probes of desired sequences can be synthesized on specific areas on the substrate of a DNA chip. An oligonucleotide N-mer in nucleotide length can be synthesized by $N \times 4$ cycles of reaction. Thus, a DNA probe 25-mer in length can be synthesized by $25 \times 4 = 100$ cycles of reaction. The nucleotide length of the DNA probes on the DNA chip of the invention for examining ischemic conditions is 10- to 30-mer, preferably 15- to 25-mer.

Since the nucleotide length of DNA probes on DNA chips of this type is usually short, the specificity of hybridization on such chips may be questioned. This problem can be solved as described below. Briefly, in order to detect the expression of a particular gene, perfect match (PM) (i.e., completely complementary) oligonucleotide DNA probes corresponding to a plurality of portions (usually, ten and several portions) of the target gene and an identical number of mismatch (MM) oligonucleotide DNA probes having a mutation at one nucleotide (usually, the central nucleotide or neighboring nucleotide) are located on a substrate (see Fig. 3). Then, hybridization is carried out on the substrate using the MM probes as an indicator of the specificity of hybridization. That is, signal ratio of PM probes to MM probes is calculated, and the pseudo-positive signal is

eliminated.

3. Method of the Invention for Examining Ischemic Conditions

Ischemic conditions can be examined by measuring the expression levels in a test sample of the genes which were revealed in the present invention to show altered expression levels under ischemic conditions. Alternatively, ischemic conditions can be examined by determining the expression profile of a gene group comprising a plurality of genes selected from the above-described genes. The expression "determining the expression profile of a gene group" means measuring the expression levels of individual genes constituting the group and arranging the results in tables, graphs, or the like. Specific examples of the ischemic conditions include compressive ischemia, occlusive ischemia and vasospastic ischemia.

By measuring the expression levels in a test sample of the genes identified in Section 1. above which show altered expression levels under ischemic conditions, it is possible to examine whether the test sample is under ischemic conditions or not. Briefly, when the expression levels of the above genes in the test sample are changed to the same extent as the expression levels under ischemic conditions revealed by the present invention are changed, then the test sample can be evaluated as being under ischemic conditions. For example, the expression levels of the genes having the nucleotide sequences shown in SEQ ID NOS: 960-1037 and SEQ ID NOS: 1065-1066 or the genes encoding the amino acid sequences shown in SEQ ID NOS: 960-1037 and SEQ ID NOS: 1065-1066 increase more than 10-fold under ischemic conditions. Thus, when the expression levels of these genes are increased more than 10-fold in a test sample, the test sample can be evaluated as being under ischemic conditions.

Further, it is possible to more accurately examine whether a test sample is under ischemic conditions or not by measuring the expression levels of ischemia marker genes, which are genes included in the genes identified in Section 1. above and show little or no changes in expression levels in diseases other than ischemia. That is, when the changes in the expression levels of the above marker genes in a test sample are the same in extent as the changes in the expression levels of those genes detected in the present invention, the test

sample can be evaluated as being under ischemic conditions.

The expression levels of the above genes may be measured by, for example, dot hybridization, slot hybridization, Northern hybridization or quantitative PCR when the number of genes to be measured is small. When the number of genes to be measured is large, their expression levels may be measured with a DNA chip.

Further, it is possible to examine with higher accuracy whether a test sample is under ischemic conditions or not by determining the expression profile of a gene group in the sample comprising a plurality of genes selected from the genes identified in Section 1. above which show altered expression levels under ischemic conditions and comparing the resultant profile with an expression profile of a normal sample which is not under ischemic conditions. The determination of expression profiles of gene groups can be performed more quickly and simply by using DNA chips. Expression profiles may be classified using cluster analysis described later. As to the DNA chip, it is preferable to use synthetic-type DNA chips from the viewpoints of accuracy, sensitivity and reproducibility. It is also possible to perform examination of ischemic conditions using the DNA chip of the invention prepared in Section 2. above. For example, as shown in Fig. 2A, genes are classified into a group of low expression level genes, a group of moderate expression level genes, and a group of high expression level genes and immobilized separately on a DNA chip for hybridization. Low expression level genes mean those genes of which transcription levels increased n -fold (where n is 2 or more but less than 5) within 24 hours when the transcription level at 0 hour is taken as 1. Moderate expression level genes mean those genes of which transcription levels increased n -fold (where n is 5 or more but less than 10). High expression level genes mean those genes of which transcription levels increased more than 10-fold.

In order to prepare a DNA chip carrying immobilized genes thereon which show altered expression levels under ischemic conditions, for example, 300 or more low expression level genes, 100-300 moderate expression level genes and 30-100 high expression level genes are selected from the genes having the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or the genes encoding the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066, and immobilized. When

the expression levels of the 30-100 high expression level genes have been changed compared with a gene expression profile obtained from a non-ischemic patient (control), the test sample can be judged under ischemic conditions of early-stage (Fig. 2B). When not only the expression levels of high expression level genes but also those of the 100-300 moderate expression level genes have been changed, the sample can be judged under ischemic conditions of intermediate-stage (Fig. 2C). Further, when the expression levels of the 300 or more low expression level genes have been changed in addition to those of the high expression level genes and the moderate expression level genes, the test sample can be evaluated under ischemic conditions of late-stage (Fig. 2D).

Expression levels may change toward increase or decrease compared to normal levels. However, the expression levels of all of the genes having the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or the genes encoding the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 change toward increase under ischemic conditions. Thus, in examining ischemic conditions using changes in the expression levels of the above genes as an indicator, a gene should be counted as having shown a change in its expression level only when an increase is observed in the expression level.

With respect to those genes which have been confirmed to show no change in expression levels under ischemic conditions, it is also possible to measure their expression levels and utilize the results for examining ischemic conditions. Briefly, the expression levels of such genes are measured in the test samples which were evaluated as ischemic as a result of the above-described measurement. If no change is observed in their expression levels, the reliability of the above evaluation that the test samples are under ischemic conditions can be enhanced.

4. Computer-Readable Record Medium Containing Gene Expression Data under Ischemic Conditions and Ischemic Condition Identification Program, as well as Ischemic Condition Identification Program

Expression level data of the genes which were revealed by the invention to show altered expression levels under ischemic conditions or expression profile data of a gene group comprising a plurality of genes selected from the above genes may be recorded in an

appropriate medium and used as comparison data in the analysis of examination data on ischemic conditions. As a record medium, any type of record media may be used, e.g., magnetic tape, CD-ROM, IC card, or RAM. Specifically, the degree of change in the expression levels of those genes of which expression levels change remarkably under ischemic conditions is examined in a test sample. If the expression levels are equal to the expression levels recorded in a record medium, the test sample (and thus the organism from which the sample is derived) can be evaluated as being under ischemic conditions. Further, more accurate evaluation of ischemic condition can be made by comparing a gene expression profile recorded (which was created from individual expression level data of a group of genes whose expression levels change under ischemic conditions) with an expression profile of corresponding genes in a test sample. That is, if the expression patterns in a test sample of a plurality of particular genes whose expression levels change under ischemic conditions resemble the expression patterns of the corresponding genes recorded in such a medium, the test sample can be evaluated as being under ischemic conditions with higher probability.

A record medium in which a program that directs a computer to execute the procedures described below has been recorded is useful as a record medium containing ischemic condition identification program. The term "ischemic condition identification program" used herein refers to a program that is able to identify the stage of ischemic conditions (i.e., early stage, intermediate stage or late stage) in a test sample when the test sample has been suspected to be under ischemic conditions or evaluated as being under such conditions. This program comprises (a) procedures to input expression level data or expression profile data of a test sample; (b) procedures to record the input data; (c) procedures to check this recorded data with already recorded expression level data or expression profile data under ischemic conditions; (d) procedures to determine whether the test sample is under ischemic conditions or not based on the checking results obtained in (c); and (e) if the test sample has been determined as being under ischemic conditions, procedures to identify the clinical stage of the ischemic conditions of the test sample based on the checking results obtained in (c). By analyzing the gene expression data of a test sample using a computer in which the above-described program has been installed, ischemic

conditions can be identified.

The ischemic condition identification program of the invention comprises (a) means for analyzing expression levels of genes isolated from test cells; and (b) means for predicting whether or not individual test samples are under ischemic conditions or not, using the analysis results obtained by (a) as an indicator. The analysis means (a) is composed of means for detecting individual expression levels of a plurality of genes in test cells or tissues (also called "detection engine"), and means for analyzing the resultant values detected (also called "analysis engine").

(1) Detection Engine for Gene Expression

In the present invention, when expression of genes has been detected, the detection data may be digitalized and used as digital information. The digitalization is performed by converting, for example, fluorescence intensities detected on DNA chips into numerical values.

(2) Analysis Engine

Analysis engine is a means for performing analysis processing by multivariate analysis such as cluster analysis, based on the data (i.e., amounts of gene expression) obtained by the detection engine. Cluster analysis, which is a technique used in the field of multivariate analysis, collects and classifies "similar objects" from a large number of objects (i.e., samples) to be observed based on specific calculation criteria (assess criteria). In other words, cluster analysis merely "classifies" a large number of samples observed by putting samples similar to each other into one group.

In order to perform cluster analysis based on the detection data, "distance matrices" that represent similarities between samples are created. As the distance, Euclidean distance, weighted Euclidean distance, standard Euclidean distance, Pearson's product-moment correlation coefficient, or the like is calculated. The concepts of these distances are known, and an appropriate distance may be selected depending on the purpose of cluster analysis. Based on the concept of the above-mentioned distance, distances between clusters or distances between a cluster and objects are calculated, followed by amalgamation of clusters (i.e., two clusters are linked together). Methods of

amalgamation are known, e.g., the nearest neighbor method, furthest neighbor method, centroid method, or Ward's method.

By the above-described procedures, clusters which are in the "shortest distance" relation are linked together as "similar" clusters to thereby generate new clusters of a higher level. When clusters at one level have been generated, distances between clusters are calculated again to create distance matrices. Then, by searching for two clusters at the shortest distance, new clusters at a higher level are generated. Thus, a dendrogram is created finally.

Samples within a cluster amalgamated at a specific level of a dendrogram are contained in that cluster because of some similarity. Those samples with such similarity can be said to possess a certain nature in common. By elucidating this nature, it is possible to reveal the characteristic of the cluster itself. Thus, according to these analysis procedures, it is possible to classify genes into a group of high expression genes and a group of low expression genes. For example, if focusing on the degree of ischemic conditions using the progress (stage) of ischemia as an indicator, it is possible to reveal such characteristics that samples belonging to one cluster are under highly ischemic conditions and that samples belonging to the other cluster are under lightly ischemic conditions.

One embodiment of the identification system of the invention is illustrated in a block diagram (Fig. 5).

The identification system shown in Fig. 5 is equipped with CPU 501, ROM 502, RAM 503, Input Unit 504, Sending/Receiving Unit 505, Output Unit 506, Hard Disk Drive (HDD) 507 and CR-ROM Drive (508).

CPU 501 controls the ischemic condition identification system entirely and executes the examination processing described below according to the programs stored in ROM 502, RAM 503 or HDD 507. ROM 502 contains programs, etc. that instruct processing necessary for the operation of the above system. RAM 503 contains those data necessary for executing the examination processing. The Input Unit 504 is composed of a keyboard, mouse, etc. and operated, e.g., for inputting necessary conditions for the execution of the examination processing. The Sending/Receiving Unit 505 executes, based on instructions

from CPU 501, the sending/receiving of data to/from External Database 510, etc. through communication circuits. The Output Unit 506 executes display processing of various conditions input from the Input Unit 504, detection data on expressed genes, etc. based on instructions from CPU 501. The Output Unit 506 may include a computer-display unit and a printer. HD 507 contains information of expression patterns of various genes in cells or tissues and, based on instructions from CPU 501, reads out stored programs or data and stores them, e.g., in RAM 503. Based on instructions from CPU 501, CR-ROM Drive 508 reads out programs or data from the identification program stored in CD-ROM 509 and stores them, e.g., in RMA 503.

CPU 501 executes prediction of whether individual test samples are under ischemic conditions or not based on the data received from the Database, while supplying data received from the Input Unit, etc. to the Output Unit 506. The Database contains accumulated information of the amounts of gene expression (including both absolute amounts and relative amounts) obtained as described above.

Fig. 6 is a flow chart showing an example of identification processing using the identification program described above. Expression patterns of genes in test samples are analyzed, followed by identification of whether individual samples are under ischemic conditions or not.

Hereinbelow, the identification processing will be described with reference to Cluster Analysis Device 601 in Fig. 6. Cluster Analysis Device 601 generates clusters to be used in the identification processing. First, gene expression data are input by Means for External Database Searching and Data Input 602. Until data input is completed, input operation of the above data is repeated. By the input of the above data, information obtained from each tissue or cell is stored in Sample Data Storage Means 603, and supplied for cluster analysis or registered in the database.

Subsequently, Data Optimizing Means 604 inputs sample data from Sample Data Storage Means 603 and optimizes the data for cluster analysis. Data optimization is performed using a method most suitable for the sample, e.g., normalization with median values, normalization with z-scores, setting the maximum and the minimum values, or log transformation.

Means for Outputting List of Variables 605 displays a list of variables in the sample data to be subjected to cluster analysis.

Subsequently, using the function of Variable Selection Means 606, a user selects variables from the variables displayed by Means for Outputting List of Variables 605.

The selection of variables by Variable Selection Means 606 allows free selection of a single or a plurality of particular variables. Since, usually, there are a large number of candidates for variables, the Means 606 allows the user selection of any variables from them.

Once the user has selected particular variables, this information is input into Means for Generating Sample Data Files for Identification 607 together with sample data. Then, sample data files for identification is generated by this Generating Means 607.

Subsequently, the resultant data files of clusters are sent to Identification Means 608, which evaluates the degree of separation of clusters. The evaluation formula to evaluate the degree of separation of clusters may be defined in various manners.

The results of evaluation of the degree of separation made by the Identification Means 608 are passed to Means for Classifying Clusters 609. Then, the Classifying Means 609 inputs the identification results by the Identification Means 608 and decides most appropriate cluster classification referring to the identification conditions set in Means for Setting Identification Conditions 612. If conditions for continuation/termination of cluster classification have been set, the Classifying Means 609 judges the continuation or termination of cluster classification. If conditions for continuation/termination of cluster classification have not been set, the Classifying Means 609 allows the user to judge the continuation or termination of cluster classification. If the Classifying Means 609 has decided to continue cluster classification, it outputs the most appropriate cluster classification obtained from the processing of that time and a signal announcing that cluster classification is continued. This signal will work later as an instruction that processing of cluster classification must be returned to the Means for Outputting List of Variables 605 after the processing by Means for Editing Dendrograms 611.

On the other hand, if the Classifying Means 609 has decided to terminate cluster classification, it specifies the most appropriate cluster at that stage and outputs a signal

announcing that cluster classification is terminated. This signal will work later as an instruction to terminate the processing of cluster classification after the processing by Means for Editing Dendrograms 611.

After completion of the processing by the Classifying Means 609, the processing by Means for Generating Dendrograms 610 starts. The Generating Means 610 inputs the cluster classification decided by the Classifying Means 609, and displays a dendrogram based on the above cluster classification and characters of the variables pertaining to the cluster classification. When the Generating Means 610 has generated this cluster classification dendrogram, the user becomes able to grasp the current state of cluster classification visually. While generating the dendrogram, the Generating Means 610 displays the amounts of gene expression which are basis for the generation of the dendrogram so that the user can grasp the amounts visually. Then, Means for Editing Dendrograms 611 allows the user on the screen of a display device to edit (i.e., make additions, changes, or deletions to) the dendrogram generated by the Generating Means 610. The addition, change, or deletion of cluster classification is performed by the user with a processing instruction input device on the screen. For example, certain clusters may be designated, and variables of clusters to be classified further at a lower level may be indicated; or a plurality of clusters may be amalgamated. Alternatively, branches of a certain cluster classification may be deleted. While providing various tools to support the user's editing operation, Means for Editing Dendrograms 611 reads the meaning of the user's editing operation and automatically corrects data files of individual clusters accordingly. Furthermore, Means for Editing Dendrograms 611 preferably presents the judgment of Cluster Classifying Means 609 to continue or terminate the cluster classification and allows the user to input his/her final decision.

If it is decided that repeated processing of cluster classification should be continued, the processing is returned to Means for Outputting List of Variables 605. Then, the above-described processing performed by Means for Outputting List of Variables 605 through Means for Editing Dendrograms 611 is repeated.

From the thus analyzed data, whether the test samples are under ischemic conditions or not can be judged by checking into which cluster (i.e., ischemic cluster or normal cluster)

they have been classified.

5. Method of Screening for Ischemic Condition-Improving Drugs or Therapeutics for Ischemic Diseases

It is possible to screen for ischemic condition-improving drugs or therapeutics for ischemic diseases using as an indicator the expression levels of the genes which were revealed in the invention to show increased expression levels under ischemic conditions. Briefly, (a) whether or not the expression levels of the above genes return to their expression levels in a normal tissue, or (b) whether or not the expression profile of a gene group comprising a plurality of above genes returns to the normal expression profile in a normal tissue, by the administration of a drug to a test animal or test cell is examined. When the expression levels of the above genes have returned to their expression levels in a normal tissue as a result of the administration of the drug, the drug is evaluated as a candidate substance for an ischemic condition-improving drug or therapeutic for ischemic diseases.

BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 shows procedures to identify genes of which expression levels change under ischemic conditions using a DNA chip.

Fig. 2 shows one embodiment of the DNA chip of the invention for examining ischemic conditions, and predicted results when test samples from patients have been hybridized on the DNA chip.

Fig. 3 shows one embodiment of synthetic-type DNA chip and procedures to detect genes in a test sample using the DNA chip.

Fig. 4 shows procedures to measure the expression levels of genes using GeneChip™.

Fig. 5 is a block diagram showing an ischemic condition identification system.

Fig. 6 is a flow chart showing an example of processing by an ischemic condition identification program.

Legend

501: CPU; 502: ROM; 503: RAM, 504: Input Unit; 505: Sending/Receiving Unit; 506: Output Unit; 507: HDD, 508: CD-ROM Drive; 509: CD-ROM; 510: Database; 601: Cluster Analysis Device; 602: Means for External Database Searching and Data Input; 603: Sample Data Storage Means; 604: Data Optimizing Means; 605: Means for Outputting List of Variables; 606: Variable Selection Means; 607: Means for Generating Sample Data File for Evaluation; 608: Evaluation Means; 609: Means for Classifying Clusters; 610: Means for Generating Dendrograms; 611: Means for Editing Dendrograms; 612: Means for Setting Evaluation Conditions.

BEST MODE FOR CARRYING OUT THE INVENTION

Hereinbelow, the present invention will be described more specifically with reference to the following Example, which should not be construed as limiting the scope of the invention.

Example 1. Identification of Genes Expressed under Ischemic Conditions using a DNA Chip

Genes expressed under ischemic conditions were identified by the procedures as shown in Fig. 4 using GeneChip System™ (Affymetrix). Briefly, 8-10 week-old bcl BLACK mice were anesthetized with inflane. Then, the carotid artery on both sides was exposed and ligated for 20 min to block the blood flow to thereby generate ischemic conditions in mice. Then, the blood flow was restored, and mice were slaughtered at 0, 2, 6, 12 and 24 hours after the blood flow restoration. The hippocampus on both sides was removed and immediately stored frozen. Subsequently, approximately 2 μ g of poly(A)+mRNA was extracted from 1 g of a frozen sample. Then, cDNA was synthesized with a reverse transcriptase. The resultant cDNA was transcribed *in vitro* to thereby obtain biotin-labeled cRNA, which was treated with heat in the presence of Mg^{2+} for fragmentation into about 50-mer fragments. Internal reference was labeled and added to the sample. Then, the sample was poured into GeneChip™ Mu6500 (Affymetrix). After hybridization in an oven, the chip was washed in Fluidic station. Then, information of the chip was read by a GeneArray scanner. The data obtained was processed and analyzed using a

bioinformatics system. The results are shown in Tables 1 through 3. Table 1 shows genes of which transcription levels increased n-fold where n is 2 or more but less than 5 within 24 hours when the transcription level at 0 hour is taken as 1. Table 2 shows genes of which transcription levels increased n-fold where n is 5 or more but less than 10. Table 3 shows genes of which transcription levels increased more than 10-fold. The accession numbers refers to GenBank accession numbers.

Table 1.

Genes of Which Transcription Levels Increased n-Fold ($2 \leq n < 5$)

ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)	ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)
M77167	SEQ ID NO.1	SEQ ID NO.2	AA103541	SEQ ID NO.465	—
AA068780	SEQ ID NO.3	—	U41736	SEQ ID NO.466	SEQ ID NO.467
M33212	SEQ ID NO.4	SEQ ID NO.5	AA103768	SEQ ID NO.468	—
D76440	SEQ ID NO.6	SEQ ID NO.7	U43900	SEQ ID NO.469	SEQ ID NO.470
M35131	SEQ ID NO.8	SEQ ID NO.9	AA140170	SEQ ID NO.471	—
AA050852	SEQ ID NO.10	—	AA104086	SEQ ID NO.472	—
W47946	SEQ ID NO.11	—	U43512	SEQ ID NO.473	—
W48104	SEQ ID NO.12	—	AA104459	SEQ ID NO.474	—
U09928	SEQ ID NO.13	—	U39545	SEQ ID NO.475	SEQ ID NO.476
M29464	SEQ ID NO.14	SEQ ID NO.15	U64445	SEQ ID NO.477	SEQ ID NO.478
X61434	SEQ ID NO.16	—	D86949	SEQ ID NO.479	SEQ ID NO.480
M90316	SEQ ID NO.17	SEQ ID NO.18	Z70023	SEQ ID NO.481	SEQ ID NO.482
M94632	SEQ ID NO.19	SEQ ID NO.20	U71202	SEQ ID NO.483	SEQ ID NO.484
W41501	SEQ ID NO.21	—	X81059	SEQ ID NO.485	SEQ ID NO.486
M20632	SEQ ID NO.22	SEQ ID NO.23	U73200	SEQ ID NO.487	SEQ ID NO.488
M13521	SEQ ID NO.24	—	U69270	SEQ ID NO.489	SEQ ID NO.490
M21285	SEQ ID NO.25	—	AA106077	SEQ ID NO.491	—
M96163	SEQ ID NO.26	—	AA106116	SEQ ID NO.492	—
X04017	SEQ ID NO.27	SEQ ID NO.28	U31758	SEQ ID NO.493	SEQ ID NO.494
M64086	SEQ ID NO.29	SEQ ID NO.30	AA106224	SEQ ID NO.495	—
W54584	SEQ ID NO.31	—	X80502	SEQ ID NO.496	SEQ ID NO.497
L12447	SEQ ID NO.32	SEQ ID NO.33	U76832	SEQ ID NO.498	SEQ ID NO.499
X62622	SEQ ID NO.34	SEQ ID NO.35	U30840	SEQ ID NO.500	SEQ ID NO.501
Z30970	SEQ ID NO.36	SEQ ID NO.37	AA107388	SEQ ID NO.502	—
M23568	SEQ ID NO.38	SEQ ID NO.39	U26459	SEQ ID NO.503	SEQ ID NO.504
J03520	SEQ ID NO.40	SEQ ID NO.41	U29055	SEQ ID NO.505	SEQ ID NO.506
M94087	SEQ ID NO.42	SEQ ID NO.43	U39302	SEQ ID NO.507	SEQ ID NO.508
L37092	SEQ ID NO.44	SEQ ID NO.45	U77630	SEQ ID NO.509	SEQ ID NO.510
M22479	SEQ ID NO.46	SEQ ID NO.47	U39473	SEQ ID NO.511	SEQ ID NO.512

AA041634	SEQ ID NO.48	—	X91043	SEQ ID NO.513	SEQ ID NO.514
M95200	SEQ ID NO.49	SEQ ID NO.50	D86603	SEQ ID NO.515	SEQ ID NO.516
M62867	SEQ ID NO.51	SEQ ID NO.52	D88792	SEQ ID NO.517	SEQ ID NO.518
AA137883	SEQ ID NO.53	—	D88793	SEQ ID NO.519	SEQ ID NO.520
L36611	SEQ ID NO.54	—	D38218	SEQ ID NO.521	SEQ ID NO.522
L19311	SEQ ID NO.55	SEQ ID NO.56	U60330	SEQ ID NO.523	SEQ ID NO.524
X74438	SEQ ID NO.57	SEQ ID NO.58	AA108925	SEQ ID NO.525	—
AA034714	SEQ ID NO.59	—	U66865	SEQ ID NO.526	SEQ ID NO.527
D32167	SEQ ID NO.60	SEQ ID NO.61	Y07836	SEQ ID NO.528	SEQ ID NO.529
U24700	SEQ ID NO.62	SEQ ID NO.63	AA110543	SEQ ID NO.530	—
U07602	SEQ ID NO.64	—	AA117787	SEQ ID NO.531	—
U66620	SEQ ID NO.65	SEQ ID NO.66	D30785	SEQ ID NO.532	SEQ ID NO.533
L25126	SEQ ID NO.67	SEQ ID NO.68	U69488	SEQ ID NO.534	—
U02982	SEQ ID NO.69	SEQ ID NO.70	Z11997	SEQ ID NO.535	SEQ ID NO.536
AA155371	SEQ ID NO.71	—	D38613	SEQ ID NO.537	SEQ ID NO.538
U16740	SEQ ID NO.72	—	X92352	SEQ ID NO.539	SEQ ID NO.540
U16741	SEQ ID NO.73	SEQ ID NO.74	AA111168	SEQ ID NO.541	—
W58941	SEQ ID NO.75	—	AA111212	SEQ ID NO.542	—
U22948	SEQ ID NO.76	SEQ ID NO.77	W07963	SEQ ID NO.543	—
U23789	SEQ ID NO.78	SEQ ID NO.79	AA114781	SEQ ID NO.544	—
X68951	SEQ ID NO.80	SEQ ID NO.81	W08033	SEQ ID NO.545	—
AA144400	SEQ ID NO.82	—	AA117064	SEQ ID NO.546	—
U06670	SEQ ID NO.83	SEQ ID NO.84	AA117128	SEQ ID NO.547	—
U09399	SEQ ID NO.85	SEQ ID NO.86	AA162093	SEQ ID NO.548	—
U10118	SEQ ID NO.87	—	U10871	SEQ ID NO.549	SEQ ID NO.550
L17069	SEQ ID NO.88	—	AA120173	SEQ ID NO.551	—
W62091	SEQ ID NO.89	—	AA123463	SEQ ID NO.552	—
U09419	SEQ ID NO.90	SEQ ID NO.91	W07927	SEQ ID NO.553	—
AA041651	SEQ ID NO.92	—	AA118546	SEQ ID NO.554	—
AA051063	SEQ ID NO.93	—	AA118294	SEQ ID NO.555	—
W62420	SEQ ID NO.94	—	AA169951	SEQ ID NO.556	—
AA110896	SEQ ID NO.95	—	AA146194	SEQ ID NO.557	—
M60057	SEQ ID NO.96	—	W08228	SEQ ID NO.558	—
U33840	SEQ ID NO.97	SEQ ID NO.98	W33440	SEQ ID NO.559	—
W63835	SEQ ID NO.99	—	AA119959	SEQ ID NO.560	—
W63876	SEQ ID NO.100	—	W08326	SEQ ID NO.561	—
AA050268	SEQ ID NO.101	SEQ ID NO.	AA125425	SEQ ID NO.562	—
W63974	SEQ ID NO.102	SEQ ID NO.	AA137580	SEQ ID NO.563	—
D14571	SEQ ID NO.103	SEQ ID NO.104	AA138848	SEQ ID NO.564	—
L20450	SEQ ID NO.105	SEQ ID NO.106	AA145188	SEQ ID NO.565	—
W64413	SEQ ID NO.107	—	AA145160	SEQ ID NO.566	—
D16262	SEQ ID NO.108	SEQ ID NO.109	W13461	SEQ ID NO.567	—
AA120109	SEQ ID NO.110	—	W13878	SEQ ID NO.568	—
X61432	SEQ ID NO.111	SEQ ID NO.112	U35623	SEQ ID NO.569	SEQ ID NO.570

D10011	SEQ ID NO.113	SEQ ID NO.114	W77121	SEQ ID NO.571	—
L16953	SEQ ID NO.115	SEQ ID NO.116	W14370	SEQ ID NO.572	—
D29016	SEQ ID NO.117	SEQ ID NO.118	AA152884	SEQ ID NO.573	—
W65920	SEQ ID NO.119	—	AA023591	SEQ ID NO.574	—
L39123	SEQ ID NO.120	SEQ ID NO.121	AA155191	SEQ ID NO.575	—
U16162	SEQ ID NO.122	—	AA050733	SEQ ID NO.576	—
AA002504	SEQ ID NO.123	—	AA096645	SEQ ID NO.577	—
U20326	SEQ ID NO.124	SEQ ID NO.125	AA165847	SEQ ID NO.578	—
U27830	SEQ ID NO.126	SEQ ID NO.127	AA170223	SEQ ID NO.579	—
U24703	SEQ ID NO.128	SEQ ID NO.129	AA170375	SEQ ID NO.580	—
W70782	SEQ ID NO.130	—	Z25524	SEQ ID NO.581	SEQ ID NO.582
U28217	SEQ ID NO.131	SEQ ID NO.132	X16857	SEQ ID NO.583	—
AA105294	SEQ ID NO.133	—	D90151	SEQ ID NO.584	SEQ ID NO.585
U28138	SEQ ID NO.134	—	D00925	SEQ ID NO.586	SEQ ID NO.587
U29396	SEQ ID NO.135	SEQ ID NO.136	ditto	ditto	SEQ ID NO.588
L29441	SEQ ID NO.137	SEQ ID NO.138	L76223	SEQ ID NO.589	—
D10061	SEQ ID NO.139	SEQ ID NO.140	D00613	SEQ ID NO.590	SEQ ID NO.591
W75403	SEQ ID NO.141	—	W13502	SEQ ID NO.592	—
M73696	SEQ ID NO.142	SEQ ID NO.143	D90344	SEQ ID NO.593	SEQ ID NO.594
W75531	SEQ ID NO.144	—	AA138226	SEQ ID NO.595	—
W75616	SEQ ID NO.145	—	AA003230	SEQ ID NO.596	—
L05439	SEQ ID NO.146	—	W30651	SEQ ID NO.597	—
D16432	SEQ ID NO.147	SEQ ID NO.148	M22531	SEQ ID NO.598	SEQ ID NO.599
L21027	SEQ ID NO.149	SEQ ID NO.150	AA118758	SEQ ID NO.600	—
AA009150	SEQ ID NO.151	—	AA027739	SEQ ID NO.601	—
U13262	SEQ ID NO.152	SEQ ID NO.153	AA168362	SEQ ID NO.602	—
W78604	SEQ ID NO.154	—	D78645	SEQ ID NO.603	SEQ ID NO.604
X56045	SEQ ID NO.155	SEQ ID NO.156	M31131	SEQ ID NO.605	SEQ ID NO.606
U36277	SEQ ID NO.157	SEQ ID NO.158	AA153320	SEQ ID NO.607	—
W82115	SEQ ID NO.159	—	W34066	SEQ ID NO.608	—
M69293	SEQ ID NO.160	—	W10606	SEQ ID NO.609	—
U36760	SEQ ID NO.161	SEQ ID NO.162	W20828	SEQ ID NO.610	—
U35142	SEQ ID NO.163	SEQ ID NO.164	L08115	SEQ ID NO.611	SEQ ID NO.612
U14420	SEQ ID NO.165	SEQ ID NO.166	Z31554	SEQ ID NO.613	SEQ ID NO.614
Y00769	SEQ ID NO.167	SEQ ID NO.168	W41861	SEQ ID NO.615	—
U37720	SEQ ID NO.169	SEQ ID NO.170	W71125	SEQ ID NO.616	—
U35368	SEQ ID NO.171	SEQ ID NO.172	AA000961	SEQ ID NO.617	—
W89939	SEQ ID NO.173	—	W82998	SEQ ID NO.618	—
W37000	SEQ ID NO.174	—	W11954	SEQ ID NO.619	—
W97373	SEQ ID NO.175	—	U43844	SEQ ID NO.620	—
W96831	SEQ ID NO.176	—	AA008650	SEQ ID NO.621	—
W82209	SEQ ID NO.177	—	W18601	SEQ ID NO.622	—
AA009169	SEQ ID NO.178	—	W30116	SEQ ID NO.623	—
U31967	SEQ ID NO.179	SEQ ID NO.180	U53456	SEQ ID NO.624	SEQ ID NO.625

D28117	SEQ ID NO.181	SEQ ID NO.182	M27073	SEQ ID NO.626	SEQ ID NO.627
U34691	SEQ ID NO.183	SEQ ID NO.184	W12720	SEQ ID NO.628	—
U32329	SEQ ID NO.185	SEQ ID NO.186	M76131	SEQ ID NO.629	SEQ ID NO.630
U10903	SEQ ID NO.187	SEQ ID NO.188	U39192	SEQ ID NO.631	—
D49949	SEQ ID NO.189	SEQ ID NO.190	W54288	SEQ ID NO.632	—
D49429	SEQ ID NO.191	SEQ ID NO.192	M76124	SEQ ID NO.633	SEQ ID NO.634
U48397	SEQ ID NO.193	SEQ ID NO.194	W12946	SEQ ID NO.635	—
D00622	SEQ ID NO.195	—	AA024288	SEQ ID NO.636	—
U38940	SEQ ID NO.196	SEQ ID NO.197	W13412	SEQ ID NO.637	—
X75313	SEQ ID NO.198	SEQ ID NO.199	AA002852	SEQ ID NO.638	—
AA008683	SEQ ID NO.200	—	W15789	SEQ ID NO.639	—
U37799	SEQ ID NO.201	SEQ ID NO.202	L39879	SEQ ID NO.640	—
U43918	SEQ ID NO.203	SEQ ID NO.204	M61215	SEQ ID NO.641	SEQ ID NO.642
AA039108	SEQ ID NO.205	—	M70641	SEQ ID NO.643	—
L10244	SEQ ID NO.206	SEQ ID NO.207	D86729	SEQ ID NO.644	SEQ ID NO.645
D78647	SEQ ID NO.208	SEQ ID NO.209	L01640	SEQ ID NO.646	SEQ ID NO.647
U36220	SEQ ID NO.210	SEQ ID NO.211	M92378	SEQ ID NO.648	—
AA051121	SEQ ID NO.212	—	K01347	SEQ ID NO.649	SEQ ID NO.650
AA003458	SEQ ID NO.213	—	M23384	SEQ ID NO.651	SEQ ID NO.652
AA003554	SEQ ID NO.214	—	W77613	SEQ ID NO.653	—
U46934	SEQ ID NO.215	SEQ ID NO.216	W18385	SEQ ID NO.654	—
D50086	SEQ ID NO.217	SEQ ID NO.218	W53188	SEQ ID NO.655	—
AA007899	SEQ ID NO.219	—	J05277	SEQ ID NO.656	SEQ ID NO.657
AA008133	SEQ ID NO.220	—	W30499	SEQ ID NO.658	—
X58876	SEQ ID NO.221	SEQ ID NO.222	W67014	SEQ ID NO.659	—
D28530	SEQ ID NO.223	SEQ ID NO.224	M31885	SEQ ID NO.660	—
AA048974	SEQ ID NO.225	—	W54228	SEQ ID NO.661	—
AA120290	SEQ ID NO.226	—	W29756	SEQ ID NO.662	—
L40406	SEQ ID NO.227	SEQ ID NO.228	W30609	SEQ ID NO.663	—
U27340	SEQ ID NO.229	SEQ ID NO.230	D17666	SEQ ID NO.664	—
AA013581	SEQ ID NO.231	—	AA033408	SEQ ID NO.665	—
AA013830	SEQ ID NO.232	—	W33728	SEQ ID NO.666	—
Z37110	SEQ ID NO.233	SEQ ID NO.234	W74850	SEQ ID NO.667	—
AA119078	SEQ ID NO.235	—	AA119191	SEQ ID NO.668	—
Z67746	SEQ ID NO.236	SEQ ID NO.237	J05205	SEQ ID NO.669	SEQ ID NO.670
U51196	SEQ ID NO.238	SEQ ID NO.239	X06746	SEQ ID NO.671	SEQ ID NO.672
AA118878	SEQ ID NO.240	—	J02870	SEQ ID NO.673	SEQ ID NO.674
X89650	SEQ ID NO.241	SEQ ID NO.242	AA124273	SEQ ID NO.675	—
U07617	SEQ ID NO.243	SEQ ID NO.244	AA008245	SEQ ID NO.676	—
U37351	SEQ ID NO.245	SEQ ID NO.246	AA106492	SEQ ID NO.677	—
Y08640	SEQ ID NO.247	SEQ ID NO.248	X07997	SEQ ID NO.678	—
U48797	SEQ ID NO.249	SEQ ID NO.250	M21041	SEQ ID NO.679	SEQ ID NO.680
AA020620	SEQ ID NO.251	—	W36757	SEQ ID NO.681	—
X01023	SEQ ID NO.252	SEQ ID NO.253	V00835	SEQ ID NO.682	—

U34920	SEQ ID NO.254	SEQ ID NO.255	Y00305	SEQ ID NO.683	SEQ ID NO.684
U17698	SEQ ID NO.256	SEQ ID NO.257	M64640	SEQ ID NO.685	—
X54352	SEQ ID NO.258	SEQ ID NO.259	W42216	SEQ ID NO.686	—
U25708	SEQ ID NO.260	SEQ ID NO.261	U73478	SEQ ID NO.687	SEQ ID NO.688
X15267	SEQ ID NO.262	SEQ ID NO.263	J00398	SEQ ID NO.689	—
X66091	SEQ ID NO.264	—	M68899	SEQ ID NO.690	SEQ ID NO.691
X55573	SEQ ID NO.265	SEQ ID NO.266	W34232	SEQ ID NO.692	—
AA119194	SEQ ID NO.267	—	D38077	SEQ ID NO.693	—
X13586	SEQ ID NO.268	SEQ ID NO.269	W29533	SEQ ID NO.694	—
Z31553	SEQ ID NO.270	SEQ ID NO.271	W29462	SEQ ID NO.695	—
Z31399	SEQ ID NO.272	SEQ ID NO.273	W62036	SEQ ID NO.696	—
AA108956	SEQ ID NO.274	—	W77226	SEQ ID NO.697	—
Z31557	SEQ ID NO.275	SEQ ID NO.276	D14340	SEQ ID NO.698	SEQ ID NO.699
AA032948	SEQ ID NO.277	—	M83118	SEQ ID NO.700	SEQ ID NO.701
Z12302	SEQ ID NO.278	SEQ ID NO.279	M21952	SEQ ID NO.702	SEQ ID NO.703
X60367	SEQ ID NO.280	SEQ ID NO.281	W11666	SEQ ID NO.704	—
X64713	SEQ ID NO.282	SEQ ID NO.283	AA015415	SEQ ID NO.705	—
AA035938	SEQ ID NO.284	—	AA097018	SEQ ID NO.706	—
AA036445	SEQ ID NO.285	—	M27796	SEQ ID NO.707	SEQ ID NO.708
X17502	SEQ ID NO.286	SEQ ID NO.287	AA016424	SEQ ID NO.709	—
X79233	SEQ ID NO.288	SEQ ID NO.289	W29543	SEQ ID NO.710	—
X13135	SEQ ID NO.290	—	AA028728	SEQ ID NO.711	—
Z22593	SEQ ID NO.291	SEQ ID NO.292	K00988	SEQ ID NO.712	—
X90875	SEQ ID NO.293	SEQ ID NO.294	AA170547	SEQ ID NO.713	—
Z36270	SEQ ID NO.295	SEQ ID NO.296	W20613	SEQ ID NO.714	—
X67056	SEQ ID NO.297	SEQ ID NO.298	AA163687	SEQ ID NO.715	—
X13605	SEQ ID NO.299	SEQ ID NO.300	M93422	SEQ ID NO.716	SEQ ID NO.717
W89699	SEQ ID NO.301	—	W12548	SEQ ID NO.718	—
X62669	SEQ ID NO.302	—	AA145181	SEQ ID NO.719	—
AA049790	SEQ ID NO.303	—	AA144057	SEQ ID NO.720	—
M33227	SEQ ID NO.304	SEQ ID NO.305	AA138791	SEQ ID NO.721	—
AA060064	SEQ ID NO.306	—	L27453	SEQ ID NO.722	SEQ ID NO.723
X70393	SEQ ID NO.307	SEQ ID NO.308	AA119571	SEQ ID NO.724	—
AA050789	SEQ ID NO.309	—	AA117227	SEQ ID NO.725	—
AA051486	SEQ ID NO.310	—	U03645	SEQ ID NO.726	SEQ ID NO.727
X61147	SEQ ID NO.311	SEQ ID NO.312	Y07711	SEQ ID NO.728	SEQ ID NO.729
AA058163	SEQ ID NO.313	—	D17571	SEQ ID NO.730	SEQ ID NO.731
W14434	SEQ ID NO.314	—	U68058	SEQ ID NO.732	SEQ ID NO.733
W82720	SEQ ID NO.315	—	U66202	SEQ ID NO.734	SEQ ID NO.735
W89958	SEQ ID NO.316	—	U56651	SEQ ID NO.736	—
AA107471	SEQ ID NO.317	—	AA110711	SEQ ID NO.737	—
AA028547	SEQ ID NO.318	—	X92122	SEQ ID NO.738	SEQ ID NO.739
X60831	SEQ ID NO.319	SEQ ID NO.320	X87257	SEQ ID NO.740	—
Z49085	SEQ ID NO.321	SEQ ID NO.322	U69695	SEQ ID NO.741	SEQ ID NO.742

X05640	SEQ ID NO.323	—	X64550	SEQ ID NO.743	—
AA059967	SEQ ID NO.324	—	U59463	SEQ ID NO.744	SEQ ID NO.745
AA163305	SEQ ID NO.325	—	AA096532	SEQ ID NO.746	—
X64837	SEQ ID NO.326	SEQ ID NO.327	W85446	SEQ ID NO.747	—
AA060704	SEQ ID NO.328	—	X94444	SEQ ID NO.748	SEQ ID NO.749
X17320	SEQ ID NO.329	SEQ ID NO.330	AA080097	SEQ ID NO.750	—
X65553	SEQ ID NO.331	SEQ ID NO.332	D32132	SEQ ID NO.751	—
X51468	SEQ ID NO.333	—	Z71268	SEQ ID NO.752	SEQ ID NO.753
X14425	SEQ ID NO.334	SEQ ID NO.335	U28419	SEQ ID NO.754	—
AA061707	SEQ ID NO.336	—	X99641	SEQ ID NO.755	SEQ ID NO.756
X95403	SEQ ID NO.337	SEQ ID NO.338	AA072611	SEQ ID NO.757	—
AA139612	SEQ ID NO.339	—	X90647	SEQ ID NO.758	—
X57277	SEQ ID NO.340	SEQ ID NO.341	X95580	SEQ ID NO.759	SEQ ID NO.760
X70067	SEQ ID NO.342	SEQ ID NO.343	U46187	SEQ ID NO.761	SEQ ID NO.762
U05245	SEQ ID NO.344	—	U43085	SEQ ID NO.763	SEQ ID NO.764
AA062237	SEQ ID NO.345	—	L29479	SEQ ID NO.765	SEQ ID NO.766
AA063841	SEQ ID NO.346	—	U20892	SEQ ID NO.767	—
X89222	SEQ ID NO.347	SEQ ID NO.348	AA064467	SEQ ID NO.768	—
AA064004	SEQ ID NO.349	—	W09407	SEQ ID NO.769	—
AA087787	SEQ ID NO.350	—	AA015354	SEQ ID NO.770	—
AA064355	SEQ ID NO.351	—	Z31370	SEQ ID NO.771	SEQ ID NO.772
X68837	SEQ ID NO.352	SEQ ID NO.353	X57349	SEQ ID NO.773	SEQ ID NO.774
Z19579	SEQ ID NO.354	SEQ ID NO.355	X81464	SEQ ID NO.775	SEQ ID NO.776
Z19581	SEQ ID NO.356	SEQ ID NO.357	W89293	SEQ ID NO.777	—
X65657	SEQ ID NO.358	SEQ ID NO.359	X58523	SEQ ID NO.778	SEQ ID NO.779
X16319	SEQ ID NO.360	SEQ ID NO.361	X53476	SEQ ID NO.780	SEQ ID NO.781
X78304	SEQ ID NO.362	SEQ ID NO.363	AA044535	SEQ ID NO.782	—
X81987	SEQ ID NO.364	SEQ ID NO.365	AA037964	SEQ ID NO.783	—
U52197	SEQ ID NO.366	SEQ ID NO.367	X81632	SEQ ID NO.784	—
AA065652	SEQ ID NO.368	—	AA035984	SEQ ID NO.785	—
U23921	SEQ ID NO.369	SEQ ID NO.370	AA035915	SEQ ID NO.786	—
AA066333	SEQ ID NO.371	—	X61800	SEQ ID NO.787	SEQ ID NO.788
U38501	SEQ ID NO.372	—	U03457	SEQ ID NO.789	SEQ ID NO.790
W46019	SEQ ID NO.373	—	AA023390	SEQ ID NO.791	—
D49744	SEQ ID NO.374	SEQ ID NO.375	AA064208	SEQ ID NO.792	—
U58497	SEQ ID NO.376	SEQ ID NO.377	L75822	SEQ ID NO.793	SEQ ID NO.794
U38252	SEQ ID NO.378	SEQ ID NO.379	U49739	SEQ ID NO.795	SEQ ID NO.796
U40930	SEQ ID NO.380	SEQ ID NO.381	U41636	SEQ ID NO.797	SEQ ID NO.798
AA118729	SEQ ID NO.382	—	X70296	SEQ ID NO.799	SEQ ID NO.800
AA068057	SEQ ID NO.383	—	AA161905	SEQ ID NO.801	—
U47104	SEQ ID NO.384	SEQ ID NO.385	AA016858	SEQ ID NO.802	—
M97635	SEQ ID NO.386	—	U50734	SEQ ID NO.803	SEQ ID NO.804
U58883	SEQ ID NO.387	SEQ ID NO.388	U36993	SEQ ID NO.805	SEQ ID NO.806
D49654	SEQ ID NO.389	SEQ ID NO.390	AA013513	SEQ ID NO.807	—

D78641	SEQ ID NO.391	SEQ ID NO.392	U31992	SEQ ID NO.808	SEQ ID NO.809
U24428	SEQ ID NO.393	SEQ ID NO.394	AA007871	SEQ ID NO.810	—
L43326	SEQ ID NO.395	SEQ ID NO.396	U43317	SEQ ID NO.811	SEQ ID NO.812
U08378	SEQ ID NO.397	SEQ ID NO.398	U41465	SEQ ID NO.813	SEQ ID NO.814
D78382	SEQ ID NO.399	SEQ ID NO.400	AA000341	SEQ ID NO.815	—
AA073296	SEQ ID NO.401	—	U39738	SEQ ID NO.816	SEQ ID NO.817
D90173	SEQ ID NO.402	SEQ ID NO.403	U28728	SEQ ID NO.818	SEQ ID NO.819
U62483	SEQ ID NO.404	SEQ ID NO.405	M85151	SEQ ID NO.820	SEQ ID NO.821
D50523	SEQ ID NO.406	—	U04827	SEQ ID NO.822	—
U63323	SEQ ID NO.407	SEQ ID NO.408	U35885	SEQ ID NO.823	SEQ ID NO.824
AA079926	SEQ ID NO.409	—	X77557	SEQ ID NO.825	SEQ ID NO.826
X99963	SEQ ID NO.410	SEQ ID NO.411	D14883	SEQ ID NO.827	SEQ ID NO.828
X97281	SEQ ID NO.412	SEQ ID NO.413	U28068	SEQ ID NO.829	—
X92411	SEQ ID NO.414	SEQ ID NO.415	W65511	SEQ ID NO.830	—
AA087332	SEQ ID NO.416	—	U17961	SEQ ID NO.831	SEQ ID NO.832
X80232	SEQ ID NO.417	SEQ ID NO.418	L32973	SEQ ID NO.833	SEQ ID NO.834
U49350	SEQ ID NO.419	SEQ ID NO.420	D16333	SEQ ID NO.835	SEQ ID NO.836
U49351	SEQ ID NO.421	SEQ ID NO.422	Z67747	SEQ ID NO.837	—
AA097087	SEQ ID NO.423	—	D16580	SEQ ID NO.838	SEQ ID NO.839
AA087616	SEQ ID NO.424	—	M18776	SEQ ID NO.840	SEQ ID NO.841
D73368	SEQ ID NO.425	SEQ ID NO.426	M91458	SEQ ID NO.842	SEQ ID NO.843
U48804	SEQ ID NO.427	SEQ ID NO.428	AA120695	SEQ ID NO.844	—
AA087986	SEQ ID NO.429	—	L29503	SEQ ID NO.845	—
AA088003	SEQ ID NO.430	—	M25811	SEQ ID NO.846	SEQ ID NO.847
Y07685	SEQ ID NO.431	SEQ ID NO.432	M34141	SEQ ID NO.848	SEQ ID NO.849
Y07693	SEQ ID NO.433	SEQ ID NO.434	W45807	SEQ ID NO.850	—
Y07688	SEQ ID NO.435	SEQ ID NO.436	M63903	SEQ ID NO.851	SEQ ID NO.852
D67015	SEQ ID NO.437	SEQ ID NO.438	U10119	SEQ ID NO.853	SEQ ID NO.854
U67874	SEQ ID NO.439	SEQ ID NO.440	L35556	SEQ ID NO.855	SEQ ID NO.856
D86344	SEQ ID NO.441	SEQ ID NO.442	X98096	SEQ ID NO.857	SEQ ID NO.858
AA097203	SEQ ID NO.443	—	AA166601	SEQ ID NO.1038	—
Y08135	SEQ ID NO.444	SEQ ID NO.445	AA125097	SEQ ID NO.1039	—
U42384	SEQ ID NO.446	SEQ ID NO.447	AA168363	SEQ ID NO.1040	—
D87899	SEQ ID NO.448	SEQ ID NO.449	U19582	SEQ ID NO.1041	SEQ ID NO.1042
D87901	SEQ ID NO.450	SEQ ID NO.451	L22482	SEQ ID NO.1043	SEQ ID NO.1044
D87902	SEQ ID NO.452	SEQ ID NO.453	W63876	SEQ ID NO.1045	—
D87903	SEQ ID NO.454	SEQ ID NO.455	U11274	SEQ ID NO.1046	SEQ ID NO.1047
X96859	SEQ ID NO.456	—	W66636	SEQ ID NO.1048	—
U56909	SEQ ID NO.457	SEQ ID NO.458	D42124	SEQ ID NO.1049	SEQ ID NO.1050
AA098588	SEQ ID NO.459	—	U41765	SEQ ID NO.1051	SEQ ID NO.1052
X70298	SEQ ID NO.460	SEQ ID NO.461	X02452	SEQ ID NO.1053	—
U62021	SEQ ID NO.462	—	X76653	SEQ ID NO.1054	SEQ ID NO.1055
D90225	SEQ ID NO.463	SEQ ID NO.464	W13425	SEQ ID NO.1056	—

Table 2.

Genes of Which Transcription Levels Increased n-Fold ($5 \leq n < 10$)

ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)	ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)
X16995	SEQ ID NO.859	—	M90364	SEQ ID NO.917	SEQ ID NO.918
W78418	SEQ ID NO.860	—	M16465	SEQ ID NO.919	SEQ ID NO.920
L10106	SEQ ID NO.861	SEQ ID NO.862	W13425	SEQ ID NO.921	—
AA060409	SEQ ID NO.863	—	M62766	SEQ ID NO.922	SEQ ID NO.923
M57999	SEQ ID NO.864	SEQ ID NO.865	U73744	SEQ ID NO.924	—
M26251	SEQ ID NO.866	SEQ ID NO.867	W29669	SEQ ID NO.925	—
M22432	SEQ ID NO.868	SEQ ID NO.869	W33838	SEQ ID NO.926	—
U00689	SEQ ID NO.870	SEQ ID NO.871	L21707	SEQ ID NO.927	SEQ ID NO.928
L22482	SEQ ID NO.872	SEQ ID NO.873	W34687	SEQ ID NO.929	—
U70662	SEQ ID NO.874	SEQ ID NO.875	AA105763	SEQ ID NO.930	—
AA064330	SEQ ID NO.876	—	M18194	SEQ ID NO.931	—
D55720	SEQ ID NO.877	SEQ ID NO.878	J04694	SEQ ID NO.932	SEQ ID NO.933
U37465	SEQ ID NO.879	SEQ ID NO.880	AA140026	SEQ ID NO.934	—
AA003413	SEQ ID NO.881	—	L35303	SEQ ID NO.935	SEQ ID NO.936
U43319	SEQ ID NO.882	SEQ ID NO.883	AA073986	SEQ ID NO.937	—
Z72000	SEQ ID NO.884	SEQ ID NO.885	X96618	SEQ ID NO.938	SEQ ID NO.939
X96639	SEQ ID NO.886	SEQ ID NO.887	X85983	SEQ ID NO.940	SEQ ID NO.941
X61940	SEQ ID NO.888	SEQ ID NO.889	X04367	SEQ ID NO.942	SEQ ID NO.943
X56518	SEQ ID NO.890	—	X07967	SEQ ID NO.944	SEQ ID NO.945
X94998	SEQ ID NO.891	SEQ ID NO.892	D90146	SEQ ID NO.946	—
X71642	SEQ ID NO.893	SEQ ID NO.894	AA014024	SEQ ID NO.947	—
X53584	SEQ ID NO.895	—	M58566	SEQ ID NO.948	SEQ ID NO.949
W89863	SEQ ID NO.896	—	AA044561	SEQ ID NO.950	—
X53257	SEQ ID NO.897	SEQ ID NO.898	W65899	SEQ ID NO.951	—
X76858	SEQ ID NO.899	SEQ ID NO.900	D10217	SEQ ID NO.952	SEQ ID NO.953
AA062131	SEQ ID NO.901	—	M55154	SEQ ID NO.954	SEQ ID NO.955
U12473	SEQ ID NO.902	SEQ ID NO.903	W46015	SEQ ID NO.956	—
M68859	SEQ ID NO.904	—	M63554	SEQ ID NO.957	SEQ ID NO.958
AA067929	SEQ ID NO.905	—	M13990	SEQ ID NO.959	—
U39066	SEQ ID NO.906	SEQ ID NO.907	W46084	SEQ ID NO.1057	—
U44088	SEQ ID NO.908	SEQ ID NO.909	AA048304	SEQ ID NO.1058	—
D87691	SEQ ID NO.910	SEQ ID NO.911	AA036574	SEQ ID NO.1059	—
U24160	SEQ ID NO.912	SEQ ID NO.913	AA030865	SEQ ID NO.1060	—
AA142376	SEQ ID NO.914	—	X51829	SEQ ID NO.1061	SEQ ID NO.1062
AA140150	SEQ ID NO.915	—	X63440	SEQ ID NO.1063	SEQ ID NO.1064
W29163	SEQ ID NO.916	—			

Table 3.

Genes of Which Transcription Levels Increased More Than 10-Fold

ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)	ACCESSION NO.	SEQ ID NO. (Nucleotide Sequence)	SEQ ID NO. (Amino Acid Sequence)
W49108	SEQ ID NO.960	—	J04115	SEQ ID NO.1000	SEQ ID NO.1001
M64292	SEQ ID NO.961	—	M22326	SEQ ID NO.1002	SEQ ID NO.1003
L25125	SEQ ID NO.962	SEQ ID NO.963	X14897	SEQ ID NO.1004	SEQ ID NO.1005
D49382	SEQ ID NO.964	SEQ ID NO.965	M88242	SEQ ID NO.1006	SEQ ID NO.1007
AA153519	SEQ ID NO.966	—	AA138777	SEQ ID NO.1008	—
AA013648	SEQ ID NO.967	—	AA061624	SEQ ID NO.1009	—
AA003990	SEQ ID NO.968	—	J00424	SEQ ID NO.1010	—
L20294	SEQ ID NO.969	SEQ ID NO.970	AA003162	SEQ ID NO.1011	—
W89900	SEQ ID NO.971	—	AA104477	SEQ ID NO.1012	—
U28656	SEQ ID NO.972	SEQ ID NO.973	J03236	SEQ ID NO.1013	SEQ ID NO.1014
U41805	SEQ ID NO.974	—	W33559	SEQ ID NO.1015	—
V00727	SEQ ID NO.975	—	AA041826	SEQ ID NO.1016	—
D78644	SEQ ID NO.976	—	L23971	SEQ ID NO.1017	SEQ ID NO.1018
X67083	SEQ ID NO.977	SEQ ID NO.978	AA117973	SEQ ID NO.1019	—
Z11911	SEQ ID NO.979	SEQ ID NO.980	AA117286	SEQ ID NO.1020	—
W17589	SEQ ID NO.981	—	U51037	SEQ ID NO.1021	SEQ ID NO.1022
X68273	SEQ ID NO.982	SEQ ID NO.983	U66203	SEQ ID NO.1023	SEQ ID NO.1024
X63535	SEQ ID NO.984	SEQ ID NO.985	X57337	SEQ ID NO.1025	SEQ ID NO.1026
D85904	SEQ ID NO.986	SEQ ID NO.987	X83972	SEQ ID NO.1027	—
AA071853	SEQ ID NO.988	—	X58251	SEQ ID NO.1028	SEQ ID NO.1029
U47543	SEQ ID NO.989	SEQ ID NO.990	AA017867	SEQ ID NO.1030	—
W13646	SEQ ID NO.991	—	W97817	SEQ ID NO.1031	—
U58513	SEQ ID NO.992	SEQ ID NO.993	W75007	SEQ ID NO.1032	—
U70210	SEQ ID NO.994	—	U27838	SEQ ID NO.1033	SEQ ID NO.1034
U18372	SEQ ID NO.995	—	U16163	SEQ ID NO.1035	SEQ ID NO.1036
AA153484	SEQ ID NO.996	—	U20264	SEQ ID NO.1037	—
AA166440	SEQ ID NO.997	—	W18950	SEQ ID NO.1065	—
W08897	SEQ ID NO.998	—	W16377	SEQ ID NO.1066	—
AA162708	SEQ ID NO.999	—			

All the publications, patents and patent applications cited in the present specification are incorporated herein by reference in their entireties.

INDUSTRIAL APPLICABILITY

According to the present invention, ischemic conditions are examined by analyzing

gene expression in a test tissue. Application of such analysis to prevention and treatment of ischemia is expected. There is also provided a novel method of screening for prophylactics and therapeutics for ischemia using, as an indicator, the expression levels of genes which are expressed specifically under ischemic conditions.

SEQUENCE LISTING FREE TEXT

SEQ ID NO: 1067: synthetic DNA

SEQ ID NO: 1068: synthetic DNA

CLAIMS

1. A method for examining ischemic conditions, comprising measuring the expression levels of particular genes in a test sample or determining the expression profile of a gene group in the sample comprising a plurality of genes selected from said particular genes.

2. The method according to claim 1, wherein said particular genes are:

- (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or
- (b) genes functionally equal to the genes having any of said nucleotide sequences or genes functionally equal to the genes encoding any of said amino acid sequences.

3. The method according to claim 1 or 2, wherein the measurement of the expression levels or the determination of the expression profile is carried out with a DNA chip.

4. The method according to claim 3, wherein the DNA chip is a synthetic-type DNA chip.

5. The method according to any one of claims 1 to 4, wherein the ischemic condition is at least one selected from the group consisting of compressive ischemia, occlusive ischemia and vasospastic ischemia.

6. A DNA chip for examining ischemic conditions, carrying a part or all of the following genes (a) or (b) immobilized on its surface:

- (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or

- (b) genes functionally equal to the genes having any of said nucleotide sequences or genes functionally equal to the genes encoding any of said amino acid sequences.

7. The DNA chip according to claim 6, wherein the ischemic condition is at least one selected from the group consisting of compressive ischemia, occlusive ischemia and vasospastic ischemia.

8. A method of screening for ischemic condition-improving drugs or therapeutics for ischemic diseases, comprising selecting candidate drugs using as an indicator whether or not:

- (a) the expression levels of particular genes of which expression levels change under ischemic conditions return to a normal expression levels; or
- (b) the expression profile of a gene group comprising a plurality of said particular genes returns to a normal expression profile;

by the administration of a drug to a test animal or test cell, wherein the returning to the normal expression levels or normal expression profile indicates that said drug is a candidate drug.

9. The method according to claim 8, wherein said particular genes of which expression levels change under ischemic conditions are:

- (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or
- (b) genes functionally equal to the genes having any of said nucleotide sequences or genes functionally equal to the genes encoding any of said amino acid sequences.

10. The method according to claim 8 or 9, wherein the ischemic condition is at least one selected from the group consisting of compressive ischemia, occlusive ischemia and vasospastic ischemia.

11. A computer-readable record medium in which the following data (a) or (b) have been recorded:

- (a) expression level data of genes of which expression levels change under ischemic conditions; or
- (b) expression profile data of a gene group comprising a plurality of genes selected from said genes.

12. The record medium according to claim 11, wherein said genes of which expression levels change under ischemic conditions are:

- (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or
- (b) genes functionally equal to the genes having said nucleotide sequences or genes functionally equal to the genes encoding said amino acid sequences.

13. The record medium according to claim 11 or 12, wherein the ischemic condition is at least one selected from the group consisting of compressive ischemia, occlusive ischemia and vasospastic ischemia.

14. A computer-readable record medium in which a program that directs a computer to execute the following procedures has been recorded:

- (a) procedures to input expression level data or expression profile data of particular genes in a test sample;
- (b) procedures to record the input data;
- (c) procedures to check the recorded data with already recorded expression level data or expression profile data of said genes under ischemic conditions;
- (d) procedures to determine whether the test sample is under ischemic conditions or not based on the checking results obtained in (c); and
- (e) if the test sample has been determined as being under ischemic conditions, procedures to identify the clinical stage of the ischemic conditions of the test sample based on the

checking results obtained in (c).

15. The record medium according to claim 14, wherein said genes are:

- (a) genes having any of the nucleotide sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066 or genes encoding any of the amino acid sequences shown in SEQ ID NO: 1 through SEQ ID NO: 1066; or
- (b) genes functionally equal to the genes having any of said nucleotide sequences or genes functionally equal to the genes encoding any of said amino acid sequences.

16. The record medium according to claim 14 or 15, wherein the ischemic condition is at least one selected from the group consisting of compressive ischemia, occlusive ischemia and vasospastic ischemia.

Fig. 1

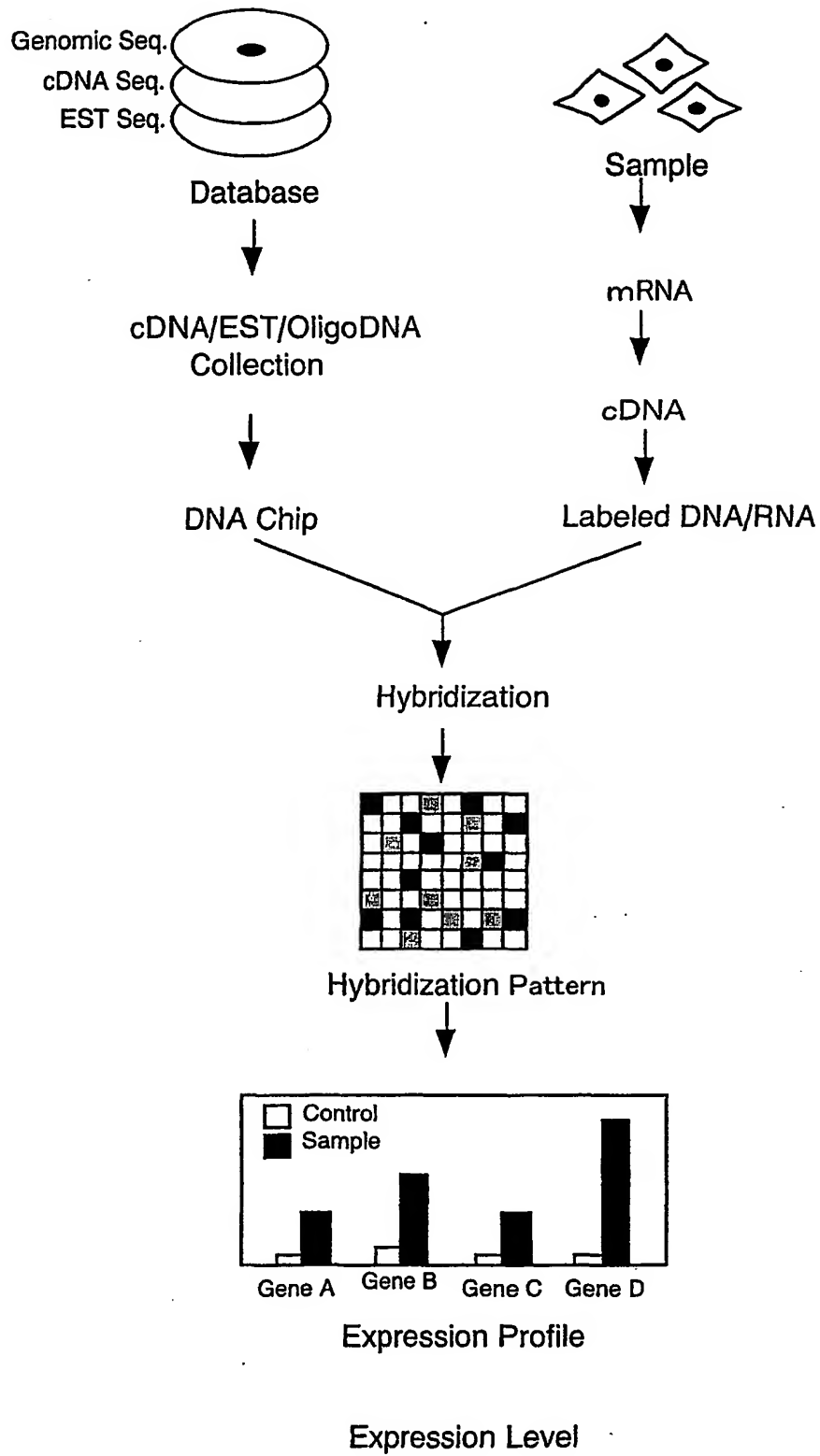


Fig. 2

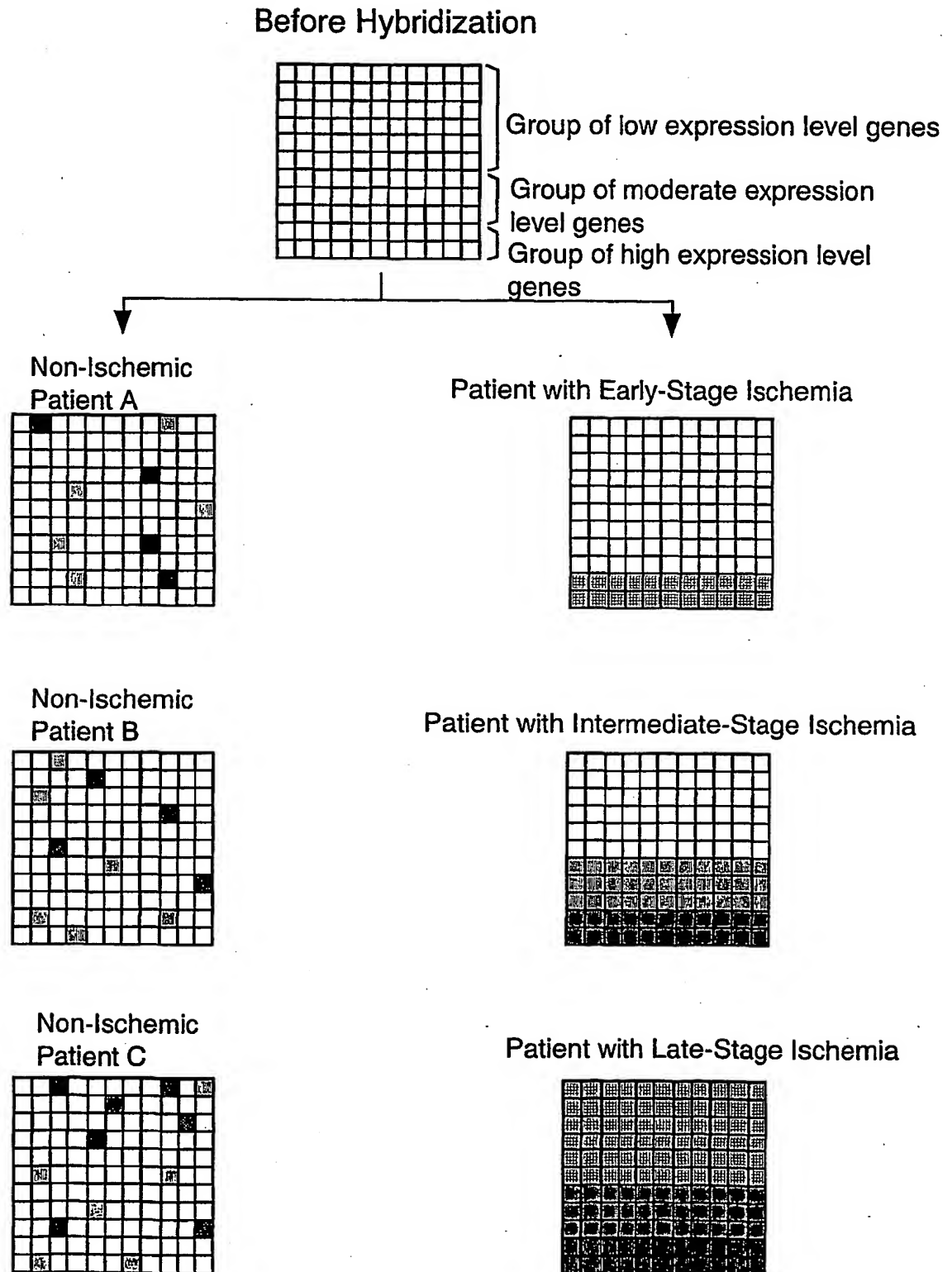


Fig. 3

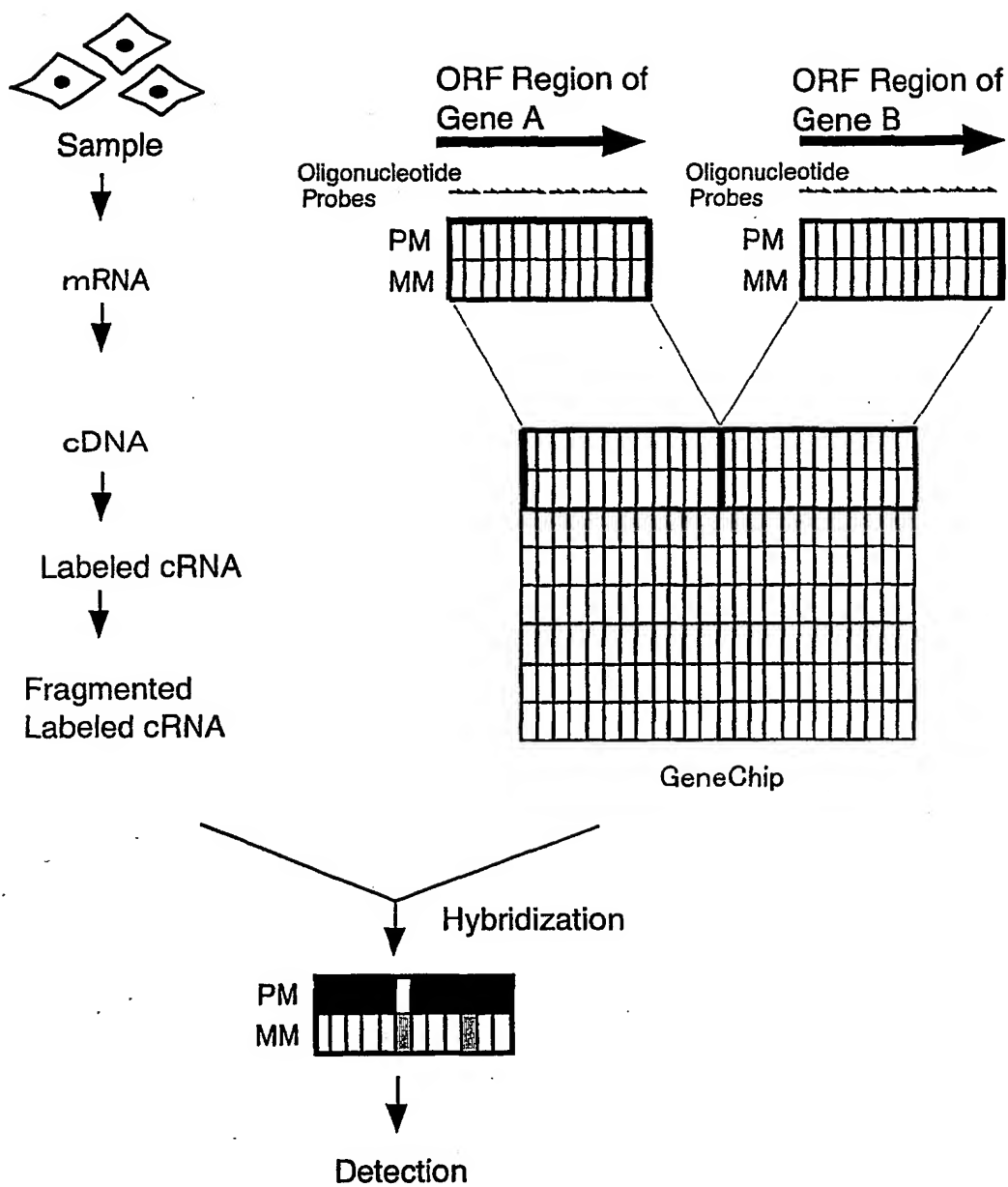


Fig.4

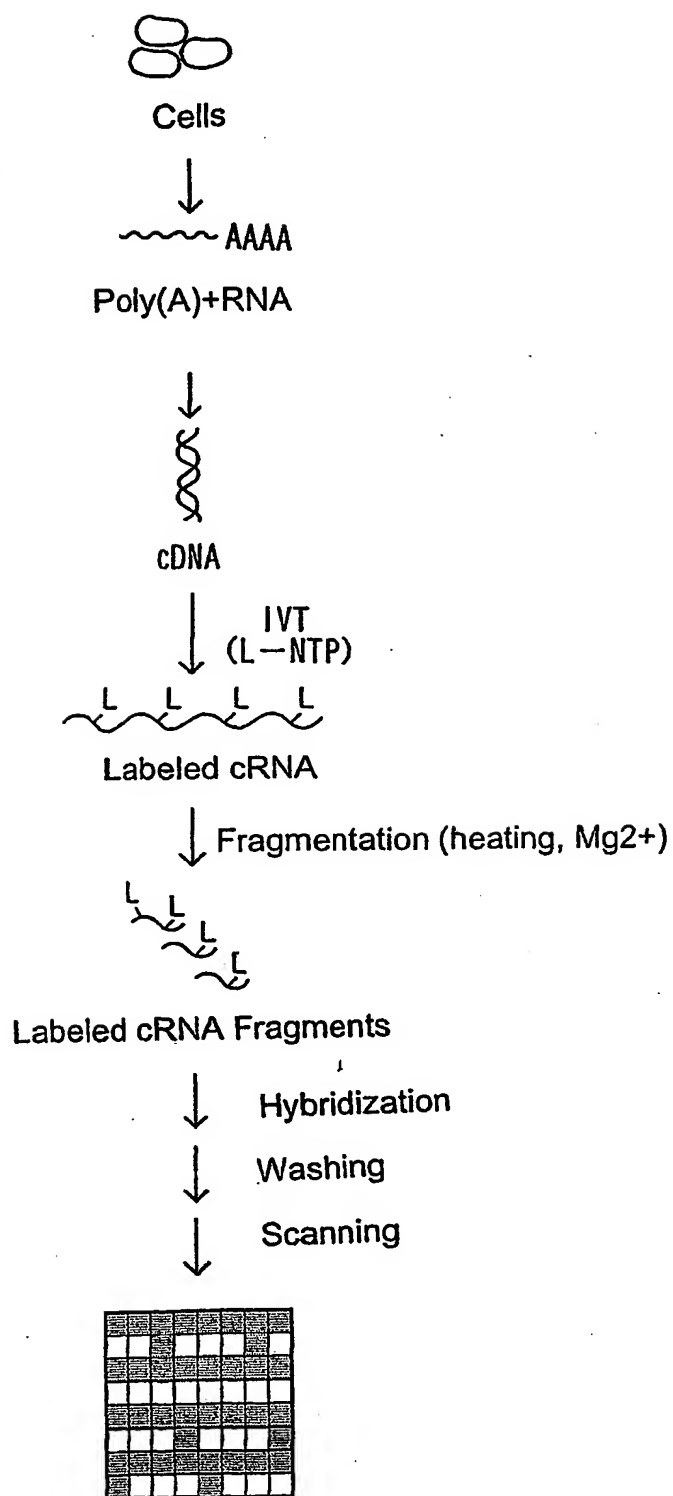


Fig.5

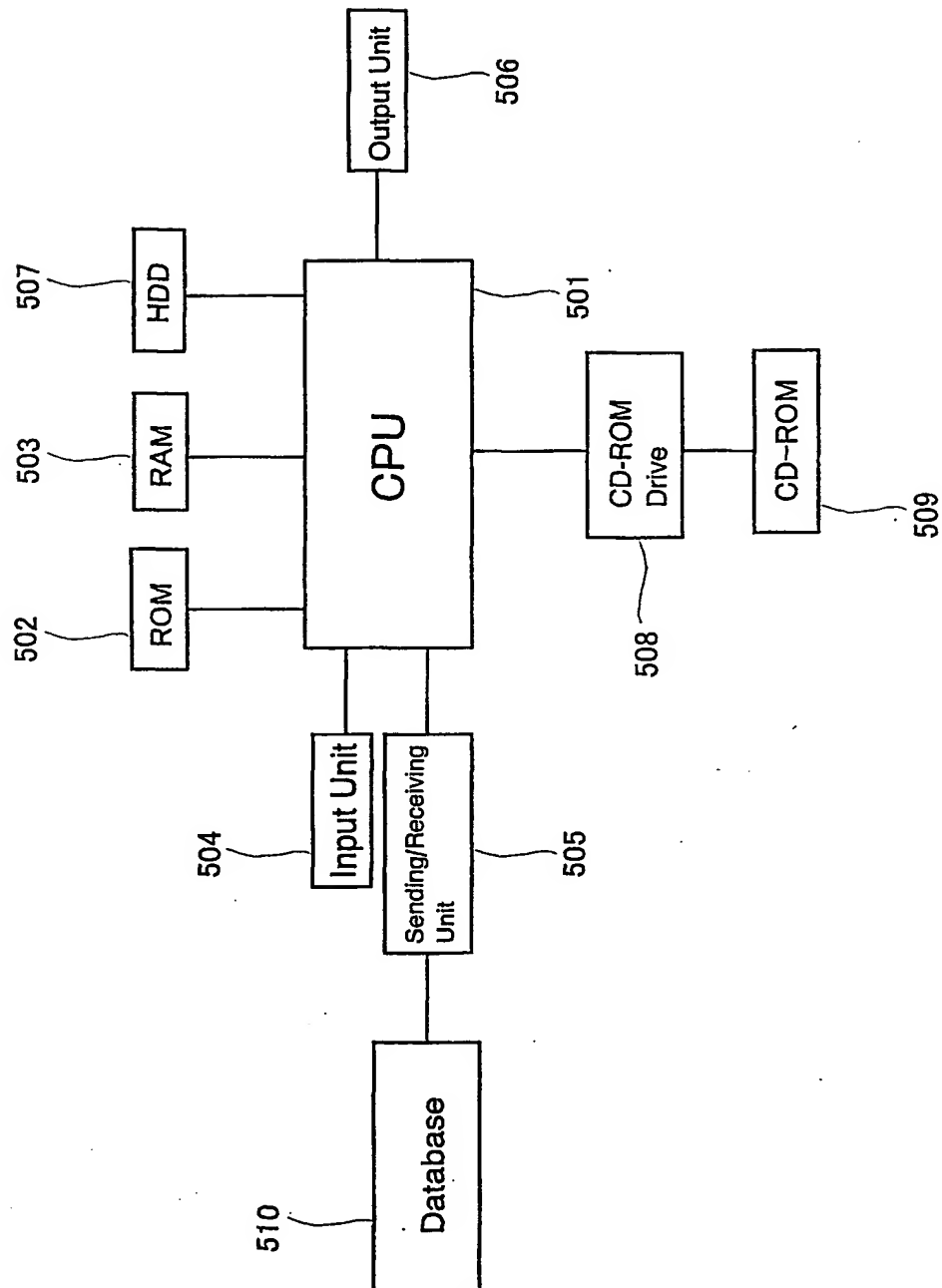
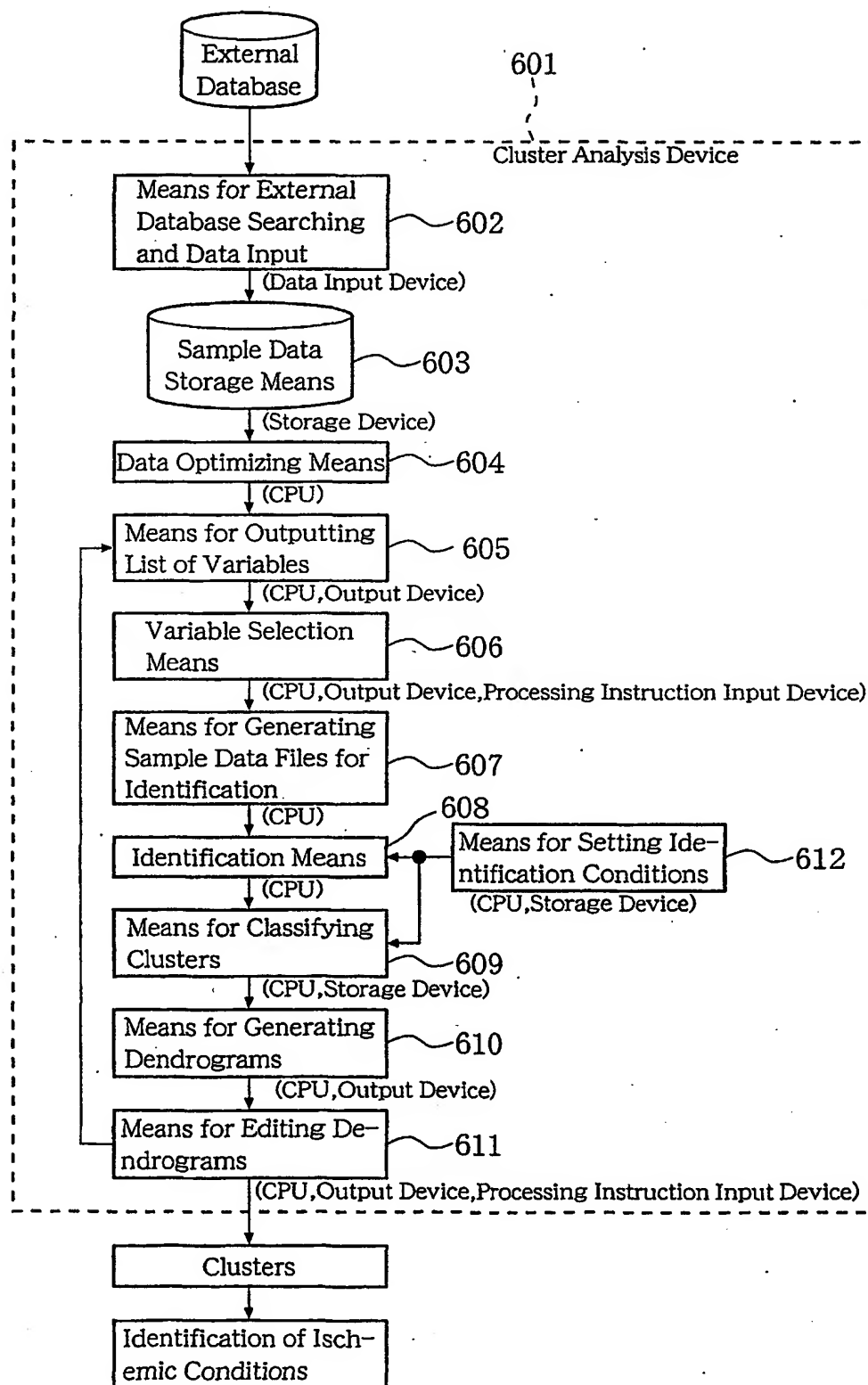


Fig.6



SEQUENCE LISTING

<110> Nihon University

<120> METHOD FOR EXAMINING ISCHEMIC CONDITIONS

<130> PH-1036PCT

<150> JP2000-145977

<151> 2000-05-18

<160> 1068

<210> 1

<211> 3217

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1).. (1236)

<400> 1

gaa ttc aag aag gct tcc gaa gat gac att aaa aaa atg cct cta gat 48

Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp

1

5

10

15

ttg tcc cct ctt gca aca ccc atc ata aga agc aaa att gag gag cct 96

Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro

20

25

30

tct gtt gta gaa aca act cac cag gac agc cct tta cct cac ccc gag	144
Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu	
35 40 45	
tcg act acc agt gat gaa aag gaa ata cca ttg gca caa act gca cag	192
Ser Thr Thr Ser Asp Glu Lys Glu Ile Pro Leu Ala Gln Thr Ala Gln	
50 55 60	
ccc aca tca gct atc gtt cgt cca gca tca tta cag gtt ccc aat gtg	240
Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val	
65 70 75 80	
ctg ctc aca agt tct gac tca agt gta att att caa caa gca gta cct	288
Leu Leu Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro	
85 90 95	
tca cca acc tca agt act gta atc acc cag gca cca tcc tct aac agg	336
Ser Pro Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg	
100 105 110	
cca att gtt cct gta cca ggc cca ttt cct ctt ctc tta cat ctt cct	384
Pro Ile Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro	
115 120 125	
aat gga caa acc atg ccc gtt gct att cct gca tca att aca agt tct	432
Asn Gly Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser	
130 135 140	
aat gtg cat gtt cca gct gca gtc cca ctt gtt cgg cca gtc acc atg	480
Asn Val His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met	
145 150 155 160	
gtg cct agt gtt cca gga atc cca ggc cct tcc tct cct caa cca gtc	528
Val Pro Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val	
165 170 175	
cag tca gaa gca aaa atg aga tta aaa gct gct ttg acc cag caa cac	576
Gln Ser Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His	

180	185	190	
cct cca gtt acc aat ggt gat act gta aaa ggc cat ggc agt gga ttg			624
Pro Pro Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu			
195	200	205	
gtt agg act cag tca gaa gag tct cgc cca cag tcc ttg cag cag cca			672
Val Arg Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro			
210	215	220	
gcc acc tcc act aca gaa act ccg gct tct cca gct cac aca act cct			720
Ala Thr Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro			
225	230	235	240
cag acc caa aat aca agt ggc cgt cga aga aga gca gct aat gaa gat			768
Gln Thr Gln Asn Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp			
245	250	255	
cct gat gag aaa agg agg aag ttt cta gaa cga aat aga gca gca gct			816
Pro Asp Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala			
260	265	270	
tca aga tgc cga caa aaa agg aaa gtg tgg gtt cag tcc tta gag aag			864
Ser Arg Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys			
275	280	285	
aaa gca gaa gac ttg agt tca cta aat ggc cag ctg cag agc gaa gtc			912
Lys Ala Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val			
290	295	300	
acc ctg ctg aga aat gaa gtg gcc cag ctg aaa cag ctt ctt ctg gct			960
Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala			
305	310	315	320
cat aaa gat tgc cct gta act gcc atg cag aag aag tct ggc tat cat			1008
His Lys Asp Cys Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His			
325	330	335	
act gct gat aaa gat gac agt tca gaa gac ctt tct gtg cca agc agt			1056

Thr Ala Asp Lys Asp Asp Ser Ser Glu Asp Leu Ser Val Pro Ser Ser
 340 345 350
 cca cat aca gaa gcg atc cag cac agc tct gtc agc aca tcc aat gga 1104
 Pro His Thr Glu Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly
 355 360 365
 gtc agt tca aca tca aaa gca gaa gct gta gcc act tca gtc ctc acc 1152
 Val Ser Ser Thr Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr
 370 375 380
 cag atg gcg gac cag agc acg gag cct gca ctt tca cag att gtc atg 1200
 Gln Met Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met
 385 390 395 400
 gct cct ccc tcc cag gca cag ccc tca gga agt tga ttaaaacctg 1246
 Ala Pro Pro Ser Gln Ala Gln Pro Ser Gly Ser
 405 410
 cagtgcaaca gttttagata ctgattagtg acttcaaagg gaaatcaagg aaagaccagt 1306
 ttgcatTTTat gcgaaatctg tggttgtaaa tttttttttt tttacttgaa gttaaatttg 1366
 tctctggagt tggatatagca gcagttgatg atcagactga atatgttttt agtcctctgga 1426
 agactgattt tccTTTTtta tacatatTgt taagatttat taattttcct gtgctcaatg 1486
 tgtaaattgt atcataactc attgtggTtg atttcacttt gatTTtagtgg catcttaata 1546
 aatgggggtg ttactgaatc actcttccca ctTccatttc ttTgcccacc cttTcaccct 1606
 gagatgtgat ggtagtcttg ttatcatTTta taccaaagtt ctgcagagtc cctattgtct 1666
 gtgtaagatg gacaaagtTg taagacacta gggaagagaa agaaagacgg aaagtTcctt 1726
 ttaatctTTTt tgccTTTTat ttTgcacatt atgcaaaagg aagaatatta gaaacacttt 1786
 tttttaagtTg agtgaaagta tggtaagacg gttagtgcTT tgtgcacttc ttagactaat 1846
 caaggTcatc catcgccctg caatgtTTTt aagattaaagt aaacaaaaat ttTggaatct 1906
 tgagcatttc aaaaaatgac ttgattTTTT aagtctTtaa ttcagtattt taaacctgtg 1966
 ttcttgaggc tgaaaactat gaaattatat aatgtatgat acagggttat cagatagtaa 2026
 tttttaaaat ttgctctTgt cattTgggat ttgtTTTgtt tgggattttg ttgtgtgtga 2086
 ttTgtTTTgt ttTgtTTTgc agattTcagg taacaaagtTg agacgcttat gcataaagaa 2146

gtgtgatgtg gttgccagaa aagcctaaaa ttatgactta gaaacgttaa gactgtttcc 2206
 cccattgtcg tactgtiactt gcgagctaac ttgtacttat tcttgtgaaa gcactgtcat 2266
 cttttagtag ccaattttga taatgtttct cgtggaaaaa aatcagtaic tatctttaga 2326
 acaatgtaat tataacgtgg gaatgtgagt gagagaatga gtaatgtgat gtgtgtgtgt 2386
 gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgcgcgc gcggtgtgtg tgcattttcc 2446
 actagtttat gccagcgata ttgcttgaat gtttaacgat gccttcagtg tgatgctggc 2506
 aatagatgac tgcagtttca gatgccatta ctgtgcaggc ttggataact aacattccat 2566
 gatgtagctt gttctgatga aatgattgta gttacacttt gctcattctc cagtcattctg 2626
 tggaaacttg agttttctaa tgtgccatta tctatittta ttctgcagtt acgttaaaaa 2686
 tacagtacaa tattttaaat agactaaatt gttaaacata aaaattaaaa aaaaaagtag 2746
 tagatgtgtg taagaaaact ttgtaaaata gttatgagtc ctaccagta gcaacttctg 2806
 gcgttcaagc aggattccat tctgtaaata cctgtaatgt gtttataata agttgtgtag 2866
 tctgttctgc atccatacta cattattgct atggictcag tgtcatctct taaagagatt 2926
 gacgtttcca aagccgtatg gaatgccctt gagagttcag gggaacaccc accccacctg 2986
 cctcctaagt tccaatctgg gaaacatgca aattatataa atgacatttc acgacttttg 3046
 agtatgaaga taataggaat titattacat ggcttattaa aatgagagca ttttggttgc 3106
 tgattctact ttgtatctat tactttcacc tgatctcata tttaatcagt ttaaattaca 3166
 attttgtcat agttatgcta aggagttgat ctcaaaggca caaaacatga a 3217

<210> 2

<211> 411

<212> PRT

<213> Mus musculus

<400> 2

Glu Phe Lys Lys Ala Ser Glu Asp Asp Ile Lys Lys Met Pro Leu Asp

1

5

10

15

Leu Ser Pro Leu Ala Thr Pro Ile Ile Arg Ser Lys Ile Glu Glu Pro

20

25

30

Ser Val Val Glu Thr Thr His Gln Asp Ser Pro Leu Pro His Pro Glu
 35 40 45
 Ser Thr Thr Ser Asp Glu Lys Glu Ile Pro Leu Ala Gln Thr Ala Gln
 50 55 60
 Pro Thr Ser Ala Ile Val Arg Pro Ala Ser Leu Gln Val Pro Asn Val
 65 70 75 80
 Leu Leu Thr Ser Ser Asp Ser Ser Val Ile Ile Gln Gln Ala Val Pro
 85 90 95
 Ser Pro Thr Ser Ser Thr Val Ile Thr Gln Ala Pro Ser Ser Asn Arg
 100 105 110
 Pro Ile Val Pro Val Pro Gly Pro Phe Pro Leu Leu Leu His Leu Pro
 115 120 125
 Asn Gly Gln Thr Met Pro Val Ala Ile Pro Ala Ser Ile Thr Ser Ser
 130 135 140
 Asn Val His Val Pro Ala Ala Val Pro Leu Val Arg Pro Val Thr Met
 145 150 155 160
 Val Pro Ser Val Pro Gly Ile Pro Gly Pro Ser Ser Pro Gln Pro Val
 165 170 175
 Gln Ser Glu Ala Lys Met Arg Leu Lys Ala Ala Leu Thr Gln Gln His
 180 185 190
 Pro Pro Val Thr Asn Gly Asp Thr Val Lys Gly His Gly Ser Gly Leu
 195 200 205
 Val Arg Thr Gln Ser Glu Glu Ser Arg Pro Gln Ser Leu Gln Gln Pro
 210 215 220
 Ala Thr Ser Thr Thr Glu Thr Pro Ala Ser Pro Ala His Thr Thr Pro
 225 230 235 240
 Gln Thr Gln Asn Thr Ser Gly Arg Arg Arg Arg Ala Ala Asn Glu Asp
 245 250 255
 Pro Asp Glu Lys Arg Arg Lys Phe Leu Glu Arg Asn Arg Ala Ala Ala

260	265	270
Ser Arg Cys Arg Gln Lys Arg Lys Val Trp Val Gln Ser Leu Glu Lys		
275	280	285
Lys Ala Glu Asp Leu Ser Ser Leu Asn Gly Gln Leu Gln Ser Glu Val		
290	295	300
Thr Leu Leu Arg Asn Glu Val Ala Gln Leu Lys Gln Leu Leu Leu Ala		
305	310	315
His Lys Asp Cys Pro Val Thr Ala Met Gln Lys Lys Ser Gly Tyr His		
325	330	335
Thr Ala Asp Lys Asp Asp Ser Ser Glu Asp Leu Ser Val Pro Ser Ser		
340	345	350
Pro His Thr Glu Ala Ile Gln His Ser Ser Val Ser Thr Ser Asn Gly		
355	360	365
Val Ser Ser Thr Ser Lys Ala Glu Ala Val Ala Thr Ser Val Leu Thr		
370	375	380
Gln Met Ala Asp Gln Ser Thr Glu Pro Ala Leu Ser Gln Ile Val Met		
385	390	395
Ala Pro Pro Ser Gln Ala Gln Pro Ser Gly Ser		
405	410	

<210> 3

<211> 503

<212> DNA

<213> Mus musculus

<400> 3

cttgctgcct tagcaccatg gaagccacca agcaagtggg taactttggg cccgggcctg 60
ccaagctgcc aactcggta ttgttgaga tccagaagca gctactagac tacagaggac 120
tcggcatcag tgtgctcgaa atgagtcaca ggtcgtcaga ttttgccaag attattggca 180

atacagagaa tcttgtgagg gaattgctag ctgttcccaa caactacaag gtgatctttg 240
 tacaaggagg tgggtctggc cagttcagtg ctgtccctt aaatctgatt ggcctgaaag 300
 ctggaaggag tgctgactac gtggtagaccg gagcttggtc agctaaggct gcggaagaag 360
 ccaagaagtt tggaacggig aacattgtcc accctaaact tggaagttaa caaaaattcc 420
 agacccaagc acctggaacg tcagcccgga cggcgtccta tgtatacttc tgtgcaaacg 480
 agactgtgca cggcngtgag ttt 503

<210> 4

<211> 1260

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (79).. (957)

<400> 4

ggcgcgtctg ttctgtggaa caggaggcag ttgttttccg tccggcttct cccacaccga 60
 agtgcgcgcc tccacctc atg gaa gac tcg atg gat atg gac atg agt cct 111
 Met Glu Asp Ser Met Asp Met Asp Met Ser Pro
 1 5 10
 ctt agg cct cag aac tac ctt ttc ggc tgt gaa cta aag gct gac aaa 159
 Leu Arg Pro Gln Asn Tyr Leu Phe Gly Cys Glu Leu Lys Ala Asp Lys
 15 20 25
 gac tat cac ttt aaa gtg gat aat gat gaa aat gag cac cag ttg tca 207
 Asp Tyr His Phe Lys Val Asp Asn Asp Glu Asn Glu His Gln Leu Ser
 30 35 40
 tta aga acg gtc agt tta gga gca ggg gca aaa gat gag tta cac atc 255
 Leu Arg Thr Val Ser Leu Gly Ala Gly Ala Lys Asp Glu Leu His Ile

45	50	55	
gta gag gca gaa gca atg aac tat gaa ggc agt cca att aaa gta aca	303		
Val Glu Ala Glu Ala Met Asn Tyr Glu Gly Ser Pro Ile Lys Val Thr			
60	65	70	75
ctg gca act ttg aaa atg tct gta caa cca aca gtt tcc cta ggg ggc	351		
Leu Ala Thr Leu Lys Met Ser Val Gln Pro Thr Val Ser Leu Gly Gly			
80	85	90	
ttt gaa att aca cca cct gtg gtc tta cgg ttg aag tgt ggt tca ggg	399		
Phe Glu Ile Thr Pro Pro Val Val Leu Arg Leu Lys Cys Gly Ser Gly			
95	100	105	
cct gtg cac att agt gga cag cat cta gta gct gta gag gaa gat gca	447		
Pro Val His Ile Ser Gly Gln His Leu Val Ala Val Glu Glu Asp Ala			
110	115	120	
gag tct gaa gat gaa gat gag gag gac gta aaa ctc tta ggc atg tct	495		
Glu Ser Glu Asp Glu Asp Glu Glu Asp Val Lys Leu Leu Gly Met Ser			
125	130	135	
gga aag cga tct gct cct gga ggt ggt aac aag gtt cca cag aaa aaa	543		
Gly Lys Arg Ser Ala Pro Gly Gly Gly Asn Lys Val Pro Gln Lys Lys			
140	145	150	155
gta aaa ctt gat gaa gat gat gag gac gat gat gag gac gat gag gat	591		
Val Lys Leu Asp Glu Asp Asp Glu Asp Asp Asp Glu Asp Asp Glu Asp			
160	165	170	
gat gag gat gat gat gat gat gat ttt gat gaa gag gaa act gaa gaa	639		
Asp Glu Asp Asp Asp Asp Asp Asp Phe Asp Glu Glu Glu Thr Glu Glu			
175	180	185	
aag gtc cca gtg aag aaa tct gta cga gat acc cca gcc aaa aat gca	687		
Lys Val Pro Val Lys Lys Ser Val Arg Asp Thr Pro Ala Lys Asn Ala			
190	195	200	
caa aaa tca aac caa aat gga aaa gac tta aaa cca tca aca ccg aga	735		

Gln Lys Ser Asn Gln Asn Gly Lys Asp Leu Lys Pro Ser Thr Pro Arg
 205 210 215
 tca aag ggt caa gag tcc ttc aaa aaa cag gaa aag act cct aaa aca 783
 Ser Lys Gly Gln Glu Ser Phe Lys Lys Gln Glu Lys Thr Pro Lys Thr
 220 225 230 235
 cca aaa gga cct agt tct gta gaa gac att aag gca aaa atg caa gca 831
 Pro Lys Gly Pro Ser Ser Val Glu Asp Ile Lys Ala Lys Met Gln Ala
 240 245 250
 agt ata gaa aaa ggc ggt tct ctt ccc aaa gtg gaa gcc aag ttc att 879
 Ser Ile Glu Lys Gly Gly Ser Leu Pro Lys Val Glu Ala Lys Phe Ile
 255 260 265
 aat tat gtg aag aat tgt ttc cgg atg act gac cag gag gct att caa 927
 Asn Tyr Val Lys Asn Cys Phe Arg Met Thr Asp Gln Glu Ala Ile Gln
 270 275 280
 gat ctc tgg cag tgg agg aaa tct ctt taa gaaaagggtt taaacagttt 977
 Asp Leu Trp Gln Trp Arg Lys Ser Leu
 285 290
 gaaatattct gtcttcattt ctgtaatagt taatatctgg ctgtcctttt tataatgcaa 1037
 agtgagaact ttccctactg tgtttgataa atgttgcca gggtcacttg ccaagaatgt 1097
 gttgtctaaa atgcctgttt agttttcaag gatggaactc caccctttac ttggttttta 1157
 gstatgtatgg aatgttatga taggacatag taatagtggc cagatgtgga aatggttagg 1217
 agacaaatat acaigtgaaa taaactcagt attttaataa agt 1260

<210> 5

<211> 292

<212> PRT

<213> Mus musculus

<400> 5

Met Glu Asp Ser Met Asp Met Asp Met Ser Pro Leu Arg Pro Gln Asn
 1 5 10 15
 Tyr Leu Phe Gly Cys Glu Leu Lys Ala Asp Lys Asp Tyr His Phe Lys
 20 25 30
 Val Asp Asn Asp Glu Asn Glu His Gln Leu Ser Leu Arg Thr Val Ser
 35 40 45
 Leu Gly Ala Gly Ala Lys Asp Glu Leu His Ile Val Glu Ala Glu Ala
 50 55 60
 Met Asn Tyr Glu Gly Ser Pro Ile Lys Val Thr Leu Ala Thr Leu Lys
 65 70 75 80
 Met Ser Val Gln Pro Thr Val Ser Leu Gly Gly Phe Glu Ile Thr Pro
 85 90 95
 Pro Val Val Leu Arg Leu Lys Cys Gly Ser Gly Pro Val His Ile Ser
 100 105 110
 Gly Gln His Leu Val Ala Val Glu Glu Asp Ala Glu Ser Glu Asp Glu
 115 120 125
 Asp Glu Glu Asp Val Lys Leu Leu Gly Met Ser Gly Lys Arg Ser Ala
 130 135 140
 Pro Gly Gly Gly Asn Lys Val Pro Gln Lys Lys Val Lys Leu Asp Glu
 145 150 155 160
 Asp Asp Glu Asp Asp Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Asp
 165 170 175
 Asp Asp Asp Phe Asp Glu Glu Glu Thr Glu Glu Lys Val Pro Val Lys
 180 185 190
 Lys Ser Val Arg Asp Thr Pro Ala Lys Asn Ala Gln Lys Ser Asn Gln
 195 200 205
 Asn Gly Lys Asp Leu Lys Pro Ser Thr Pro Arg Ser Lys Gly Gln Glu
 210 215 220
 Ser Phe Lys Lys Gln Glu Lys Thr Pro Lys Thr Pro Lys Gly Pro Ser

225 230 235 240
 Ser Val Glu Asp Ile Lys Ala Lys Met Gln Ala Ser Ile Glu Lys Gly
 245 250 255
 Gly Ser Leu Pro Lys Val Glu Ala Lys Phe Ile Asn Tyr Val Lys Asn
 260 265 270
 Cys Phe Arg Met Thr Asp Gln Glu Ala Ile Gln Asp Leu Trp Gln Trp
 275 280 285
 Arg Lys Ser Leu
 290

<210> 6

<211> 3899

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (957).. (1934)

<400> 6

gatcattttc cactagaatc ttaacggaag cttagatga aaacaaagt acctaataga 60
 aatggagagc ccaaattctat agttattaaa ataattcaaa accaacaac tgagcatcca 120
 atgatgaatg aatgcatata tatatatatt ttatatatcc ctcatittca tgtggggcct 180
 gggggattta aattctgggt ctcattgctt aactgcaaaa gctcttaacc actgaaccaa 240
 gtctcatitt aattaaaatt tttaaactccc atcaattatg ctatatgaat ctactacttc 300
 tagaacattc aaatctcaca tggatttatc tccagtgtct gtaactaac ttacattct 360
 tccttgittg atctgcattc agatatgtaa gaatttatct ctattaataa tttctcaata 420
 ttccaatctt aaacaactca tcatcatcat catcatcata aggtacagct ttccaaaaga 480
 aaaaagaaaa aaaagtcatt tctgtttctc ttattcttct gtagaaaaac caaatcaag 540

aattaagtica ttctccagga ccttcacatt taatttgatt ttgcccaaac tcagtgtgtc 600
cgaacttaac ttcaccatct cagctacatc ttcttccttc aacttggttc tttccctacc 660
atcatctagt tctgtgccat acaggagacc agggaaatct ttacataag cctagtggtta 720
cccttccttt aagaccccca ttggttgggc ttigactctt cggctccttt cccagcccta 780
ccactcttct ggcttcccaa cacgcatgcg caatatcgcg tcagccccgc ccgcccgtg 840
ctgcggaagg cgcagtgtc agtaaagcgc acttcctctg ctggtctcca ccgagggagt 900
gcccgtctcca agagctccaa gccgcatcgg tcctgctctg atccgaaggc gcagac atg 959

Met

1

tcg gaa caa agt aag gac ctg agc gac cct aac ttt gca gcc gag gcc 1007
Ser Glu Gln Ser Lys Asp Leu Ser Asp Pro Asn Phe Ala Ala Glu Ala
5 10 15
ccc gac tgt gag atg cag gac agc gat gcc gtt ccg gtg ggg atc cct 1055
Pro Asp Cys Glu Met Gln Asp Ser Asp Ala Val Pro Val Gly Ile Pro
20 25 30
cct ccc gct tct ctg gcc gct aac ctc gca ggg cca ccg tgc gct ccc 1103
Pro Pro Ala Ser Leu Ala Ala Asn Leu Ala Gly Pro Pro Cys Ala Pro
35 40 45
gaa ggc cct atg gca gcc caa cag gcc tcg cca ccg ccc gaa gaa cgg 1151
Glu Gly Pro Met Ala Ala Gln Gln Ala Ser Pro Pro Pro Glu Glu Arg
50 55 60 65
ata gaa gat gtt gac cct aaa atc ctg cag cag gcc gca gag gag ggc 1199
Ile Glu Asp Val Asp Pro Lys Ile Leu Gln Gln Ala Ala Glu Glu Gly
70 75 80
cgc gcc cac cag ccc cag agt cca gcc cgg ccg atc cca gca ccg cca 1247
Arg Ala His Gln Pro Gln Ser Pro Ala Arg Pro Ile Pro Ala Pro Pro
85 90 95
gcc cct gcc cag ctg gtg cag aag gcg cac gag ctc atg tgg tac gtg 1295
Ala Pro Ala Gln Leu Val Gln Lys Ala His Glu Leu Met Trp Tyr Val

100	105	110	
ttg gtg aag gac cag aag agg atg gtc ctc tgg ttt cca gac atg gtg			1343
Leu Val Lys Asp Gln Lys Arg Met Val Leu Trp Phe Pro Asp Met Val			
115	120	125	
aaa gag gtc atg ggc agc tac aag aaa tgg tgc aga agc atc ctc agg			1391
Lys Glu Val Met Gly Ser Tyr Lys Lys Trp Cys Arg Ser Ile Leu Arg			
130	135	140	145
cgc acc agc gtc atc ctc gcc aga gtg ttc ggg ctg cac ctg agg ctg			1439
Arg Thr Ser Val Ile Leu Ala Arg Val Phe Gly Leu His Leu Arg Leu			
150	155	160	
acc aat ctc cac acc atg gag ttt gcc ctg gtc aaa gcc ctc agc cca			1487
Thr Asn Leu His Thr Met Glu Phe Ala Leu Val Lys Ala Leu Ser Pro			
165	170	175	
gag gag cta gac agg gtg gcg ctc aac aac cgt atg ccc atg aca ggc			1535
Glu Glu Leu Asp Arg Val Ala Leu Asn Asn Arg Met Pro Met Thr Gly			
180	185	190	
ctc ctg ctc atg atc ctg agc ctc atc tat gtg aag ggc cgc ggg gcc			1583
Leu Leu Leu Met Ile Leu Ser Leu Ile Tyr Val Lys Gly Arg Gly Ala			
195	200	205	
aga gag ggt gcg gtc tgg aat gtg ctg cgc atc ctg ggg ctg agg ccc			1631
Arg Glu Gly Ala Val Trp Asn Val Leu Arg Ile Leu Gly Leu Arg Pro			
210	215	220	225
tgg aag aag cac tcc acc ttc gga gac gtg agg aag ata atc acc gag			1679
Trp Lys Lys His Ser Thr Phe Gly Asp Val Arg Lys Ile Ile Thr Glu			
230	235	240	
gag ttc gtc cag cag aat tac ctg aag tac cag cgt gtg ccc cac atc			1727
Glu Phe Val Gln Gln Asn Tyr Leu Lys Tyr Gln Arg Val Pro His Ile			
245	250	255	
gag cct ccc gag tac gag ttc ttc tgg ggg tcc aga gct aac cgt gaa			1775

Glu Pro Pro Glu Tyr Glu Phe Phe Trp Gly Ser Arg Ala Asn Arg Glu
 260 265 270
 atc acc aag atg cag atc atg gag ttc ctg gcc aga gtc ttc aag aaa 1823
 Ile Thr Lys Met Gln Ile Met Glu Phe Leu Ala Arg Val Phe Lys Lys
 275 280 285
 gat ccc cag gcg tgg cct tcc cga tac agg gag gct ctg gag cag gcc 1871
 Asp Pro Gln Ala Trp Pro Ser Arg Tyr Arg Glu Ala Leu Glu Gln Ala
 290 295 300 305
 aga gct ctg cgg gag gct aat ctt gct gcc cag gcc ccc cgc agc agt 1919
 Arg Ala Leu Arg Glu Ala Asn Leu Ala Ala Gln Ala Pro Arg Ser Ser
 310 315 320
 gtc tct gag gac taa aaaggtccag gggcacactg atagtttctg acccatacta 1974
 Val Ser Glu Asp
 325
 gggctgtgta aggggtgggt tgagtcattt gagtatccca aatccacagt gcagtatttc 2034
 aigtataatt ttttaagtttt ccatacagtg cttttgtacc ttgtaatgct attcatttgt 2094
 gtactcgtgt agtgtttaag attgatgcat gtgtgataag tatttggtac tttcactttt 2154
 gtgcittcgt gcatttttgt acaagagatg tgctgtgcta aacttgtgaa atacattgag 2214
 gtgttctgta tcttgttcct ttgtatggga ctgatgatct gtatcgacaa agaaggccct 2274
 ggagagttag caggacttaa cagcaacgca gacctgagca agagaaaggc caaggccitt 2334
 ctccatatga cttcaactgg cacaggaagc atccatgtgg aatggactga tttgaactgg 2394
 actgttctca gtgtaggcac ttagcacctt ttacaaaaca tgtatgcaac cccaccataa 2454
 ataaacgtta aaatgagcat taaagatact gtgaaataat ttcttggggg ggggaggagg 2514
 catttatatt tgatgaaagg gggagtggga atgggtgggg atgagaaaga ttctccctgt 2574
 gtgcagcata agcataagca aacaggggtgt cctaacacag tgggagacca cagaccact 2634
 cagaagaaac ttgcagtgtt ttaatcaatt tgtcacataa aaggtataac aacaacaaca 2694
 aaaaagctca ttatcacata acatggggat aataacaggc atatggaggg cctgcccctt 2754
 ttctgttgca ttttttaaaa tagtctttga tggacacttt agcagaataa acccttatcg 2814
 tgcatttctt ctttattttg tcttcccacc agccataaga agtaagggat aactgtatca 2874

tcacagagca agaaaaaata aaaggggtgt tggtaatgaa ctatcctaaa acctttatac 2934
 aggagtcttg acaccaagct ccccatggcc accactcaca caagcactct ggccctccctg 2994
 ctgtatgcat taagggttga tttttctaata taattccaag agtttcacag aaaatttagct 3054
 tctgaatgta caaatttagga aactcgtttc agaaagaatt gatgacctaa tcaagtcctt 3114
 atcttgctaa ggggtaaaaa caagatctga aatttcactt ttccagaagg atgaagatga 3174
 gcgaaactat tctgacagtc gtaccagtaa gagccatggc actaatgaaa tagaggaggg 3234
 gttgggattt aggagctgcc ccagaagca tagtcacatt tgccactcag cagtcagtat 3294
 gttgcagtgg gcagtaggtg aagagaaggt gaaatgggat gagaatcact gtaaacagca 3354
 acaactgggg taaaaatctc cttagaaagc ttttggctcg gggagaaaaga gagacacgag 3414
 gctttaatga gattagaaat cctttagaat ttgtggtaaa agtcatttag taaaagcaaa 3474
 aaagtaattt cccacctggg aaaggtgaat aaggggagat acctgtcaca ccataccgag 3534
 taaagagtaa acgaggagtc ctattaatat gaaagagatg caaccagtgt gttgacgtgc 3594
 agaactgccg acatttagtg gcattaccta gcttgtaatg caggaatta aaaggcttat 3654
 aatccatgtg tctgttaaaa cggaactcat catatttagt tgtgcccata gtctttcact 3714
 ggagtgagaa tggaaagtgg gaagatactg actgtaaccc caatgtgagt gacctggctt 3774
 tcagcagact tcataaagag ctgatgctag ctggcacacc taittaagac gtttaggggt 3834
 tttctgctgt aagaatattg aatctgcttt gcatggatct gcttggcaaa gtctgttctg 3894
 cagat 3899

<210> 7

<211> 325

<212> PRT

<213> Mus musculus

<400> 7

Met Ser Glu Gln Ser Lys Asp Leu Ser Asp Pro Asn Phe Ala Ala Glu

1

5

10

15

Ala Pro Asp Cys Glu Met Gln Asp Ser Asp Ala Val Pro Val Gly Ile

20

25

30

Pro Pro Pro Ala Ser Leu Ala Ala Asn Leu Ala Gly Pro Pro Cys Ala
 35 40 45
 Pro Glu Gly Pro Met Ala Ala Gln Gln Ala Ser Pro Pro Pro Glu Glu
 50 55 60
 Arg Ile Glu Asp Val Asp Pro Lys Ile Leu Gln Gln Ala Ala Glu Glu
 65 70 75 80
 Gly Arg Ala His Gln Pro Gln Ser Pro Ala Arg Pro Ile Pro Ala Pro
 85 90 95
 Pro Ala Pro Ala Gln Leu Val Gln Lys Ala His Glu Leu Met Trp Tyr
 100 105 110
 Val Leu Val Lys Asp Gln Lys Arg Met Val Leu Trp Phe Pro Asp Met
 115 120 125
 Val Lys Glu Val Met Gly Ser Tyr Lys Lys Trp Cys Arg Ser Ile Leu
 130 135 140
 Arg Arg Thr Ser Val Ile Leu Ala Arg Val Phe Gly Leu His Leu Arg
 145 150 155 160
 Leu Thr Asn Leu His Thr Met Glu Phe Ala Leu Val Lys Ala Leu Ser
 165 170 175
 Pro Glu Glu Leu Asp Arg Val Ala Leu Asn Asn Arg Met Pro Met Thr
 180 185 190
 Gly Leu Leu Leu Met Ile Leu Ser Leu Ile Tyr Val Lys Gly Arg Gly
 195 200 205
 Ala Arg Glu Gly Ala Val Trp Asn Val Leu Arg Ile Leu Gly Leu Arg
 210 215 220
 Pro Trp Lys Lys His Ser Thr Phe Gly Asp Val Arg Lys Ile Ile Thr
 225 230 235 240
 Glu Glu Phe Val Gln Gln Asn Tyr Leu Lys Tyr Gln Arg Val Pro His
 245 250 255
 Ile Glu Pro Pro Glu Tyr Glu Phe Phe Trp Gly Ser Arg Ala Asn Arg

260 265 270
 Glu Ile Thr Lys Met Gln Ile Met Glu Phe Leu Ala Arg Val Phe Lys
 275 280 285
 Lys Asp Pro Gln Ala Trp Pro Ser Arg Tyr Arg Glu Ala Leu Glu Gln
 290 295 300
 Ala Arg Ala Leu Arg Glu Ala Asn Leu Ala Ala Gln Ala Pro Arg Ser
 305 310 315 320
 Ser Val Ser Glu Asp
 325

<210> 8

<211> 3959

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (154).. (3372)

<400> 8

ggggccgcgg gggaggaggt ggagcccact gccgaggggc cggaccgggc caccgcgata 60
 taaaagagcc ggagtcaccag agctgccgca gtgctgcctg ccccgctcca gcccgcact 120
 cccgctccgc tggcggccgc acctgctccg gcc atg atg agc ttc ggc agc gcc 174

Met Met Ser Phe Gly Ser Ala

1

5

gat gcg ctg ctg ggc gcc ccg ttc gcg ccg ctg cac gga ggc ggc agc 222
 Asp Ala Leu Leu Gly Ala Pro Phe Ala Pro Leu His Gly Gly Gly Ser

10

15

20

ctg cac tac tcg ctg agc cgc aag gca ggc ccg ggc ggc acg cgc tcc 270

Leu His Tyr Ser Leu Ser Arg Lys Ala Gly Pro Gly Gly Thr Arg Ser
 25 30 35
 gcg gcc ggc tcc tcc agc ggc ttc cac tcg tgg gcg cgg acg tcc gtg 318
 Ala Ala Gly Ser Ser Ser Gly Phe His Ser Trp Ala Arg Thr Ser Val
 40 45 50 55
 agc tcc gtg tcc gcc tca ccc agc cgc ttc cgc ggc gcc gcc tcg agc 366
 Ser Ser Val Ser Ala Ser Pro Ser Arg Phe Arg Gly Ala Ala Ser Ser
 60 65 70
 acc gac tcg cta gac acc cta agc aac ggc cca gag ggc tgc gtg gtg 414
 Thr Asp Ser Leu Asp Thr Leu Ser Asn Gly Pro Glu Gly Cys Val Val
 75 80 85
 gcg gcg gtg gcg gcg cgc agc gag aag gag cag ctg cag gct ctg aac 462
 Ala Ala Val Ala Ala Arg Ser Glu Lys Glu Gln Leu Gln Ala Leu Asn
 90 95 100
 gac cgc ttc gcg ggc tac atc gac aag gtg agg cag ctc gag gcg cac 510
 Asp Arg Phe Ala Gly Tyr Ile Asp Lys Val Arg Gln Leu Glu Ala His
 105 110 115
 aac cgc agc ctg gag ggc gag gcg gcg gcg ctg cgg cag caa caa gcc 558
 Asn Arg Ser Leu Glu Gly Glu Ala Ala Ala Leu Arg Gln Gln Gln Ala
 120 125 130 135
 ggc cgc gcc gcc atg ggc gag ctg tac gag cgc gag gtg cgc gag atg 606
 Gly Arg Ala Ala Met Gly Glu Leu Tyr Glu Arg Glu Val Arg Glu Met
 140 145 150
 cgc ggc gcc gtg ctg cgc ctc ggg gcg gcg cgc ggg cag ctg cgc ctg 654
 Arg Gly Ala Val Leu Arg Leu Gly Ala Ala Arg Gly Gln Leu Arg Leu
 155 160 165
 gag cag gag cac ctg ctg gag gac atc gct cac gtc cgc cag cgg ctg 702
 Glu Gln Glu His Leu Leu Glu Asp Ile Ala His Val Arg Gln Arg Leu
 170 175 180

gac gag gag gcc cgg cag cgt gag gag gcg gag gcg gcg gcg cgc gcc 750
 Asp Glu Glu Ala Arg Gln Arg Glu Glu Ala Glu Ala Ala Ala Arg Ala
 185 190 195
 ctg gcg cgc ttc gcg cag gag gcg gaa gcg gcg cgc gtg gag ctg cag 798
 Leu Ala Arg Phe Ala Gln Glu Ala Glu Ala Ala Arg Val Glu Leu Gln
 200 205 210 215
 aag aag gcg cag gcg ctg cag gag gag tgc ggc tac ctg cgg cgc cac 846
 Lys Lys Ala Gln Ala Leu Gln Glu Glu Cys Gly Tyr Leu Arg Arg His
 220 225 230
 cac cag gag gag gtg ggc gag ctg ctc ggt cag atc cag ggc tgc ggg 894
 His Gln Glu Glu Val Gly Glu Leu Leu Gly Gln Ile Gln Gly Cys Gly
 235 240 245
 gcc gcg cag gcg cag gct cag gcc gag gct cgc gac gcc ctc aag tgc 942
 Ala Ala Gln Ala Gln Ala Gln Ala Glu Ala Arg Asp Ala Leu Lys Cys
 250 255 260
 gac gtg acg tcg gcg ctg cgg gag atc cgc gcg cag ctc gaa ggc cac 990
 Asp Val Thr Ser Ala Leu Arg Glu Ile Arg Ala Gln Leu Glu Gly His
 265 270 275
 gcg gtg cag agc acg ctg cag tcc gag gag tgg ttc cga gtg agg ttg 1038
 Ala Val Gln Ser Thr Leu Gln Ser Glu Glu Trp Phe Arg Val Arg Leu
 280 285 290 295
 gac cga ctc tca gag gca gcc aaa gtg aac aca gat gct atg cgc tcg 1086
 Asp Arg Leu Ser Glu Ala Ala Lys Val Asn Thr Asp Ala Met Arg Ser
 300 305 310
 gcc caa gag gag ata act gag tac cgg cgg cag ctg caa gcc agg acc 1134
 Ala Gln Glu Glu Ile Thr Glu Tyr Arg Arg Gln Leu Gln Ala Arg Thr
 315 320 325
 aca gag ttg gag gcc ctg aaa agc acc aag gag tca ctg gag agg cag 1182
 Thr Glu Leu Glu Ala Leu Lys Ser Thr Lys Glu Ser Leu Glu Arg Gln


```

      330              335              340
cgc tct gag cta gag gac cgt cat cag gca gac att gcc tcc tac cag 1230
Arg Ser Glu Leu Glu Asp Arg His Gln Ala Asp Ile Ala Ser Tyr Gln

      345              350              355
gac gct att cag cag ctg gac agt gag ctg aga aac acc aag tgg gag 1278
Asp Ala Ile Gln Gln Leu Asp Ser Glu Leu Arg Asn Thr Lys Trp Glu

360              365              370              375
atg gct gca cag ctc cga gag tac cag gac ctg ctc aac gtc aag atg 1326
Met Ala Ala Gln Leu Arg Glu Tyr Gln Asp Leu Leu Asn Val Lys Met

              380              385              390
gcc ctg gac att gag att gcc gct tac aga aag ctc ctg gaa ggc gaa 1374
Ala Leu Asp Ile Glu Ile Ala Ala Tyr Arg Lys Leu Leu Glu Gly Glu

              395              400              405
gag tgt cgg att ggc ttt ggt ccg agt ccc ttc tct ctt act gaa gga 1422
Glu Cys Arg Ile Gly Phe Gly Pro Ser Pro Phe Ser Leu Thr Glu Gly

      410              415              420
ctc cca aaa att ccc tcc ata tcc acg cac ata aaa gtc aaa agc gaa 1470
Leu Pro Lys Ile Pro Ser Ile Ser Thr His Ile Lys Val Lys Ser Glu

      425              430              435
gag atg ata aag gta gta gag aaa tcc gag aag gaa act gtg att gta 1518
Glu Met Ile Lys Val Val Glu Lys Ser Glu Lys Glu Thr Val Ile Val

440              445              450              455
gaa gga cag aca gaa gag atc cgg gtg acg gaa gga gtg aca gaa gag 1566
Glu Gly Gln Thr Glu Glu Ile Arg Val Thr Glu Gly Val Thr Glu Glu

              460              465              470
gag gac aaa gag gcc caa ggt cag gaa gga gaa gaa gca gaa gag gga 1614
Glu Asp Lys Glu Ala Gln Gly Gln Glu Gly Glu Glu Ala Glu Glu Gly

      475              480              485
gaa gaa aaa gaa gaa gag gaa gga gca gca gct aca tct ccc cct gca 1662

```

Glu Glu Lys Glu Glu Glu Glu Gly Ala Ala Ala Thr Ser Pro Pro Ala	
490	495
500	
gaa gag gct gca tct cca gaa aaa gaa acc aag tct cgt gtg aaa gaa	1710
Glu Glu Ala Ala Ser Pro Glu Lys Glu Thr Lys Ser Arg Val Lys Glu	
505	510
515	
gag gcc aag tcc cca ggt gag gcc aag tcc cca ggt gag gcc aag tcc	1758
Glu Ala Lys Ser Pro Gly Glu Ala Lys Ser Pro Gly Glu Ala Lys Ser	
520	525
530	535
cca ggt gag gcc aag tcc cca gct gag gcc aag tcc cca ggt gag gcc	1806
Pro Gly Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Gly Glu Ala	
540	545
550	
aag tcc cca cgt gag gcc aag tcc cca ggt gag gcc aag tct cca gct	1854
Lys Ser Pro Arg Glu Ala Lys Ser Pro Gly Glu Ala Lys Ser Pro Ala	
555	560
565	
gag ccc aag tct cca gct gag ccc aag tct cca gct gag gcc aag tca	1902
Glu Pro Lys Ser Pro Ala Glu Pro Lys Ser Pro Ala Glu Ala Lys Ser	
570	575
580	
cca gct gag ccc aag tct cca gct aca gtg aag tct cca ggt gag gcc	1950
Pro Ala Glu Pro Lys Ser Pro Ala Thr Val Lys Ser Pro Gly Glu Ala	
585	590
595	
aag tca cca tct gag gcc aaa tct cca gct gaa gcc aaa tct cca gct	1998
Lys Ser Pro Ser Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala	
600	605
610	615
gag gcc aaa tct cca gct gag gcc aaa tct cca gct gag gcc aag tca	2046
Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser	
620	625
630	
cca gct gaa gcc aag tca cca gct gaa gcc aaa tct cca gct aca gtg	2094
Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Thr Val	
635	640
645	

aag tct cca ggt gag gcc aag tca cca tct gag gcc aaa tct cca gct	2142
Lys Ser Pro Gly Glu Ala Lys Ser Pro Ser Glu Ala Lys Ser Pro Ala	
650 655 660	
gaa gcc aaa tct cca gct gag gcc aaa tct cca gct gag gcc aaa tct	2190
Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser	
665 670 675	
cca gct gag gtc aag tca cca ggt gag gcc aag tct cca gct gag ccc	2238
Pro Ala Glu Val Lys Ser Pro Gly Glu Ala Lys Ser Pro Ala Glu Pro	
680 685 690 695	
aag tca cca gct gag gcc aaa tct cca gct gca gtg aag tca cca gct	2286
Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Ala Val Lys Ser Pro Ala	
700 705 710	
gag gcc aag tct cca gct gca gtc aag tcc cca ggt gag gcc aag tcc	2334
Glu Ala Lys Ser Pro Ala Ala Val Lys Ser Pro Gly Glu Ala Lys Ser	
715 720 725	
cca ggt gag gcc aag tca cca gct gag gcc aaa tct cca gct gag gcc	2382
Pro Gly Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala	
730 735 740	
aag tca cca att gag gta aaa tct cca gag aag gcc aag acc ccc gtc	2430
Lys Ser Pro Ile Glu Val Lys Ser Pro Glu Lys Ala Lys Thr Pro Val	
745 750 755	
aag gaa gga gca aaa tct cca gct gag gcc aag tct cct gag aag gcc	2478
Lys Glu Gly Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Glu Lys Ala	
760 765 770 775	
aag tcc ccc gtg aag gaa gat atc aag ccc cca gct gag gcg aaa tcc	2526
Lys Ser Pro Val Lys Glu Asp Ile Lys Pro Pro Ala Glu Ala Lys Ser	
780 785 790	
cct gag aag gcc aag agc ccc atg aag gaa gga gca aag cct cct gag	2574
Pro Glu Lys Ala Lys Ser Pro Met Lys Glu Gly Ala Lys Pro Pro Glu	

795	800	805	
aag gcc aag cct cta gat gtg aag tct ccg gaa gcc cag act cca gta			2622
Lys Ala Lys Pro Leu Asp Val Lys Ser Pro Glu Ala Gln Thr Pro Val			
810	815	820	
cag gag gaa gcg aac gac ccc aca gac atc aga ccc cct gag cag gtg			2670
Gln Glu Glu Ala Asn Asp Pro Thr Asp Ile Arg Pro Pro Glu Gln Val			
825	830	835	
aaa agt cct gcc aag gag aag gcc aag tcc cct gag aag gaa gaa gcc			2718
Lys Ser Pro Ala Lys Glu Lys Ala Lys Ser Pro Glu Lys Glu Glu Ala			
840	845	850	855
aag act tct gaa aag gtg gct ccc aag aag gaa gag gtg aag tcc cct			2766
Lys Thr Ser Glu Lys Val Ala Pro Lys Lys Glu Glu Val Lys Ser Pro			
860	865	870	
gtg aag gag gag gta aaa gcc aaa gaa ccc cca aag aag gta gaa gaa			2814
Val Lys Glu Glu Val Lys Ala Lys Glu Pro Pro Lys Lys Val Glu Glu			
875	880	885	
gag aag aca ctg cct aca cca aag aca gag gcg aag gag agt aag aaa			2862
Glu Lys Thr Leu Pro Thr Pro Lys Thr Glu Ala Lys Glu Ser Lys Lys			
890	895	900	
gac gaa gct ccc aag gag gcc ccg aag ccc aag gtg gag gag aag aag			2910
Asp Glu Ala Pro Lys Glu Ala Pro Lys Pro Lys Val Glu Glu Lys Lys			
905	910	915	
gaa act ccc acg gaa aag ccc aag gac tct aca gca gaa gcc aag aag			2958
Glu Thr Pro Thr Glu Lys Pro Lys Asp Ser Thr Ala Glu Ala Lys Lys			
920	925	930	935
gaa gag gct gga gag aag aag aaa gcc gtg gcc tca gag gag gag act			3006
Glu Glu Ala Gly Glu Lys Lys Lys Ala Val Ala Ser Glu Glu Glu Thr			
940	945	950	
cct gcc aag ttg ggt gtg aag gaa gaa gct aaa ccc aaa gag aag aca			3054

Pro Ala Lys Leu Gly Val Lys Glu Glu Ala Lys Pro Lys Glu Lys Thr
 955 960 965
 gag aca acc aag aca gaa gca gaa gac acc aag gcc aaa gaa cct agc 3102
 Glu Thr Thr Lys Thr Glu Ala Glu Asp Thr Lys Ala Lys Glu Pro Ser
 970 975 980
 aaa ccc aca gag acg gaa aag cca aag aaa gag gag atg cca gcg gca 3150
 Lys Pro Thr Glu Thr Glu Lys Pro Lys Lys Glu Glu Met Pro Ala Ala
 985 990 995
 cca gag aag aaa gac acc aag gag gag aag acc aca gag tcc agg aag 3198
 Pro Glu Lys Lys Asp Thr Lys Glu Glu Lys Thr Thr Glu Ser Arg Lys
 1000 1005 1010 1015
 cct gag gag aag ccc aaa atg gag gcc aag gtc aag gag gat gac aag 3246
 Pro Glu Glu Lys Pro Lys Met Glu Ala Lys Val Lys Glu Asp Asp Lys
 1020 1025 1030
 agc ctt tcc aaa gag cct agc aaa ccc aag aca gaa aag gct gaa aaa 3294
 Ser Leu Ser Lys Glu Pro Ser Lys Pro Lys Thr Glu Lys Ala Glu Lys
 1035 1040 1045
 tcc tct agc aca gac cag aaa gaa agc cag ccc cca gag aag acc aca 3342
 Ser Ser Ser Thr Asp Gln Lys Glu Ser Gln Pro Pro Glu Lys Thr Thr
 1050 1055 1060
 gag gac aag gcc acc aag gga gag aag taa gagaacaaga gaaacaccca 3392
 Glu Asp Lys Ala Thr Lys Gly Glu Lys
 1065 1070
 gaatagccaa agaaactcag gacgggtccca gtactcaggg gtcggcgtaa taaattttat 3452
 ttcttccttt cctccgtaa gaagaaacac tgcttagatg gtgggcctgc cctcaccaaa 3512
 caggaatttc tattaagatt aagttagcaa gagaagataa ccctgagcct tgtccccac 3572
 gccgaaaacc ctccccaggt gatggacaat taigatagct tcttgtagcc gaacgtgatg 3632
 tatgctgaac gctacgcgta aaacacgcgt ctaaaaactg cccctcctt tccaagtaag 3692
 tgcatttatt tctgtatgt ccaactgaca gatgaccgca ataatgaatg agcagttaga 3752

aacgcattat gcttgaaatg ttgtaacctt ttcctgaatg ccttcttggt ttccaaagga 3812
 gtggtcaggc ccttgcccag tacacgtcc tggaagagct gcagcaggtg aggcaggcg 3872
 ctggccactg aaccacgcca ggggtgtact tccactgaag tccactttca attgcttcca 3932
 tgcaataaaa ccaagtgcct ctgaaat 3959

<210> 9

<211> 1072

<212> PRT

<213> Mus musculus

<400> 9

Met Met Ser Phe Gly Ser Ala Asp Ala Leu Leu Gly Ala Pro Phe Ala
 1 5 10 15
 Pro Leu His Gly Gly Gly Ser Leu His Tyr Ser Leu Ser Arg Lys Ala
 20 25 30
 Gly Pro Gly Gly Thr Arg Ser Ala Ala Gly Ser Ser Ser Gly Phe His
 35 40 45
 Ser Trp Ala Arg Thr Ser Val Ser Ser Val Ser Ala Ser Pro Ser Arg
 50 55 60
 Phe Arg Gly Ala Ala Ser Ser Thr Asp Ser Leu Asp Thr Leu Ser Asn
 65 70 75 80
 Gly Pro Glu Gly Cys Val Val Ala Ala Val Ala Ala Arg Ser Glu Lys
 85 90 95
 Glu Gln Leu Gln Ala Leu Asn Asp Arg Phe Ala Gly Tyr Ile Asp Lys
 100 105 110
 Val Arg Gln Leu Glu Ala His Asn Arg Ser Leu Glu Gly Glu Ala Ala
 115 120 125
 Ala Leu Arg Gln Gln Gln Ala Gly Arg Ala Ala Met Gly Glu Leu Tyr
 130 135 140

Glu Arg Glu Val Arg Glu Met Arg Gly Ala Val Leu Arg Leu Gly Ala
 145 150 155 160
 Ala Arg Gly Gln Leu Arg Leu Glu Gln Glu His Leu Leu Glu Asp Ile
 165 170 175
 Ala His Val Arg Gln Arg Leu Asp Glu Glu Ala Arg Gln Arg Glu Glu
 180 185 190
 Ala Glu Ala Ala Ala Arg Ala Leu Ala Arg Phe Ala Gln Glu Ala Glu
 195 200 205
 Ala Ala Arg Val Glu Leu Gln Lys Lys Ala Gln Ala Leu Gln Glu Glu
 210 215 220
 Cys Gly Tyr Leu Arg Arg His His Gln Glu Glu Val Gly Glu Leu Leu
 225 230 235 240
 Gly Gln Ile Gln Gly Cys Gly Ala Ala Gln Ala Gln Ala Gln Ala Glu
 245 250 255
 Ala Arg Asp Ala Leu Lys Cys Asp Val Thr Ser Ala Leu Arg Glu Ile
 260 265 270
 Arg Ala Gln Leu Glu Gly His Ala Val Gln Ser Thr Leu Gln Ser Glu
 275 280 285
 Glu Trp Phe Arg Val Arg Leu Asp Arg Leu Ser Glu Ala Ala Lys Val
 290 295 300
 Asn Thr Asp Ala Met Arg Ser Ala Gln Glu Glu Ile Thr Glu Tyr Arg
 305 310 315 320
 Arg Gln Leu Gln Ala Arg Thr Thr Glu Leu Glu Ala Leu Lys Ser Thr
 325 330 335
 Lys Glu Ser Leu Glu Arg Gln Arg Ser Glu Leu Glu Asp Arg His Gln
 340 345 350
 Ala Asp Ile Ala Ser Tyr Gln Asp Ala Ile Gln Gln Leu Asp Ser Glu
 355 360 365
 Leu Arg Asn Thr Lys Trp Glu Met Ala Ala Gln Leu Arg Glu Tyr Gln

370	375	380
Asp Leu Leu Asn Val Lys Met Ala Leu Asp Ile Glu Ile Ala Ala Tyr		
385	390	395
Arg Lys Leu Leu Glu Gly Glu Glu Cys Arg Ile Gly Phe Gly Pro Ser		400
405	410	415
Pro Phe Ser Leu Thr Glu Gly Leu Pro Lys Ile Pro Ser Ile Ser Thr		
420	425	430
His Ile Lys Val Lys Ser Glu Glu Met Ile Lys Val Val Glu Lys Ser		
435	440	445
Glu Lys Glu Thr Val Ile Val Glu Gly Gln Thr Glu Glu Ile Arg Val		
450	455	460
Thr Glu Gly Val Thr Glu Glu Glu Asp Lys Glu Ala Gln Gly Gln Glu		
465	470	475
Gly Glu Glu Ala Glu Glu Gly Glu Glu Lys Glu Glu Glu Glu Gly Ala		480
485	490	495
Ala Ala Thr Ser Pro Pro Ala Glu Glu Ala Ala Ser Pro Glu Lys Glu		
500	505	510
Thr Lys Ser Arg Val Lys Glu Glu Ala Lys Ser Pro Gly Glu Ala Lys		
515	520	525
Ser Pro Gly Glu Ala Lys Ser Pro Gly Glu Ala Lys Ser Pro Ala Glu		
530	535	540
Ala Lys Ser Pro Gly Glu Ala Lys Ser Pro Arg Glu Ala Lys Ser Pro		
545	550	555
Gly Glu Ala Lys Ser Pro Ala Glu Pro Lys Ser Pro Ala Glu Pro Lys		560
565	570	575
Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Pro Lys Ser Pro Ala Thr		
580	585	590
Val Lys Ser Pro Gly Glu Ala Lys Ser Pro Ser Glu Ala Lys Ser Pro		
595	600	605

Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys
 610 615 620
 Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu
 625 630 635 640
 Ala Lys Ser Pro Ala Thr Val Lys Ser Pro Gly Glu Ala Lys Ser Pro
 645 650 655
 Ser Glu Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Ala Lys
 660 665 670
 Ser Pro Ala Glu Ala Lys Ser Pro Ala Glu Val Lys Ser Pro Gly Glu
 675 680 685
 Ala Lys Ser Pro Ala Glu Pro Lys Ser Pro Ala Glu Ala Lys Ser Pro
 690 695 700
 Ala Ala Val Lys Ser Pro Ala Glu Ala Lys Ser Pro Ala Ala Val Lys
 705 710 715 720
 Ser Pro Gly Glu Ala Lys Ser Pro Gly Glu Ala Lys Ser Pro Ala Glu
 725 730 735
 Ala Lys Ser Pro Ala Glu Ala Lys Ser Pro Ile Glu Val Lys Ser Pro
 740 745 750
 Glu Lys Ala Lys Thr Pro Val Lys Glu Gly Ala Lys Ser Pro Ala Glu
 755 760 765
 Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Val Lys Glu Asp Ile Lys
 770 775 780
 Pro Pro Ala Glu Ala Lys Ser Pro Glu Lys Ala Lys Ser Pro Met Lys
 785 790 795 800
 Glu Gly Ala Lys Pro Pro Glu Lys Ala Lys Pro Leu Asp Val Lys Ser
 805 810 815
 Pro Glu Ala Gln Thr Pro Val Gln Glu Glu Ala Asn Asp Pro Thr Asp
 820 825 830
 Ile Arg Pro Pro Glu Gln Val Lys Ser Pro Ala Lys Glu Lys Ala Lys

835	840	845
Ser Pro Glu Lys Glu Glu Ala Lys Thr Ser Glu Lys Val Ala Pro Lys		
850	855	860
Lys Glu Glu Val Lys Ser Pro Val Lys Glu Glu Val Lys Ala Lys Glu		
865	870	875
Pro Pro Lys Lys Val Glu Glu Glu Lys Thr Leu Pro Thr Pro Lys Thr		
885	890	895
Glu Ala Lys Glu Ser Lys Lys Asp Glu Ala Pro Lys Glu Ala Pro Lys		
900	905	910
Pro Lys Val Glu Glu Lys Lys Glu Thr Pro Thr Glu Lys Pro Lys Asp		
915	920	925
Ser Thr Ala Glu Ala Lys Lys Glu Glu Ala Gly Glu Lys Lys Lys Ala		
930	935	940
Val Ala Ser Glu Glu Glu Thr Pro Ala Lys Leu Gly Val Lys Glu Glu		
945	950	955
Ala Lys Pro Lys Glu Lys Thr Glu Thr Thr Lys Thr Glu Ala Glu Asp		
965	970	975
Thr Lys Ala Lys Glu Pro Ser Lys Pro Thr Glu Thr Glu Lys Pro Lys		
980	985	990
Lys Glu Glu Met Pro Ala Ala Pro Glu Lys Lys Asp Thr Lys Glu Glu		
995	1000	1005
Lys Thr Thr Glu Ser Arg Lys Pro Glu Glu Lys Pro Lys Met Glu Ala		
1010	1015	1020
Lys Val Lys Glu Asp Asp Lys Ser Leu Ser Lys Glu Pro Ser Lys Pro		
1025	1030	1035
Lys Thr Glu Lys Ala Glu Lys Ser Ser Ser Thr Asp Gln Lys Glu Ser		
1045	1050	1055
Gln Pro Pro Glu Lys Thr Thr Glu Asp Lys Ala Thr Lys Gly Glu Lys		
1060	1065	1070

<210> 10

<211> 665

<212> DNA

<213> *Mus musculus*

<400> 10

```
agcgtttccg gtgcgggcag tcgcagccgg cggtaaagcc ttgtcatctg aaggggacca 60
tggccaacag tgagcgcacc ttcatcgcca tcaagccctga tgggggtccag cgggggctgg 120
tgggcgagat catcaagcgg ttcgagcaga aggggttccg ccttgttggg ctgaagtctc 180
tgcaggcttc agaggacctt ctcaaggagc actacactga cctgaaggac cgccccctct 240
ttactggcct ggtgaaatac atgcactcag gaccagtggg tgctatgggc tgggagggtc 300
tgaatgtggg gaagacaggc cgcgigatgc ttggagagac caaccccgca gactctaagc 360
ctgggaccat acgaggagac ttctgcatcc aagtltggcag gaacatcatt catggcagcg 420
attctgtaaa gagcgcagag aaggagatca gcttgtgggt tcagcctgag gagctgggtg 480
agtacaagag ctgtcgcaga actggatcta tgagtgcagc gacgggtgctg gttttctacc 540
tgcttactct tgttttcaca ggcaggggac aagaaccgta gatatttctg gaattctttg 600
acctgnaang accctttggg actgtgactc ctgtgcagtg ttacgtcact gttagattaa 660
gtgtt 665
```

<210> 11

<211> 364

<212> DNA

<213> *Mus musculus*

<400> 11

```
gattgatgct acctccaaag acagagcagt acgtggaact tcacaaaggc gaggtggtag 60
atgtcatggg cattggacgg ctatgatggg gaccaacagg agaaagtttt gatgcatgtc 120
cacatatcat tgactgtatc ctgtaatatg caacggcaca gctagttttt ctgatctgga 180
```

taaaagt tga tctgtat agt caacatc ttg aactatattt caaatgaaat ttaaatacct 240
 tttaaagaaa aaaaaaacac ctaagaataa atctcaacag acaactctat tctgattata 300
 tcaaagcaaa attttccttt ctgcaaatt gctttgtgtg ttcaatgcta ggctc gatag 360
 cgat 364

<210> 12

<211> 470

<212> DNA

<213> Mus musculus

<400> 12

t c g g t t t g g g c t c a g c a c g c c t g a a g c a g a a a a a g a a a a a g c t t a a a a a a a c a c a a a a 60
 g c c t c a a a a a c c t t a a a a a a a a a a a a a g a a a g a a a a g a g a g g a a a a a a a a a g c a a a 120
 a g g g a t c c c t c g t t g a g a a a a t c t g g g g t g g g a a t g t c t t c a t c a a g a a c c t g g a c a a a 180
 t c c a t a g a c a a c a a g g c a c t g t a t g a c a c t t t c t c t g c c t t t g g a a c a t c t t g t c c t g t 240
 a a g g t g g t c t g t g a t g a g a a c g g c t c t a a g g g c t a t g c t t t t g t t c a c t t c g a g a c c c a a 300
 g a g g c c g c c g a c a a g g g c a t c g a g a a g a t g a a t g g c a t g c t t c t c a a t g a c c g t a a a g t g 360
 t t c g t g g g t a g a t t c a a g t c t c g c a a a a a c c g g a a a c g g a t t t t g g g a g c c a a g g g c a a 420
 g g a a t t t c a c a a t g t t t a t a t t c a a a a c t t t t g g a g a a a g t g g a t t a t g 470

<210> 13

<211> 814

<212> DNA

<213> Mus musculus

<220>

<221> exon

<222> (13).. (762)

<400> 13

tatcattaac ag aaa agc ctt cta aaa aaa cta ctc tca gag aaa ccc aag 51
 gac cga cct gag aca tct gaa atc ctg aag acc ttg gct gaa tgg agg 99
 aac atc tca gag aaa aag aaa aga aac aca tgt tag ggc ctt tct gag 147
 aaa aca ttc ctc tgc cgt ggt ttt cct tta acg atc tgc agt ctg agg 195
 gga gta tca gtg aat att atc ctt ctt ttc tta ata cca ctc tcc cag 243
 aca ggt ttt ggt tag ggt gac cca cag aca ttg tat tta tta ggc tat 291
 gaa aaa gta tgc cca ttt cct caa ttg tta att gct ggg cct gtg gct 339
 ggc tag cta gcc aaa tat gta aat gct tgt ttc tcg tct gcc caa aga 387
 gaa agg cag gct cct gtg tgg gaa gtc aca gag ccc cca aag cca act 435
 gga tga gga agg act ctg gct ttt ggc ata aaa aag agc tgg tag tca 483
 gag ctg ggg cag aag gtc ctg cag aca gac aga cag aca gac aga cag 531
 aca gac aga cag aca gag aca caa aga cat gga cta gaa tgg agg agg 579
 gag gga gga agg gag gga ggg aga gag aga gag aga aag aaa gag aga 627
 gag acc aca tgg aga caa aat ggc tta agt tag ctg ggc tac ctg aga 675
 gac tgt ccc aga aaa cag gcc aac aac ctt cct tat gct ata tag atg 723
 tct cag tgt ctt tat cat taa aca cca agc agg act gct aaaaactctg 772
 caataggggt tttttttcct gttacttcaa aagcaatcct ac 814

<210> 14

<211> 906

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (63).. (653)

<400> 14

cgggctggag cgcccgcccc ggccctcgcc tccctgccga gcttccagcg cctcgggacg 60
 cg atg agg acc tgg gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc 107
 Met Arg Thr Trp Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu
 1 5 10 15
 gcc cat gcc ctg gcc gag gaa gcc gag ata ccc cgg gag ttg atc gag 155
 Ala His Ala Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Leu Ile Glu
 20 25 30
 cgg ctg gct cga agt cag atc cac agc atc cgg gac ctc cag cga ctc 203
 Arg Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu
 35 40 45
 ttg gag ata gac tcc gta ggg gct gag gat gcc ttg gag aca agt ctg 251
 Leu Glu Ile Asp Ser Val Gly Ala Glu Asp Ala Leu Glu Thr Ser Leu
 50 55 60
 aga gcc cat ggg tcc cat gcc att aac cat gtg ccc gag aag cgg cct 299
 Arg Ala His Gly Ser His Ala Ile Asn His Val Pro Glu Lys Arg Pro
 65 70 75
 gtg ccc att cgc agg aag aga agt att gag gaa gcc att cct gca gtt 347
 Val Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Ile Pro Ala Val
 80 85 90 95
 tgc aag acc agg acg gtc att tac gag ata cct cgg agc cag gtg gac 395
 Cys Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp
 100 105 110
 ccc aca tcg gcc aac ttc ctg atc tgg ccc cca tgt gtg gag gtg aag 443
 Pro Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys
 115 120 125
 cgc tgc act ggc tgt tgt aac acc agc agc gtc aag tgc cag cct tca 491
 Arg Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser
 130 135 140
 cgg gtc cac cac cgc agt gtc aag gtg gcc aaa gtg gag tat gtc agg 539

Arg Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg
 145 150 155
 aag aag cca aaa ttg aaa gag gtc cag gtg agg tta gag gaa cac ctg 587
 Lys Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu
 160 165 170 175
 gag tgt gca tgt gcg acc tcc aac ctg aac cca gac cat cgg gag gag 635
 Glu Cys Ala Cys Ala Thr Ser Asn Leu Asn Pro Asp His Arg Glu Glu
 180 185 190
 gag aca gat gtg agg tga gatagagccg gccgcccctc tcccggggac 683
 Glu Thr Asp Val Arg
 195
 acgatgtgcg tggcgtgtga cattcctgaa catactatgt atgggtgcttc attgccaatg 743
 tgcgtgcggt ctttgttctc ctccgtgaaa aaccgtgtcc gaggacaaag agacagtgtc 803
 cgtttgttca gttgtgacatc aaagcaagta ctgtagcact cagagagaca gtgagaaagc 863
 ttccttgtca cagagagcga aaacaaaacc acaaaaaaga aaa 906

<210> 15

<211> 196

<212> PRT

<213> Mus musculus

<400> 15

Met Arg Thr Trp Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
 1 5 10 15
 His Ala Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Leu Ile Glu Arg
 20 25 30
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 Glu Ile Asp Ser Val Gly Ala Glu Asp Ala Leu Glu Thr Ser Leu Arg

50 55 60
 Ala His Gly Ser His Ala Ile Asn His Val Pro Glu Lys Arg Pro Val
 65 70 75 80
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Ile Pro Ala Val Cys
 85 90 95
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Ser Asn Leu Asn Pro Asp His Arg Glu Glu Glu
 180 185 190
 Thr Asp Val Arg
 195

<210> 16

<211> 2146

<212> DNA

<213> Mus musculus

<400> 16

agcgattcgg gaacctgaag aacggcgtga gtgacataaa gaccacaaag tggtttgcca 60
 caactgactg gattgctatt tatcagagaa aggttgaggc tccattcata ccaaagtica 120
 gaggctctgg cgataccagc aacttcgatg actatgaaga agaagaaatc cgtgtgtcta 180

taacagaaaa atgtggaaag gaatittgtg aatittaggg aggagaaaga tagcctggag 240
ctcacactca gcccttgcac gctgtggagg tggaaaggtg agccgagacc tgcctgttgg 300
agcgggttcc aatcccttca ttccagcaac tgcgtgaggt ctttcctgcg tcatcagtgt 360
gcgcicgctc tgcaaccacc tgtgtcccca ggcacgcgtc cgcagcatcg tctgccataa 420
cacgggtgtgc accacgtcct cctggtttgg tttttctcca ccttcctaca tctttctcat 480
tcacttctct gaccagtgtc ccttttattt tcttggtgtt tcagatgggc agtgttatgg 540
ctgtgtgata tttaaaagga aagctacatg ttgctttttg tagttttgag caatatTTTT 600
gctgaccagt ggcttgaaga taaactctct aatgattatt tttatTTTga gtagcttgaa 660
ttcagttttg ccaaaactct tagtaatttt gaagatggaa tgtcttgtca gcatgggaat 720
ttgcataagt aaagataact ttccaggggt cactgatgca gcagtgagtc agagcgccia 780
gagagcagtg aggactcctg gacgagaggc tacgttcccc tgggccttct agtgctcttc 840
actccgtgag atagtaagtg accagacaga taagtgaggg gcatggctcc tgcgcgcagc 900
tgtctccctt ggtaccgacc tctctgtggg ctggagagag gcctaagggt tctgagcctt 960
ggctcttcca tgggggcttc agccagtatt tgaggaaagt gtgactgaga aatgacactt 1020
tgggaggitt ctccgtccct atcgggtgggc tcttaaggga aaagagcaaa cgtgcatttg 1080
gataaatgct aagtcagcag aagccttgat acctgcttgc agcttagagg ttctctcctt 1140
taagggaact tgtctgtttg ctttggttcg taccaggtaa gaaaacaagc aaagcagtag 1200
cttattgcgt cctcttctga gggaagaaga cggcaggcgg gcactgccgc agctctgccg 1260
tgtccctgcc tggctagtga caggagaacg caaagcttga gacactgccca catttgtatt 1320
tcatgctgag ctgtgatata ttaagtacgt cagaattgct aacctcttcc ttctctttca 1380
tagacaggat atgatcatgc ggatacagtt ttcatatttg cttttcctta atttttctat 1440
acattttgcc aattgactta acaatgttgc catcgtgagg acatttcaag cactcttgca 1500
catttagttc agtgttcctt tgtgaataaa tggcttcaact ttttttttac tatactttga 1560
ttagttttaa tttctcacc tcatttatc tctgtatcag tgacctacct taaatagtcc 1620
acttacccaa atagtttaaa atatttcatt tcatgatgaa tctccaagga tataagattg 1680
ttttaagtca gacaaaccct gtgtatatag agcctctcta tctgcctcct tactgggtgca 1740
ggtagggtcat tgacagcagt cctagtcata tgcacacaca cctcaccaa acccttgaag 1800
acattgaaaa tctatctga gacctctct ccacctatct gcatgtgttt tggttgtcaa 1860
gtgtttctgc atggcaatgt cccacagtaa caaataatga tttcagttgg tccacctgta 1920

tttaaaatgt gcaagaaaaa ctgaaatact ctgctgtagc aagtctctgtg taacaaagat 1980
 atatcatcgt gtttaataact gaaagcatca ttgtatataa atactttatt tacttttatg 2040
 tatttcattt aaatccaaga acatgctaata catgtgttct agtatgctac aaatttctctg 2100
 gtagtgttgt tgtatattaa tgtaaaatta cttcaataaa tttatc 2146

<210> 17

<211> 1827

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (460).. (1446)

<400> 17

acaaaaaggaa agcagctgct aagcatcctg agaaaggaga gggagagag acccacagaa 60
 acaggggtcca gggacagtgg aagggcctgg ggctgccatc tgggagccag cccagaccc 120
 cccccccac ggctggagg gctgagacag acagatatcc ttcagacaga cagatggagg 180
 agacagggaa gggctgtcag agcctgagag accagacaga ctgacagggg gaggagggt 240
 gggacaagga cacaagaga gggacaagga gaaggacag ggcagggcag ggaagaagaa 300
 aggaaaagaa aaaagggaag gggaaagagg agaaaggga gaaggcagag gagaacagag 360
 gtgctgggcc agagcaccag gagcctttga agctgcaggc tgtgtcccca gggccagggg 420
 tcaggccagg tcatcagcgt cgtcgggcag gcctgcagc atg aat ggc ccc gca 474

Met Asn Gly Pro Ala

1

5

ctc ctg agg aga aat gct agc aaa cgg ggc ctg gag aag ctg ctg agg 522
 Leu Leu Arg Arg Asn Ala Ser Lys Arg Gly Leu Glu Lys Leu Leu Arg

10

15

20

ctc aca act cag tgg aga gaa gaa gac gag gaa gag gct gcc cgt gag 570

Leu Thr Thr Gln Trp Arg Glu Glu Asp Glu Glu Glu Ala Ala Arg Glu
 25 30 35
 cag cgt caa cgg gag cga gag agg cag cta cag gac cag gac aaa gat 618
 Gln Arg Gln Arg Glu Arg Glu Arg Gln Leu Gln Asp Gln Asp Lys Asp
 40 45 50
 aaa gaa gat gat ggt ggc cat tcc ctg gaa cag cca gga cag cag aca 666
 Lys Glu Asp Asp Gly Gly His Ser Leu Glu Gln Pro Gly Gln Gln Thr
 55 60 65
 ctc atc agc ctg aag tcc tct gaa ctg gat gaa gat gag ggt ttt ggt 714
 Leu Ile Ser Leu Lys Ser Ser Glu Leu Asp Glu Asp Glu Gly Phe Gly
 70 75 80 85
 gac tgg tcc caa aag ccg gag cca cgg cag caa ttc tgg ggg aat gag 762
 Asp Trp Ser Gln Lys Pro Glu Pro Arg Gln Gln Phe Trp Gly Asn Glu
 90 95 100
 ggg act gca gaa ggg act gaa ccc tct caa agc gag aga cca gag gag 810
 Gly Thr Ala Glu Gly Thr Glu Pro Ser Gln Ser Glu Arg Pro Glu Glu
 105 110 115
 aaa caa aca gag gag agt tct cac caa gcc aaa gtc cac ttg gag gag 858
 Lys Gln Thr Glu Glu Ser Ser His Gln Ala Lys Val His Leu Glu Glu
 120 125 130
 tca aac ctg agc tac agg gag ccc gat cca gag gat gct gtt ggg ggt 906
 Ser Asn Leu Ser Tyr Arg Glu Pro Asp Pro Glu Asp Ala Val Gly Gly
 135 140 145
 tct ggg gag gcg gaa gag cat ctg ata cgt cat cag gtc agg acc ccc 954
 Ser Gly Glu Ala Glu Glu His Leu Ile Arg His Gln Val Arg Thr Pro
 150 155 160 165
 agc cct ttg gcc tta gaa gac acc gtt gag ctg agt tca cct ccc ctg 1002
 Ser Pro Leu Ala Leu Glu Asp Thr Val Glu Leu Ser Ser Pro Pro Leu
 170 175 180

agc cct acc acc aaa ctg gct gat agg acc gag tcc ctg aac cgc tcc 1050
 Ser Pro Thr Thr Lys Leu Ala Asp Arg Thr Glu Ser Leu Asn Arg Ser
 185 190 195
 att aaa aag agc aac agt gtg aag aag tct caa cca acc itg ccc att 1098
 Ile Lys Lys Ser Asn Ser Val Lys Lys Ser Gln Pro Thr Leu Pro Ile
 200 205 210
 tcc aca att gat gaa cgc ctg cag cag tat acc cag gcc act gag tct 1146
 Ser Thr Ile Asp Glu Arg Leu Gln Gln Tyr Thr Gln Ala Thr Glu Ser
 215 220 225
 tct ggc cga act cct aag ctg tcc cgc cag ccc tcc ata gag ctg ccc 1194
 Ser Gly Arg Thr Pro Lys Leu Ser Arg Gln Pro Ser Ile Glu Leu Pro
 230 235 240 245
 agc atg gcc gta gcc agt acc aag act ctt tgg gaa aca gga gaa gtg 1242
 Ser Met Ala Val Ala Ser Thr Lys Thr Leu Trp Glu Thr Gly Glu Val
 250 255 260
 cag agt cag tct gct tct aag aca ccc tcc tgc cag gat ata gta gct 1290
 Gln Ser Gln Ser Ala Ser Lys Thr Pro Ser Cys Gln Asp Ile Val Ala
 265 270 275
 gga gac atg agc aag aaa agt ctg tgg gag cag aaa gga ggc tcc aag 1338
 Gly Asp Met Ser Lys Lys Ser Leu Trp Glu Gln Lys Gly Gly Ser Lys
 280 285 290
 atc tca tcc acc atc aag agc acc cca tct gga aag cgg tac aag ttc 1386
 Ile Ser Ser Thr Ile Lys Ser Thr Pro Ser Gly Lys Arg Tyr Lys Phe
 295 300 305
 gtg gcc act gga cat ggg aag tac gag aaa gta ctt gtg gat gag ggc 1434
 Val Ala Thr Gly His Gly Lys Tyr Glu Lys Val Leu Val Asp Glu Gly
 310 315 320 325
 tca gca cca tag accatgtttg catcctggat agactccggc cggatgccac 1486
 Ser Ala Pro

tcccagccct gaccaagaaa ttgtttcttg ttgccagtct ggcttgctct cctgcctcca 1546
 acaaccaagc tgccgatagc ctctcctttt gctcctggac cctccatctt ctcttccttc 1606
 tcattcctttg accaaccctc caactctgct tctcaccatc agctaaagg accagtcctt 1666
 aggggagcca agagctccca aggaaggatg aaggagagaa ggcaagcatc ccaaccagat 1726
 ccaaggggac actgtcccca tgctgaatgc tcaggactct tgggtcctgc cctgtttacg 1786
 gatccctcat ttgtgtaat aaagtgcatt gagtgtcccc t 1827

<210> 18

<211> 328

<212> PRT

<213> Mus musculus

<400> 18

Met	Asn	Gly	Pro	Ala	Leu	Leu	Arg	Arg	Asn	Ala	Ser	Lys	Arg	Gly	Leu
1				5					10					15	
Glu	Lys	Leu	Leu	Arg	Leu	Thr	Thr	Gln	Trp	Arg	Glu	Glu	Asp	Glu	Glu
				20				25						30	
Glu	Ala	Ala	Arg	Glu	Gln	Arg	Gln	Arg	Glu	Arg	Glu	Arg	Gln	Leu	Gln
				35				40						45	
Asp	Gln	Asp	Lys	Asp	Lys	Glu	Asp	Asp	Gly	Gly	His	Ser	Leu	Glu	Gln
				50				55						60	
Pro	Gly	Gln	Gln	Thr	Leu	Ile	Ser	Leu	Lys	Ser	Ser	Glu	Leu	Asp	Glu
65				70				75						80	
Asp	Glu	Gly	Phe	Gly	Asp	Trp	Ser	Gln	Lys	Pro	Glu	Pro	Arg	Gln	Gln
				85				90						95	
Phe	Trp	Gly	Asn	Glu	Gly	Thr	Ala	Glu	Gly	Thr	Glu	Pro	Ser	Gln	Ser
				100				105						110	
Glu	Arg	Pro	Glu	Glu	Lys	Gln	Thr	Glu	Glu	Ser	Ser	His	Gln	Ala	Lys
				115				120						125	

Val His Leu Glu Glu Ser Asn Leu Ser Tyr Arg Glu Pro Asp Pro Glu
 130 135 140
 Asp Ala Val Gly Gly Ser Gly Glu Ala Glu Glu His Leu Ile Arg His
 145 150 155 160
 Gln Val Arg Thr Pro Ser Pro Leu Ala Leu Glu Asp Thr Val Glu Leu
 165 170 175
 Ser Ser Pro Pro Leu Ser Pro Thr Thr Lys Leu Ala Asp Arg Thr Glu
 180 185 190
 Ser Leu Asn Arg Ser Ile Lys Lys Ser Asn Ser Val Lys Lys Ser Gln
 195 200 205
 Pro Thr Leu Pro Ile Ser Thr Ile Asp Glu Arg Leu Gln Gln Tyr Thr
 210 215 220
 Gln Ala Thr Glu Ser Ser Gly Arg Thr Pro Lys Leu Ser Arg Gln Pro
 225 230 235 240
 Ser Ile Glu Leu Pro Ser Met Ala Val Ala Ser Thr Lys Thr Leu Trp
 245 250 255
 Glu Thr Gly Glu Val Gln Ser Gln Ser Ala Ser Lys Thr Pro Ser Cys
 260 265 270
 Gln Asp Ile Val Ala Gly Asp Met Ser Lys Lys Ser Leu Trp Glu Gln
 275 280 285
 Lys Gly Gly Ser Lys Ile Ser Ser Thr Ile Lys Ser Thr Pro Ser Gly
 290 295 300
 Lys Arg Tyr Lys Phe Val Ala Thr Gly His Gly Lys Tyr Glu Lys Val
 305 310 315 320
 Leu Val Asp Glu Gly Ser Ala Pro
 325

<210> 19

<211> 2170

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (24).. (1802)

<400> 19

```

tccggcggct ggcggagtgc gcc atg ccc agc agg acg gac ccc aag atg gac 53
      Met Pro Ser Arg Thr Asp Pro Lys Met Asp
                1                5                10

cgg agc ggc ggc cgc gtc cgt ctg aag gcg cac tac ggc ggg gac atc 101
Arg Ser Gly Gly Arg Val Arg Leu Lys Ala His Tyr Gly Gly Asp Ile
                15                20                25

ctg att acc agc gtg gat gcc atg aca aca ttc aag gac ctc tgt gag 149
Leu Ile Thr Ser Val Asp Ala Met Thr Thr Phe Lys Asp Leu Cys Glu
                30                35                40

gaa gtg cga gac atg tgt ggc ctg cac cag cag cac cca ctc acc ctc 197
Glu Val Arg Asp Met Cys Gly Leu His Gln Gln His Pro Leu Thr Leu
                45                50                55

aag tgg gtg gac agt gaa ggt gac cct tgt act gtg tcc tca cag atg 245
Lys Trp Val Asp Ser Glu Gly Asp Pro Cys Thr Val Ser Ser Gln Met
                60                65                70

gag ctg gag gag gcc ttc cgc ctg gtc tgt cag ggc agg gac gaa gtg 293
Glu Leu Glu Glu Ala Phe Arg Leu Val Cys Gln Gly Arg Asp Glu Val
                75                80                85                90

ctc atc att cat gtt ttc cca agc atc cca gag cag ccg ggc atg cct 341
Leu Ile Ile His Val Phe Pro Ser Ile Pro Glu Gln Pro Gly Met Pro
                95                100                105

```

tgt cct gga gaa gac aag tcc atc tac cgc cgt gga gcc aga aga tgg	389
Cys Pro Gly Glu Asp Lys Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp	
110 115 120	
agg aag ctg tac cga gcc aac ggc cac ctc ttc caa gcc aag cgc ttt	437
Arg Lys Leu Tyr Arg Ala Asn Gly His Leu Phe Gln Ala Lys Arg Phe	
125 130 135	
aac agg gga gcg tac tgc ggc cag tgc agc gaa agg ata tgg ggt ctc	485
Asn Arg Gly Ala Tyr Cys Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu	
140 145 150	
tcg agg cag ggc tac agg tgc atc aac tgc aag ctg ctg gtc cat aaa	533
Ser Arg Gln Gly Tyr Arg Cys Ile Asn Cys Lys Leu Leu Val His Lys	
155 160 165 170	
cgc tgc cac gtc ctc gtc ccg ctg acc tgc agg agg cat atg gat tct	581
Arg Cys His Val Leu Val Pro Leu Thr Cys Arg Arg His Met Asp Ser	
175 180 185	
gtc atg cct tcc caa gag cct cca gta gat ggc aag aac gat ggt gta	629
Val Met Pro Ser Gln Glu Pro Pro Val Asp Gly Lys Asn Asp Gly Val	
190 195 200	
gac ctt cct tca gaa gaa act gat gga att gct tat att tct tca tct	677
Asp Leu Pro Ser Glu Glu Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser	
205 210 215	
cgg aaa cat gat aat atc aaa gat gat tct gag gac ctt aag cct gtc	725
Arg Lys His Asp Asn Ile Lys Asp Asp Ser Glu Asp Leu Lys Pro Val	
220 225 230	
atc gat ggg gtg gat ggg atc aaa atc tct cag ggg ctg ggg ctg caa	773
Ile Asp Gly Val Asp Gly Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln	
235 240 245 250	
gac ttc gac ctc atc aga gtc atc ggg cgt gga agc tat gcc aag gtc	821
Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Ser Tyr Ala Lys Val	

255	260	265	
ctc ctg gtg cgg ttg .aag aaa aac gac cag att tac gcc atg aag gtg			869
Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala Met Lys Val			
270	275	280	
gta aag aag gag ctt gtc cac gac gac gag gat atc gac tgg gtg cag			917
Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp Trp Val Gln			
285	290	295	
aca gag aaa cat gtg ttt gag cag gcg tcc agc aac ccc ttc ctg gtt			965
Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro Phe Leu Val			
300	305	310	
ggc tta cac tcc tgc ttc cag aca acg agc cgg ttg ttc ctg gtc atc			1013
Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe Leu Val Ile			
315	320	325	330
gag tat gtc aat ggc ggg gac ctc atg ttc cac atg cag agg cag aga			1061
Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln Arg Gln Arg			
335	340	345	
aaa ctt cca gag gag cat gcc agg ttc tat gct gct gag atc tgt atc			1109
Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile			
350	355	360	
gct ctc aac ttc ttg cat gag agg ggg atc atc tac cgg gac cta aaa			1157
Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys			
365	370	375	
ctg gac aac gtc ctc ctt gat gcc gac gga cac att aag ctg acg gac			1205
Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys Leu Thr Asp			
380	385	390	
tac ggc atg tgc aag gaa ggt cta ggc ccc ggt gat aca aca agc act			1253
Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr			
395	400	405	410
ttt tgt gga acc ccg aac tat atc gcc ccc gaa atc ctg cga gga gaa			1301

Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu	
415	420
gag tac ggg ttc agc gtg gac tgg tgg gca ctg ggt gtc ctt atg ttt	1349
Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val Leu Met Phe	
430	440
gag atg atg gct ggg cgc tcc ccc ttt gac atc atc acg gac aac cct	1397
Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro	
445	455
gac atg aac act gaa gac tac ctt ttc caa gtt atc ctg gaa aag cca	1445
Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro	
460	470
att cgg att ccc cgt ttc ctg tct gtc aag gcc tca cac gtc tta aaa	1493
Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His Val Leu Lys	
475	485
gga ttt tta aat aag gat ccc aaa gag agg ctt ggc tgc cgg cca cag	1541
Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln	
495	505
act ggg ttt tcc gac atc aag tct cat gcc ttc ttc cga agc ata gac	1589
Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg Ser Ile Asp	
510	520
tgg gac ctg ctg gaa aag aag cag acc ctg cct ccc ttc cag ccc cag	1637
Trp Asp Leu Leu Glu Lys Lys Gln Thr Leu Pro Pro Phe Gln Pro Gln	
525	535
atc aca gat gac tat ggc ctg gac aac ttt gac acg cag ttc acc agc	1685
Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser	
540	550
gag cct gtg cag ctg acc cca gat gat gag gac gtc ata aag agg atc	1733
Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Val Ile Lys Arg Ile	
555	565
	570

gac cag tcc gaa ttt gaa ggc ttt gag tac atc aac cca ctt ctg ctg 1781
 Asp Gln Ser Glu Phe Glu Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu
 575 580 585
 tct gct gag gag tcc gtg tga ggccatgagc atctctgttg tggacacgcc 1832
 Ser Ala Glu Glu Ser Val
 590
 tgtgaatgac cctgtcactt tacccttaac tacagcatat gcatgccagg ccgggcaccg 1892
 aggctccaag cagccaggga gggatgctgg ccaccaagac cgaagagggg gcgtccaaca 1952
 ggcacttcta gacagagcaa tctcttgtgt ccaggcccca gaggctggct ttgtgctgga 2012
 ggaaccgctt cctgtgcaca gaggccctac cggaggggtga gacagccagc cacgccgttt 2072
 ggaaagggtgc acatcttcca cagaaacaga actcgatgca ctgacccgct ccaggaaaag 2132
 ttagcgtgta atgccctgag gaataaagtg taccgatg 2170

 <210> 20
 <211> 592
 <212> PRT
 <213> Mus musculus

 <400> 20
 Met Pro Ser Arg Thr Asp Pro Lys Met Asp Arg Ser Gly Gly Arg Val
 1 5 10 15
 Arg Leu Lys Ala His Tyr Gly Gly Asp Ile Leu Ile Thr Ser Val Asp
 20 25 30
 Ala Met Thr Thr Phe Lys Asp Leu Cys Glu Glu Val Arg Asp Met Cys
 35 40 45
 Gly Leu His Gln Gln His Pro Leu Thr Leu Lys Trp Val Asp Ser Glu
 50 55 60
 Gly Asp Pro Cys Thr Val Ser Ser Gln Met Glu Leu Glu Glu Ala Phe
 65 70 75 80

Arg Leu Val Cys Gln Gly Arg Asp Glu Val Leu Ile Ile His Val Phe
 85 90 95
 Pro Ser Ile Pro Glu Gln Pro Gly Met Pro Cys Pro Gly Glu Asp Lys
 100 105 110
 Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu Tyr Arg Ala
 115 120 125
 Asn Gly His Leu Phe Gln Ala Lys Arg Phe Asn Arg Gly Ala Tyr Cys
 130 135 140
 Gly Gln Cys Ser Glu Arg Ile Trp Gly Leu Ser Arg Gln Gly Tyr Arg
 145 150 155 160
 Cys Ile Asn Cys Lys Leu Leu Val His Lys Arg Cys His Val Leu Val
 165 170 175
 Pro Leu Thr Cys Arg Arg His Met Asp Ser Val Met Pro Ser Gln Glu
 180 185 190
 Pro Pro Val Asp Gly Lys Asn Asp Gly Val Asp Leu Pro Ser Glu Glu
 195 200 205
 Thr Asp Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Asn Ile
 210 215 220
 Lys Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Val Asp Gly
 225 230 235 240
 Ile Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg
 245 250 255
 Val Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg Leu Lys
 260 265 270
 Lys Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val
 275 280 285
 His Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe
 290 295 300
 Glu Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe

305 310 315 320
 Gln Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly
 325 330 335
 Asp Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His
 340 345 350
 Ala Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His
 355 360 365
 Glu Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu
 370 375 380
 Asp Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu
 385 390 395 400
 Gly Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn
 405 410 415
 Tyr Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val
 420 425 430
 Asp Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg
 435 440 445
 Ser Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp
 450 455 460
 Tyr Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe
 465 470 475 480
 Leu Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp
 485 490 495
 Pro Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile
 500 505 510
 Lys Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys
 515 520 525
 Lys Gln Thr Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly
 530 535 540

Leu Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr
 545 550 555 560
 Pro Asp Asp Glu Asp Val Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu
 565 570 575
 Gly Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Ala Glu Glu Ser Val
 580 585 590

<210> 21

<211> 1021

<212> DNA

<213> Mus musculus

<400> 21

ggcgagactc acaagctggt ggtcgtaggc ggcggcggcg tgggcaagag cgcgctgacc 60
 atccagttca tccagtccta ctttgtgtct gactatgata ccaccattga agattcctac 120
 acaaagatct gcactgtgga cggcatccct gcacggctgg acatcctgga cactgcgggg 180
 caagaggaat ttggtgccat gcgggacgag tacatgcgtg ctggcaacgg ctccctgctg 240
 gtgtttgcca ttaacgacag gcagagtttc aatgagggtg gcaagctcct cacacagatc 300
 ctccagagtca aggaccggga tgatttccca ttgtgttggt tgggacaagg cagatctgga 360
 gaaccacgcc aggtccctcc ggtctgaagc ctctctttcg tgttccacga catgacitac 420
 tttagaggcct cagcagactg cgtctgaatg tcatgaggc atttagcagc tggtcgcgct 480
 gtccggaata caggacaaga ctcccgtag ccacctagtc gtcccagaga agatgaggat 540
 gccctgtgcg tgctgtacca aatagcctaa gtgcnacgaa acgtnttgga cnagtgccta 600
 cattactgtt tgccaagggt gtctactgac gtctgttaac tctggctcga gaaagataac 660
 atcgtaatta atcgtgcccc tgggtacatg tgcgtttgca tcacgcttgt cgagagcctt 720
 aggtgnggag atgctacggt atagcccatc caaaaaactt tgagaaaaaa aaaaattgcg 780
 cggggttgct tctttgggtg ttgcacggcg ggggtgtgagg tgtggtggaa ggagagagaa 840
 gtgtgtctgc ttactggacc taggactcta tgacgccnng gaggggggtg gaaccacgac 900
 gttttgtgta cgggatggtt gaaaaggggg ggggtgtgtg aatcttagtg ttatctgcct 960

gcncctntnnn nnnnnnnnnn nnnnnngnnn gnnnnnnnnn nnnnnnnnnn nngnnnnnnn 1020
g 1021

<210> 22

<211> 1728

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1023).. (1688)

<400> 22

gggttcacat tgcccttttt tatttgtaac aggggagcat cctcttccca tcaaggtctc 60
ggcctcacag gcgtccctgt tggcataagg tgatcatctgc ctgcgtacga ggacaacatg 120
gcaggagtg gcgtcctaa cagttctata tctccactgt ccagcaggaa atctctgctc 180
ctgggaaccc ttcttggtaa ctcaacttga gctctctggt agccaggtag tcaactcctt 240
gaactttgac tgtccgtttt gtattatcgt ggctcgacgg gtggctccca gacgatgtcc 300
cgtataaact gaccaagctc ccttttaact gtgggagaat gctggtgtca ttcaaaagca 360
gcattagtc tctctgaggg tcatccaggg acaggaggcc gatggtgact ttgtctgggc 420
cactgagctg taggagtccc atcatattca tggatcatctt caagccaggt aacacagaga 480
acagcgtctt ctccacttg tattcagtg ttttcttgcc tctgttcacc accagtcgtt 540
caggggttgc atggacctgc aggtgaggct tctggatggt cacttcgagc cagagaacc 600
cagtattctc atacttacca gtcacctcca gacctaaaga gccagacca gagatttcaa 660
agtcaattca gagcaatggc ccaaacaagg aatctccctt atgtcctttc tggaacgggg 720
tccccagaag aatctttctt ctctctcttc ttcttcttct tcttcttctt ctctctcttc 780
ttcttcttct tctgggagaac accaaatggc ggatgacgcc ggtgcagcgg gagggcccg 840
aggaccggg ggcccaggat taggtggccg cggccggctt ccgcggagga ttcggcagcg 900
gtcttagggg ccgtggtcgt ggccgaggcc gtggccgtgg tcgaggccgc ggggctcgtg 960

gaggtaaagc tgaagacaag gagtggatcc ccgtcaccaa gctgggccgt ctggttaagg 1020
 ac atg aag atc aag tcc ttg gag gag atc tac ctg ttc tcc ctg ccc 1067
 Met Lys Ile Lys Ser Leu Glu Glu Ile Tyr Leu Phe Ser Leu Pro
 1 5 10 15
 att aag gag tct gag atc att gat ttc ttc ctg ggt gcg tcc cta aag 1115
 Ile Lys Glu Ser Glu Ile Ile Asp Phe Phe Leu Gly Ala Ser Leu Lys
 20 25 30
 gat gag gtt ctg aaa atc atg cca gtg cag aag cag act cgg gct ggc 1163
 Asp Glu Val Leu Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly
 35 40 45
 cag cgg acc agg ttc aag gct ttc gtc gct att ggg gac tac aat ggt 1211
 Gln Arg Thr Arg Phe Lys Ala Phe Val Ala Ile Gly Asp Tyr Asn Gly
 50 55 60
 cac gtt ggt ctt ggt gtt aag tgc tcc aag gag gtt gcc act gcc atc 1259
 His Val Gly Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala Ile
 65 70 75
 cga ggg gcc atc atc ttg gcc aag ctt tcc atc gtc cct gtg cgg aga 1307
 Arg Gly Ala Ile Ile Leu Ala Lys Leu Ser Ile Val Pro Val Arg Arg
 80 85 90 95
 ggc tac tgg ggg aac aag att ggc aag ccc cac act gtt cca tgc aag 1355
 Gly Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys
 100 105 110
 gtg aca ggc cgc tgt ggc tct gtg ctg gtg cgt ctc atc cct gcc ccc 1403
 Val Thr Gly Arg Cys Gly Ser Val Leu Val Arg Leu Ile Pro Ala Pro
 115 120 125
 aga ggc act ggc att gtc tct gct cct gtg ccc aag aag ctc ctg atg 1451
 Arg Gly Thr Gly Ile Val Ser Ala Pro Val Pro Lys Lys Leu Leu Met
 130 135 140
 atg gcc ggt ata gat gac tgc tac act tca gcc aga ggc tgc act gcc 1499

Met Ala Gly Ile Asp Asp Cys Tyr Thr Ser Ala Arg Gly Cys Thr Ala
 145 150 155
 acc ctg ggc aac ttt gct aag gcc acc ttt gat gcc atc tcc aag act 1547
 Thr Leu Gly Asn Phe Ala Lys Ala Thr Phe Asp Ala Ile Ser Lys Thr
 160 165 170 175
 tac agc tac ctg acc ccc gac ctc tgg aaa gag act gtc ttc acc aag 1595
 Tyr Ser Tyr Leu Thr Pro Asp Leu Trp Lys Glu Thr Val Phe Thr Lys
 180 185 190
 tct cct tat cag gaa ttc tcg gat cat ctt gtg aaa acc cac acc aga 1643
 Ser Pro Tyr Gln Glu Phe Ser Asp His Leu Val Lys Thr His Thr Arg
 195 200 205
 gtc tct gtt cag agg acc cag gct cca gct gtg gct acc aca taa 1688
 Val Ser Val Gln Arg Thr Gln Ala Pro Ala Val Ala Thr Thr
 210 215 220
 gggtttttat atgagaaaaa taaaagaatt aagtctgctg 1728

<210> 23

<211> 221

<212> PRT

<213> Mus musculus

<400> 23

Met Lys Ile Lys Ser Leu Glu Glu Ile Tyr Leu Phe Ser Leu Pro Ile
 1 5 10 15
 Lys Glu Ser Glu Ile Ile Asp Phe Phe Leu Gly Ala Ser Leu Lys Asp
 20 25 30
 Glu Val Leu Lys Ile Met Pro Val Gln Lys Gln Thr Arg Ala Gly Gln
 35 40 45
 Arg Thr Arg Phe Lys Ala Phe Val Ala Ile Gly Asp Tyr Asn Gly His

50	55	60
Val Gly Leu Gly Val Lys Cys Ser Lys Glu Val Ala Thr Ala Ile Arg		
65	70	75
Gly Ala Ile Ile Leu Ala Lys Leu Ser Ile Val Pro Val Arg Arg Gly		80
	85	90
Tyr Trp Gly Asn Lys Ile Gly Lys Pro His Thr Val Pro Cys Lys Val		95
	100	105
Thr Gly Arg Cys Gly Ser Val Leu Val Arg Leu Ile Pro Ala Pro Arg		110
	115	120
Gly Thr Gly Ile Val Ser Ala Pro Val Pro Lys Lys Leu Leu Met Met		125
	130	135
Ala Gly Ile Asp Asp Cys Tyr Thr Ser Ala Arg Gly Cys Thr Ala Thr		140
145	150	155
Leu Gly Asn Phe Ala Lys Ala Thr Phe Asp Ala Ile Ser Lys Thr Tyr		160
	165	170
Ser Tyr Leu Thr Pro Asp Leu Trp Lys Glu Thr Val Phe Thr Lys Ser		175
	180	185
Pro Tyr Gln Glu Phe Ser Asp His Leu Val Lys Thr His Thr Arg Val		190
	195	200
Ser Val Gln Arg Thr Gln Ala Pro Ala Val Ala Thr Thr		205
	210	215
		220

<210> 24

<211> 4281

<212> DNA

<213> Mus musculus

<400> 24

ggcccagcct tccccctgggt gctgttcctt ggagacacag tgcctccttc cttgcctctg 60

cttgtgtggg agtttcttac gcccataagc cttggtacta atttcatgat tctaggattg 120
tgctaaggaa gaagtagagt tccctgtggg gccaggttta attcatctcc ttgtcacatt 180
aacaagcagg tggggtagag gtgccttccc caagagctga gaacttatgc tagtaaaatg 240
ctagtagaag cctcttcaaa aacacagact gtctggtgga tctggctggt cagttttaca 300
aatctagttt agacatgcat tcaaagaaat ttaatatcag tcagagaacg gtgatggcat 360
gcctttaatc agagactggg gggactgagg caggcagatt ctctgagttt gaggacagcc 420
tggtctacag agtgagticc aaggacagcc agggctacat agagaaatcc tgtcataaga 480
aatgaaagaa ggtaaaatgg ggggcagggg gagaacagag acagacagaa ggagagagag 540
cgacacacac acactgtctt cctcttggca tcttctatct tccctcagta ttgaccccag 600
gctactatgc cccagaagac tgctacagca cagaaaactg tctcctgtgc tcccatigca 660
caatgaggga gaatgacctg tggatgaaga gctcacagga caccgggaag atttctgtca 720
cagtcctttac aagaaatgac ttgtctggag ttttcccaag ggtggtgcca ggctgtcctt 780
gccctcacct gagcaggag gctcagcata aatgcctgcc tctctcacc tacaccata 840
gatcaccaga tctgcccagg agacaccagg tgagaggcag atccgggcac agaaactgat 900
tgattgctgt gtttctctc agtggaaacct cctggcttct gctcacttgt ggggtttgtg 960
ccaggctgag gagacacatg ggaaatgctt cctactgaat caggggctcc tggaggaagt 1020
ggcgacctg gtggtccctg cctccagac cctctctac tgcctgctg cttctttaga 1080
cagaggtagt tgagcaggca ggatggatgg atgagaactg agcagccttg tggctctgat 1140
ggggggaggt cctgctgaga ggtctcagga ggcactgcta ggacacacat gaatagcagt 1200
aaggagaaat gagcagggcc tgtgtggatg agaggccaag ggggaggcac cagtctgtga 1260
gggtctcctc cagcctctcc tctacccca gcaggatgaa gctactcacc agcctggctt 1320
tctgctccct gctcctggga gtctgcatg gagggttttt ttcatttgtt cagaggctt 1380
tccaaggiaa gctgagaagg cccccactc taggggtgtc ctgagcattc aggggggttg 1440
gactcactgc tctgcttgct ggaaggacca ggggttcctg caagacttcc tgctaagcac 1500
tgcatacagc aggaggcaga caggattatg acccagaatg cttagagcca atctgatctg 1560
actgaaagtc ggcctgacaa ttctcagtg catttatgaa gaacatgagc tactgctggc 1620
atcacctaaa gagctgtgat agctcagagg tccagacagg ctccctgca cctagagtct 1680
caggactggc ttgcatgtg gcctggcatg gagacgtca gtgtttcctt gggaggtcag 1740
aacttgcacc cacagctgag atcatttctc ctaagtttct ttctgcaaga cagcacaaga 1800

cccatgcatt ctactcaaag ggcagtcagc aggtcacggt ggtgcgcatg ttctctgtca 1860
ggatagattc tcgcatcaga gcagatgctc tctgtatgca gccctcctct gccttttgtc 1920
acctcatgat ggaacttcct agattagggg agctacatcc acagcactgt cccttggcta 1980
caggcagtgt gttccctggg ggcattgtca atggctgtag gacattaggt ggctctacta 2040
gggaaaatgtg ctgtggggtc tgtggtagga gctggaaagc atggaagtgg ttagcctgtg 2100
gtaaacagct tccagggctg cagctggcag gccctgatct gtgatgtcat tgccctgcct 2160
ctgtggagtg ctccaccgg ggtgagcggc ctaggcagca ctgtgggcag aaaaacaaac 2220
acagaccata gaagatgtcc taagggctct cctggtttac tctgagaagc cagaggggac 2280
caggccatga tctccagtt catcctctca ggctgctctg agcacagact caggccagga 2340
gtagtttcaa tgtctctgtc ctctcaaagg catgggcaga gtcttttggg tcaagttcct 2400
gtggcttttc ccatgcaggg gctggggaca tgtggcgagc ctacactgac atgaaggaag 2460
ctaactggaa aaactcagac aaatacttcc atgctcgggg gaactatgat gctgctcaaa 2520
ggggtc ccgg gggagtctgg gctgctgaga aaatcaggta actcagaagg ctgggtagca 2580
gggctcgact ctcttgggga aagcagtggc aggtgaactc tggagaagat tctgccactc 2640
taacgtccct cctcctcttg ctgcgaaggc tagtgtgtcc atcaaagccc aatgtatgcc 2700
ctggctgtgt gcagagccag cacacagcca tgctctgtga gcctgctccc aaatgtagac 2760
agggagggac tctcagctca gccctgtgtt tctggctttg tttatctagt gtgagaggac 2820
cagcctgggc tgcccagtgt ctcagcttct atttcctggc actatctggt tectcctgag 2880
ccagcccatg caaaggggag aactggagga tagattgtgt ccacacagct tggtgactga 2940
ctgactcct gtgtgtctgc ttctcctagt gatggaagag aggcctttca ggaattcttc 3000
ggcagaggac atgaggacac cattgtgac caggaagcca acagacatgg ccgcagtggc 3060
aaagacccca attactacag acctcctgga ctgcctgaca aatactgagc gtctcctat 3120
tagctcagta ggttgtgtg ggggcctgag ggtgggtct gggcttcttc ctacctagga 3180
acactgaaga tgctctctgg ggaaacattg tatactcttc atgtgtglat ccacaagg 3240
tttcagaact gagttactct tgcagtagta actgcttgag gaggagagg taataaacag 3300
aaacttgga gtggatctga gcctgcatat ctgtcatga cgatgctttg gggaacactc 3360
ggggcagaca ccactcttct agactctgac atgagtcgct ctagccctt tctcgggcc 3420
tgtgactgtg tgtgtttgtt gtlatttgtg ggctttctg tgtccaggac ctactccct 3480
gtcaatcgtg tgcactgacc agttcctgtg cccagctt agttctcagt ggtgctgcct 3540

ccaggacac acccatgggc cacctcatac gtgggtgtgc tgcagctgtc agtgtggtcc 3600
 tgctccittcc tctacaacac acaatcccaa ggccactcac ctctccatc ctaagaaata 3660
 ctgaggaggg ctttcccttt gacttaggag tgttgctgtc gtgaggaaac accatgtcaa 3720
 agcatctaag gggtgtattg actcgtgtat gtctgtcag tattagaaaa taagtagagt 3780
 cccitgtatg tgaatggttt gattgggcaa gtccgtgtca gtaaaaacat ggtggtgtctg 3840
 aaccccttca aagaacaacc aagcaggctt ttgcatttcc ttgctatgaa accctaggta 3900
 aagcctagat ttacctgtga ccttgatgta aaagagattt tcagtcctct ggtctttgtc 3960
 atagagaacc taggacagaa tccggacagt gtgagctggt gacttacaag gtaaaaggac 4020
 tggtttagagt tgaacaggaa gctaccagg gatgtcaacg tgcataagagc acacaagccc 4080
 ttggcgaccc cgctggacca ggatcacact ggtatctcc tgcaacatct ccaaggcgat 4140
 cagggctcag gccccactgt tatgccccca ttacatcaa ccagtagtcc cctatacag 4200
 gatgtagcat gtgctaattg tacaggatgg ctgcaatcct ggattatagt catcagcaag 4260
 ccttcttcta ctggttaaag c 4281

<210> 25

<211> 3660

<212> DNA

<213> Mus musculus

<400> 25

ttgcaggcga gggcttccac aactaccacc acacctccc cttegactac tctgccagtg 60
 agtaccgctg gcacatcaac ttaccacgt tcttcatega ctgcatggct gccctgggcc 120
 tggcttacga ccggaagaaa gtttctaagg ctactgtctt agccaggatt aagagaactg 180
 gagacgggag tcacaagagt agctgagctt tgggcttctg agttcctgtt tcaaacgttt 240
 tctggcagag atttaatat ctgttgatta actaacaact ggatattgct atcggggtgt 300
 taatgatgca tttaacctat tccggtacag tattcttata aaatgagaaa gctttgatca 360
 cgttttgagg taataaatat tttatttagc taggattaac catgccaaa gacattatat 420
 atttctaagc acacatgata aatgcatata caattttgca caacagcttt aaataataac 480
 aataaatttg aacattctat acagagagga tcaaagccaa ggaacatgct gttttgatgc 540

tagggtgagc atgggtgctca gtccctgttt gtttgcatgg tgtccagctt tgtttcttct 600
ctgtcatcac caccctcagg caaatagttg accaaccact ggccgtgtgc tgtccaccct 660
ccaaagccca ggccaccttt ctgttttctg aaatactgat ccttctctct gaatacatcc 720
ctccctgttc ctagcttcaa gactgtgtcc tcaaataagg atagagcaag tccccgtgc 780
aggttgtgct agatgggatg gagaaattat cttcatttga tacagagcaa gtagattgtc 840
tcgagagaaa agttagcatg cgtgggtatga tttgtaagta aagatggaag agagagagag 900
agagagagag agagagagag agagagagag agaggtagcc atatctaaca gcctacttac 960
caaagacccc aggcctctct gcttggcatg cctcctttct gtccatcctc tgaaccccag 1020
agattagtga gatttgaata attaaatcat tttcagagtg aagggggta atgcagggtc 1080
tgtgctaggg gagggtttta gcttttggta actgaagatt ttttcatgga aaaagtcttc 1140
gtgttcaatg tgcctagaac tgataactaa acagctgaca tttgtcgggg acagatatgg 1200
tgtgaaacta tgaaaatata agcaaaatct tcacttggaa catgaaacta tttcacttag 1260
aaaataatcg aaggaccga ggtgttgctt gggttgccag tttctttcgt ggctgggcag 1320
gaactagtga ggttgagggg cagtgtctgt aagtagctgc taagagggtc atttccagat 1380
gaagcccttg gggaacatct gccagggatc cgcatgggtg tggctccatc cattgcctta 1440
gtttctctct tggatttgtt agaaacttgg cttcccatgg ttttgaacct tccatgcctt 1500
ctttgctttg tggccacca gccgtgctag tgcgtgctag gaagctctta cccacctgat 1560
ttcttctgac atttcttctt ttggcctttt tttctttctc cggacatgca gctagtgtcc 1620
tgagtgtatc aagagcacc aggacttgc tctgtccagg cctgttctc cccagiatc 1680
cgtgggtgtg gaagagctgt gtagcttcag gaagcagagc caggtgccac ctttctgttg 1740
cttccagatc ctccctacct ccaactcatg tgcctctgtc acagtgattt caggaaagct 1800
tggtagaccc tctagcaaca tctcgggtca gaaagtctct ctggtttgtg agttaacagc 1860
tcagctaagt gctgttttgt ctcatgagt taaccactga atgcgagggt tggttgttga 1920
tctgtctcgg tgtgtgtcgg agtagacagc atatgcactt ctccctgtgc gctttgcaag 1980
gtaatgtggc tttggctgat ccatgcaggc aggtagtgtt acagtgtgtc tgaaaggaag 2040
aagttcccca ttttatctgt taaaacacca gagacatggg caagtgtctaa tggacctcac 2100
ttcaggaaga gggctctgct cctgaagcca gtgtgtgatg aaaagtgact gagacctgat 2160
atctaaggtg agacctgata cctaacactc tgtcacacag tccagggccca acagtgtat 2220
aggaaagtct agaagaaaac atcacatcag tatttttagaa ccatcaacca tctcttgtcc 2280

ctatagccca atccagaggc ctggtttita gaactggctg tgtaaggctc caaacactca 2340
gttcacttgt agaatacagag ccttttttcc cccctatgtt aatigaacac gcgctctgag 2400
ctgttttgtt gaagtagaaa atcicataga aaaatcactg tagatctact gacctatagc 2460
cctctggaaa tgcctttgag atggttttac ttttctaggt catagatgcc tgattataaa 2520
gatgaacaat aaaatcagct ttttttctt cttctctgat cttattcccc agatctgatt 2580
caggccatgt tccaaagcaa ggctacattg aggtcctggt gtctttaagt aaaggacatc 2640
tticagatcc tctcaaagaa ggatttataa cagtttccag atgaatgtac taatagcttt 2700
gggtgcctta tctcttttct aatctgtagt gcctgtgagc tcagttctac tctttccctt 2760
agcccgagga ccccttagat cgagtgggaa tagtcaagag gctggctgga gagtcacag 2820
tacattgggt tgcagaaatc ttttacaggc tacattttgg aatttttttt tttttagtaa 2880
gtgatcaaat ttggtgggaa gtaattcgag tgtattcgat tgtattgtcg tctctgttat 2940
cattgtcaaa catgttatag acggcagttg gcactggggc tgctaattct tgggtgtagt 3000
ctctgaaact gtagctccag tgagggtgtg tgaaagggtt gcaaagccac catctgctgg 3060
tgctccagcc aagggtgctc ttagccactg aattgctatg ttatcctttc tcttgtaaca 3120
aaccacccc agagataaag cctttaatca acccaagaaa ctcttgggct aagtatctga 3180
cagttctaca tctcaacagt gtgaattaa tgctcatagc atcagctcag gaggacactc 3240
tgggagagtg ctgacaaaaa agggttatta atactgacct actacttcaa gggcagttct 3300
gaggtgatta gagctttttt taaaaacca gttttgggg atcctcagca gaggtattca 3360
tacagactcc caaagaacta tatatgttcc tgagaccatc gtttagtcta cattgtcttt 3420
cccagagact gacagatatg accagtcaaa gtgcaagact acctaccac tgccatgaaa 3480
accattgcag gaaacctttc ctttctgaa tgagattttt tttttccctt tttatgtggg 3540
gtaattattt gtgaccaag tgtaatttgg atgatitcca ttaatatcaa ctcttgaagc 3600
ctacttgtac tgattgagat tgtatttgtt cctaataaaa gtggatctgg ttgtactgtc 3660

<210> 26

<211> 2772

<212> DNA

<213> Mus musculus

<400> 26

cgtagggaga gagactgggtg ctgagggagc agggctagcc cggacgcgtg tccgcgcctc 60
 ggaggtggca agtaggcagt gtcgggtggc gaggcaacga tggagctcct gcggactatc 120
 acctaccagc cggccgcccgg caccaagatg tgcgagcagg ctctgggcaa agcttgccggc 180
 ggggactcaa agaagaagcg accacagcag ccttctgaag atgggcagcc ccaagcccag 240
 gtgaccccg gggcccgca ccaccatcac caccattccc actcgggacc cgagatctcg 300
 cggattatag tcgaccccac gacggggaag cgctactgcc ggggcaaagt gctgggcaag 360
 ggtggatttg caaagtgtta cgaaatgaca gatctgacaa acaacaagt ctacgctgca 420
 aaaattattc ctacagcag agtagctaaa cctcatcaga gggaaaagat cgacaaagaa 480
 atcgagcttc acagactact gcaccataag catgtcgtgc agttttacca ctactttgaa 540
 gacaaagaaa acatttacat tctcttgaa tactgcagta gaaggccat ggctcacatc 600
 ttgaaagcaa gaaaggigt gacagagcca gaagtccgat actacctcag gcagattgtg 660
 tcaggactca agtatcttca cgaacaagaa atcttgaca gggatctcaa gctagggaaac 720
 ttttttatta atgaagccat ggagctgaag gtgggagact ttggtttggc agccagactg 780
 gaaccactgg aacacagaag gagaacaata tgtggaacc caaattatct ctccccgaa 840
 gtctcaaca aacaaggaca cggctgtgaa tcagacatct gggccttagg ctgtglaatg 900
 tatacgatgc tgctaggaag acctccattc gaaaccacaa atctgaaaga aacgtacagg 960
 tgcataaggg aagcaaggta taccatgccg tctcatctgc tggcccctgc taagcacttg 1020
 atagctagca tgctgtccaa aaaccagag gaccgcccc gtttggatga catcattcgg 1080
 catgacttct tcttcaggg tttcactccg gacagactct ctccagctg ttgccacaca 1140
 gtccagatt tccactgtc aagcccagcc aagaatttct ttaagaaagc cgcagccgct 1200
 ctttttgggtg gcaagaagga caaagcaaga tatacgaca cacacaataa ggtgtctaag 1260
 gaagatgaag acatttaca gcttcggcat gatttgaaga aagtgtcgat aaccagcag 1320
 cctagcaaac acagagcaga cgaggagccc cagccgcctc ccactactgt tgccagatct 1380
 ggaacgtccg cagtggaaaa caaacagcag attggggatg caatccgat gatagtcagg 1440
 gggactctcg gcagctgcag cagcagcagc gaatgccttg aagacagcac catgggaagt 1500
 gttgcagaca cagtggcaag agtccttcga ggatgtctag aaaacatgcc ggaagctgac 1560
 tgtatcccca aagagcagct gagcacgtcc tttcagtggg tcaccaagtg ggtcgactac 1620
 tccaacaaat atggcittgg gtaccagctc tcggaccaca ctgttggcgt ctttticaac 1680


```

aacggggctc acatgagcct ccttccggac aaaaagacag ttcactatta tgcggaactt 1740
ggccaatgct ctgttttccc agcaacagat gccctgaac aatttattag tcaagtgcag 1800
gtgctgaaat acttttctca ttacatggag gagaacctca tggatggtag tgatctcccg 1860
agtggttactg acattcgaag acctcggctc taccctctgc agtgggttaa gtctgataaa 1920
gccttaaatga tgctcttcaa tgacggcaca ttacaggtag atttctacca cgatcataca 1980
aaaatcatca tctgtaacca gaggaagaa taccttctca cctacatcaa tgaggacagg 2040
atctctacaa ctttcagact gacgactctg ctgatgtctg gctgttcgtt agaattgaaa 2100
aatcgaatgg aatatgccct gaacatgctc ttacagagat gtaactgaaa acattattat 2160
tattattatt ataattattt cgagcggacc tcatgggact cttttccact gtgagatcaa 2220
cagggaagcc agcggaaaga tacagagcat gttagagaag tcggacaggi ggtggtagca 2280
atacaattcc tctgtggcct gctggactgc tggaaccaga ccagcctaag gtgtagagtt 2340
gactttggac aatcctgagt gtggagccga gtgcagtttt ccttgagata cctgtcgtga 2400
aaaggtttat gggacagttt ttacagaaaga tgcattgact ctgaagttct ctctgttgag 2460
agcgtcttca gttggaagac ttggaactgt gaatacactt cctgaagggg aggagaagg 2520
gaggttgctc ccttgctgtt taaaggctac aatcagagca gcttttggct gcttaactgt 2580
gaactatggc catacatttt tttttttttt ggttattttt gaatacactt gtggttgga 2640
aagtgcattc cttgttaata aactttttat ttattacagc cccaagagca gtatttatta 2700
tcaagatgtt ctcttttttt atgttgacca ttccaactc ttggcaataa agagtatgac 2760
atagaaaaaa aa 2772

```

<210> 27

<211> 2079

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (90).. (998)

<400> 27

```

gcattcctgc agcccttcag accgccagaa ctcttctgcc gcctgccctgc ctgccctgcct 60
gccctgccctgt gccgagagtt cccagcattc atg agg gcc tgg atc ttc ttt ctc 113
Met Arg Ala Trp Ile Phe Phe Leu
1 5
ctt tgc ctg gcc ggg agg gcc ctg gca gcc cct cag cag act gaa gtt 161
Leu Cys Leu Ala Gly Arg Ala Leu Ala Ala Pro Gln Gln Thr Glu Val
10 15 20
gct gag gag ata gtg gag gag gaa acc gtg gtg gag gag aca ggg gta 209
Ala Glu Glu Ile Val Glu Glu Glu Thr Val Val Glu Glu Thr Gly Val
25 30 35 40
cct gtg ggt gcc aac cca gtc cag gtg gaa atg gga gaa ttt gag gac 257
Pro Val Gly Ala Asn Pro Val Gln Val Glu Met Gly Glu Phe Glu Asp
45 50 55
ggt gca gag gaa acg gtc gag gag gtg gtg gct gac aac ccc tgc cag 305
Gly Ala Glu Glu Thr Val Glu Glu Val Val Ala Asp Asn Pro Cys Gln
60 65 70
aac cat cat tgc aaa cat ggc aag gtg tgt gag ctg gac gag agc aac 353
Asn His His Cys Lys His Gly Lys Val Cys Glu Leu Asp Glu Ser Asn
75 80 85
acc ccc atg tgt gtg tgc cag gac ccc acc agc tgc cct gct ccc att 401
Thr Pro Met Cys Val Cys Gln Asp Pro Thr Ser Cys Pro Ala Pro Ile
90 95 100
ggc gag ttt gag aag gta tgc agc aat gac aac aag acc ttc gac tct 449
Gly Glu Phe Glu Lys Val Cys Ser Asn Asp Asn Lys Thr Phe Asp Ser
105 110 115 120
tcc tgc cac ttc ttt gcc acc aag tgc acc ctg gag ggc acc aag aag 497
Ser Cys His Phe Phe Ala Thr Lys Cys Thr Leu Glu Gly Thr Lys Lys
125 130 135

```

ggc cac aag ctc cac ctg gac tac atc gga cca tgc aaa tac atc gcc 545
 Gly His Lys Leu His Leu Asp Tyr Ile Gly Pro Cys Lys Tyr Ile Ala
 140 145 150
 ccc tgc ctg gat tcc gag ctg acc gaa ttc cct ctg cgc atg cgt gac 593
 Pro Cys Leu Asp Ser Glu Leu Thr Glu Phe Pro Leu Arg Met Arg Asp
 155 160 165
 tgg ctc aaa aat gtc ctg gtc acc ttg tac gag aga gat gag ggc aac 641
 Trp Leu Lys Asn Val Leu Val Thr Leu Tyr Glu Arg Asp Glu Gly Asn
 170 175 180
 aac ctc ctc act gag aag cag aag ctg cgt gtg aag aag atc cat gag 689
 Asn Leu Leu Thr Glu Lys Gln Lys Leu Arg Val Lys Lys Ile His Glu
 185 190 195 200
 aat gag aag cgc ctg gag gct gga gac cac ccc gtg gag ctg ttg gcc 737
 Asn Glu Lys Arg Leu Glu Ala Gly Asp His Pro Val Glu Leu Leu Ala
 205 210 215
 cga gac ttt gag aag aac tac aat atg tac atc ttc cct gtc cac tgg 785
 Arg Asp Phe Glu Lys Asn Tyr Asn Met Tyr Ile Phe Pro Val His Trp
 220 225 230
 cag ttt ggc cag ctg gat cag cac cct att gat ggg tac ctg tcc cac 833
 Gln Phe Gly Gln Leu Asp Gln His Pro Ile Asp Gly Tyr Leu Ser His
 235 240 245
 act gag ctg gcc cca ctg cgt gct ccc ctc atc ccc atg gaa cat tgc 881
 Thr Glu Leu Ala Pro Leu Arg Ala Pro Leu Ile Pro Met Glu His Cys
 250 255 260
 acc aca cgt ttc ttt gag acc tgt gac cta gac aac gac aag tac att 929
 Thr Thr Arg Phe Phe Glu Thr Cys Asp Leu Asp Asn Asp Lys Tyr Ile
 265 270 275 280
 gcc ctg gag gaa tgg gcc ggc tgc ttt ggc atc aag gag cag gac atc 977
 Ala Leu Glu Glu Trp Ala Gly Cys Phe Gly Ile Lys Glu Gln Asp Ile

	285	290	295	
aac aag gat ctg gig atc taa gttcacgcct cctgctgcag tectgaactc				1028
Asn Lys Asp Leu Val Ile				
300				
tctccctctg atgtgtcacc cctcccatta ccccttgtt taaaatgttt ggatggttgg				1088
ctgttcgccc tggggataag gigctaacat agatttaact gaatacatta acgggtgctaa				1148
aaaaaaaaaa aaaacaaagt aagaaagaaa ctagaacca agtcacagca ttttcccaca				1208
taactctgag gccatggccc atccacagcc tcttggctccc ctgcactacc cagtgtctca				1268
ctggctgtgt tggaaacgga gttgcataag ctaccgtcc acaagcacga gatattctta				1328
gcattcatit caattttgca ttgactctt aacactcacc cagactctgt gcttatitca				1388
ttttggggga tgtgggcttt ttcccttgtt ggittggagt taggcagagg gaagttacag				1448
acacaggtac aaaatttggg taaagatact gtgagacctg aggaccacc agtcagaacc				1508
cacatggcaa gtcttagtag cctaggtcaa ggaaagacag aataatccag agctgtggca				1568
cacatgacag actcccagca gcccgggacc ttgctgtctt ctgactctt cgggcgtttc				1628
tttccatgitt tggctgttgg ttttagtttt ggtgagccat gggtagggcca gaacatcact				1688
caactgcaat tgggcatttca ggttcttggc gggagctcta ggcactggga ggctgtttca				1748
ggaaagttag actcaagagg aagacagaaa aggttgtaac gtagaggaag tgagactggt				1808
gaattggttt gatttttttc acatctagat ggctgtcata aagtttctag catgttcccc				1868
ctcacctctc cccacccctt gccacttgaa accttctact aatcaagaga aacttccaag				1928
ccaacggaat ggtcagatct cacaggctga gaaattgttc cctccaagc atttcatgaa				1988
aaagctgctt ctcatiaacc atgcaaactc tcacagcgat gtgaagagct tgacaagtct				2048
ttcaaaataa aaagtaacaa cttagaaacg g				2079

<210> 28

<211> 302

<212> PRT

<213> Mus musculus

<400> 28

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1 5 10 15
 Ala Ala Pro Gln Gln Thr Glu Val Ala Glu Glu Ile Val Glu Glu Glu
 20 25 30
 Thr Val Val Glu Glu Thr Gly Val Pro Val Gly Ala Asn Pro Val Gln
 35 40 45
 Val Glu Met Gly Glu Phe Glu Asp Gly Ala Glu Glu Thr Val Glu Glu
 50 55 60
 Val Val Ala Asp Asn Pro Cys Gln Asn His His Cys Lys His Gly Lys
 65 70 75 80
 Val Cys Glu Leu Asp Glu Ser Asn Thr Pro Met Cys Val Cys Gln Asp
 85 90 95
 Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys Ser
 100 105 110
 Asn Asp Asn Lys Thr Phe Asp Ser Ser Cys His Phe Phe Ala Thr Lys
 115 120 125
 Cys Thr Leu Glu Gly Thr Lys Lys Gly His Lys Leu His Leu Asp Tyr
 130 135 140
 Ile Gly Pro Cys Lys Tyr Ile Ala Pro Cys Leu Asp Ser Glu Leu Thr
 145 150 155 160
 Glu Phe Pro Leu Arg Met Arg Asp Trp Leu Lys Asn Val Leu Val Thr
 165 170 175
 Leu Tyr Glu Arg Asp Glu Gly Asn Asn Leu Leu Thr Glu Lys Gln Lys
 180 185 190
 Leu Arg Val Lys Lys Ile His Glu Asn Glu Lys Arg Leu Glu Ala Gly
 195 200 205
 Asp His Pro Val Glu Leu Leu Ala Arg Asp Phe Glu Lys Asn Tyr Asn
 210 215 220
 Met Tyr Ile Phe Pro Val His Trp Gln Phe Gly Gln Leu Asp Gln His

225 230 235 240
 Pro Ile Asp Gly Tyr Leu Ser His Thr Glu Leu Ala Pro Leu Arg Ala
 245 250 255
 Pro Leu Ile Pro Met Glu His Cys Thr Thr Arg Phe Phe Glu Thr Cys
 260 265 270
 Asp Leu Asp Asn Asp Lys Tyr Ile Ala Leu Glu Glu Trp Ala Gly Cys
 275 280 285
 Phe Gly Ile Lys Glu Gln Asp Ile Asn Lys Asp Leu Val Ile
 290 295 300

<210> 29

<211> 2035

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (61).. (1317)

<400> 29

caccagcacaga gaggctggca gctggctggt ttcagctctg cagactgcag aacacagaag 60
 atg gct ttc att gca gct ctg ggg ctc ttg atg gct ggg atc tgc cct 108
 Met Ala Phe Ile Ala Ala Leu Gly Leu Leu Met Ala Gly Ile Cys Pro
 1 5 10 15
 gct gtc ctc tgc ttc cca gat ggc acg ttg gga atg gat gct gca gtc 156
 Ala Val Leu Cys Phe Pro Asp Gly Thr Leu Gly Met Asp Ala Ala Val
 20 25 30
 caa gaa gac cat gac aat ggg aca caa ctg gac agt ctc aca ttg gcc 204
 Gln Glu Asp His Asp Asn Gly Thr Gln Leu Asp Ser Leu Thr Leu Ala

35	40	45	
tcc atc aac act gac ttt gcc ttc agc ctc tac aag gag ctg gtt ttg	252		
Ser Ile Asn Thr Asp Phe Ala Phe Ser Leu Tyr Lys Glu Leu Val Leu			
50	55	60	
aag aat cca gat aaa aat att gtc ttc tcc cca ctt agc atc tca gcg	300		
Lys Asn Pro Asp Lys Asn Ile Val Phe Ser Pro Leu Ser Ile Ser Ala			
65	70	75	80
gcc ttg gct gtc atg tcc ctg gga gca aag ggc aac acc ctg gaa gag	348		
Ala Leu Ala Val Met Ser Leu Gly Ala Lys Gly Asn Thr Leu Glu Glu			
	85	90	95
att cta gaa ggt ctc aag ttc aat ctt aca gag acc tct gag gca gac	396		
Ile Leu Glu Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu Ala Asp			
100	105	110	
atc cac cag ggc ttt ggg cac ctc cta cag agg ctc aac cag cca aag	444		
Ile His Gln Gly Phe Gly His Leu Leu Gln Arg Leu Asn Gln Pro Lys			
115	120	125	
gac cag gta cag atc agc acg ggt agt gcc ctg ttt att gaa aag cgc	492		
Asp Gln Val Gln Ile Ser Thr Gly Ser Ala Leu Phe Ile Glu Lys Arg			
130	135	140	
cag cag atc ctg aca gaa ttc cag gag aag gca aag act ctg tac cag	540		
Gln Gln Ile Leu Thr Glu Phe Gln Glu Lys Ala Lys Thr Leu Tyr Gln			
145	150	155	160
gct gag gcc ttc aca gca gac ttc cag cag cct cga cag gcc aaa aag	588		
Ala Glu Ala Phe Thr Ala Asp Phe Gln Gln Pro Arg Gln Ala Lys Lys			
	165	170	175
ctc atc aat gac tat gtg agg aaa cag acc cag ggg atg atc aag gaa	636		
Leu Ile Asn Asp Tyr Val Arg Lys Gln Thr Gln Gly Met Ile Lys Glu			
180	185	190	
ctg gtc tca gac ctg gat aaa agg aca ttg atg gtg ctg gtg aat tat	684		

Leu Val Ser Asp Leu Asp Lys Arg Thr Leu Met Val Leu Val Asn Tyr	
195 200 205	
atc tac ttt aaa gcc aaa tgg aag gtg ccc ttt gac cct ctt gac acg	732
Ile Tyr Phe Lys Ala Lys Trp Lys Val Pro Phe Asp Pro Leu Asp Thr	
210 215 220	
ttc aag tct gag ttc tac tgc ggc aag agg agg ccc gtg ata gtg ccc	780
Phe Lys Ser Glu Phe Tyr Cys Gly Lys Arg Arg Pro Val Ile Val Pro	
225 230 235 240	
atg atg agc atg gag gac ctg acc aca ccc tac ttc cga gat gag gag	828
Met Met Ser Met Glu Asp Leu Thr Thr Pro Tyr Phe Arg Asp Glu Glu	
245 250 255	
ctg tcc tgc act gtg gtg gag ctg aag tac aca gga aat gcc agc gcc	876
Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala Ser Ala	
260 265 270	
ctg ttc atc ctc cct gac cag ggc agg atg cag cag gtg gaa gcc agc	924
Leu Phe Ile Leu Pro Asp Gln Gly Arg Met Gln Gln Val Glu Ala Ser	
275 280 285	
tta caa cca gag acc ctg agg aag tgg aag aat tct ctg aaa ccc agg	972
Leu Gln Pro Glu Thr Leu Arg Lys Trp Lys Asn Ser Leu Lys Pro Arg	
290 295 300	
atg ata gat gag ctc cac ctg ccc aag ttc tcc atc tcc acc gac tac	1020
Met Ile Asp Glu Leu His Leu Pro Lys Phe Ser Ile Ser Thr Asp Tyr	
305 310 315 320	
agc ctg gag gat gtc ctt tca aag ctg ggc atc agg gaa gtc ttc tcc	1068
Ser Leu Glu Asp Val Leu Ser Lys Leu Gly Ile Arg Glu Val Phe Ser	
325 330 335	
aca cag gct gac ctg tct gca atc aca gga acc aag gat ctg aga gtg	1116
Thr Gln Ala Asp Leu Ser Ala Ile Thr Gly Thr Lys Asp Leu Arg Val	
340 345 350	

tct cag gtg gtc cac aag gct gtg ctg gat gtg gct gag aca ggc aca 1164
 Ser Gln Val Val His Lys Ala Val Leu Asp Val Ala Glu Thr Gly Thr
 355 360 365
 gaa gca gct gct gcc act gga gtc aaa ttt gtc cca atg tct gcg aaa 1212
 Glu Ala Ala Ala Ala Thr Gly Val Lys Phe Val Pro Met Ser Ala Lys
 370 375 380
 ctg tac cct ctg act gta tat ttc aat cgg cct ttc ctg ata atg atc 1260
 Leu Tyr Pro Leu Thr Val Tyr Phe Asn Arg Pro Phe Leu Ile Met Ile
 385 390 395 400
 ttt gac aca gaa act gaa att gcc ccc ttt ata gcc aag ata gcc aac 1308
 Phe Asp Thr Glu Thr Glu Ile Ala Pro Phe Ile Ala Lys Ile Ala Asn
 405 410 415
 ccc aaa tga gactagaact cccaagtgt tgacgttct tcccgggagc 1357
 Pro Lys
 caggcattga gccgtgtctgt ggggtctccat gtgcattttg gcttccatgc tctgcttggc 1417
 cttagcatgc ctggattaga tagtgactaa ctgigtata acctcatgta cagacatccc 1477
 tgtgggaagt cagtgcctgt ctcccagact tcttggtagc actagcccat gttcctgagc 1537
 ctgaaatttg tcttggtccc taccctgtct ctctccctgt atctgcttcc acccaaaagc 1597
 ctgggcccga tcaagtaagc tcagtcccag tttagactct ggttatgtct cccttcagcc 1657
 ttgtgtctt gatgggactg tgcaaccita caggccaacc catatggacc aagaggaaag 1717
 cttaggtggc cgtgtctat ccgcagcatc taggactact tggtgcccag tctgcctcac 1777
 tctttcattt ctccaggctt tgctccagg cactgcccc ctgcaggatc tcttcacttt 1837
 gtccacatct ggcacagagt tagagccctc acttctgcag ctgcatgggg tctgtgggtc 1897
 agagcagatc ctttcccctg gcactcctac ttagaacaaa gtagcctttc ttttagttcc 1957
 cagctgacca acctcacaca aaagaggaac accaaccaga ataaagaggt aggagcaaag 2017
 gatcaataaa catgtaac 2035

<210> 30

<211> 418

<212> PRT

<213> Mus musculus

<400> 30

Met Ala Phe Ile Ala Ala Leu Gly Leu Leu Met Ala Gly Ile Cys Pro

1 5 10 15

Ala Val Leu Cys Phe Pro Asp Gly Thr Leu Gly Met Asp Ala Ala Val

20 25 30

Gln Glu Asp His Asp Asn Gly Thr Gln Leu Asp Ser Leu Thr Leu Ala

35 40 45

Ser Ile Asn Thr Asp Phe Ala Phe Ser Leu Tyr Lys Glu Leu Val Leu

50 55 60

Lys Asn Pro Asp Lys Asn Ile Val Phe Ser Pro Leu Ser Ile Ser Ala

65 70 75 80

Ala Leu Ala Val Met Ser Leu Gly Ala Lys Gly Asn Thr Leu Glu Glu

85 90 95

Ile Leu Glu Gly Leu Lys Phe Asn Leu Thr Glu Thr Ser Glu Ala Asp

100 105 110

Ile His Gln Gly Phe Gly His Leu Leu Gln Arg Leu Asn Gln Pro Lys

115 120 125

Asp Gln Val Gln Ile Ser Thr Gly Ser Ala Leu Phe Ile Glu Lys Arg

130 135 140

Gln Gln Ile Leu Thr Glu Phe Gln Glu Lys Ala Lys Thr Leu Tyr Gln

145 150 155 160

Ala Glu Ala Phe Thr Ala Asp Phe Gln Gln Pro Arg Gln Ala Lys Lys

165 170 175

Leu Ile Asn Asp Tyr Val Arg Lys Gln Thr Gln Gly Met Ile Lys Glu

180 185 190

Leu Val Ser Asp Leu Asp Lys Arg Thr Leu Met Val Leu Val Asn Tyr

195	200	205
Ile Tyr Phe Lys Ala Lys Trp Lys Val Pro Phe Asp Pro Leu Asp Thr		
210	215	220
Phe Lys Ser Glu Phe Tyr Cys Gly Lys Arg Arg Pro Val Ile Val Pro		
225	230	235
Met Met Ser Met Glu Asp Leu Thr Thr Pro Tyr Phe Arg Asp Glu Glu		
245	250	255
Leu Ser Cys Thr Val Val Glu Leu Lys Tyr Thr Gly Asn Ala Ser Ala		
260	265	270
Leu Phe Ile Leu Pro Asp Gln Gly Arg Met Gln Gln Val Glu Ala Ser		
275	280	285
Leu Gln Pro Glu Thr Leu Arg Lys Trp Lys Asn Ser Leu Lys Pro Arg		
290	295	300
Met Ile Asp Glu Leu His Leu Pro Lys Phe Ser Ile Ser Thr Asp Tyr		
305	310	315
Ser Leu Glu Asp Val Leu Ser Lys Leu Gly Ile Arg Glu Val Phe Ser		
325	330	335
Thr Gln Ala Asp Leu Ser Ala Ile Thr Gly Thr Lys Asp Leu Arg Val		
340	345	350
Ser Gln Val Val His Lys Ala Val Leu Asp Val Ala Glu Thr Gly Thr		
355	360	365
Glu Ala Ala Ala Ala Thr Gly Val Lys Phe Val Pro Met Ser Ala Lys		
370	375	380
Leu Tyr Pro Leu Thr Val Tyr Phe Asn Arg Pro Phe Leu Ile Met Ile		
385	390	395
Phe Asp Thr Glu Thr Glu Ile Ala Pro Phe Ile Ala Lys Ile Ala Asn		
405	410	415
Pro Lys		

<210> 31

<211> 596

<212> DNA

<213> Mus musculus

<400> 31

```

tgaagttgac ctcagagcct cacaccgagg ataaggaagc cctcgttacg attcggctcc 60
tgtgatgtct tgtgtgaaat gtacgtccaa cactgagctt ctcggatacc tgcaggtttt 120
ccctgacctg atggaacgcg tgattgatgt gtgacgagtg attcatgaag ttggagtaga 180
aagcacgaac atcttcagtc gctcagactc tctaaaagct gatcggtagc atcgagcaca 240
tgactgaagg ctttaagtct catctcatcc gtgctgattg gagatctgtg ctacaagaat 300
aacgatgacc aagacaaaagt ggatgagctg gatggcattc ctcgtatcct ggacagcagc 360
aacatcgaat gcaacaactc ctttatgatg cagtgggtgg tgtatgctgt gcgaaatctc 420
actgaagaca tcagccaaaa cgatgatgtc gttaggccaga tggaggagca gggcttggct 480
gacgccaccc tactgaagaa aatgggcttt gaaattgaaa agattgcgga tacctgattc 540
tgaagtctaa taatgcgttc cctcggcct tggaatgcac ttccatttaa acattc 596

```

<210> 32

<211> 5561

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (388).. (1203)

<400> 32

```

ttttttttct tcacctctc ctttttcaag gccccaagc taattatttc tgttgctttg 60
gagtgagcaa ttctgtgggt cctccacca ccaccccaa ttctgaccgg atcccgcctg 120

```

ggggtttctta cggctcgcgc tcactctgcg tgcacctggc ggcctctttt ttttaccccc 180
 caacctgttg caagtcctta atcctcgcaa ttgggacttg cgtgcaggca cctgaatcct 240
 ccttgcctca tatittgcaa gtgtttgggg gagagcacct gctctacctg caagagattt 300
 aaaaggaaaa aaatctccag gctccctctt tctccacaca ctctcgctct cctgccccgc 360
 cccgaggtaa agccagactc cgagaaa atg gtg atc agc gtg gtc ctc ctg ctg 414

Met Val Ile Ser Val Val Leu Leu Leu

1

5

ctg gcc gcc tat gcc gta ccg gct caa ggc ctg ggt tct ttc gtg cat 462
 Leu Ala Ala Tyr Ala Val Pro Ala Gln Gly Leu Gly Ser Phe Val His

10

15

20

25

tgt gaa ccc tgc gac gag aaa gct ctg tcc atg tgt ccc ccc agc cct 510
 Cys Glu Pro Cys Asp Glu Lys Ala Leu Ser Met Cys Pro Pro Ser Pro

30

35

40

ctg ggc tgt gag ctg gtc aaa gag ccc ggc tgt ggc tgc tgc atg act 558
 Leu Gly Cys Glu Leu Val Lys Glu Pro Gly Cys Gly Cys Cys Met Thr

45

50

55

tgc gcc ctg gcg gag gga cag tcg tgt ggt gtc tac aca gag cgc tgc 606
 Cys Ala Leu Ala Glu Gly Gln Ser Cys Gly Val Tyr Thr Glu Arg Cys

60

65

70

gcc cag ggt ttg cgc tgc ctc ccc cgg cag gat gag gag aag ccg ctg 654
 Ala Gln Gly Leu Arg Cys Leu Pro Arg Gln Asp Glu Glu Lys Pro Leu

75

80

85

cac gcc ctg ctg cac ggc cgc ggg gtt tgc ctc aac gaa aag agc tac 702
 His Ala Leu Leu His Gly Arg Gly Val Cys Leu Asn Glu Lys Ser Tyr

90

95

100

105

ggc gag caa acc aag ata gag aga gac tct cgg gaa cac gag gaa ccc 750
 Gly Glu Gln Thr Lys Ile Glu Arg Asp Ser Arg Glu His Glu Glu Pro

110

115

120

acc acc tcc gag atg gct gaa gag acc tac tcc ccc aag gtc ttc cgg 798

Thr Thr Ser Glu Met Ala Glu Glu Thr Tyr Ser Pro Lys Val Phe Arg
 125 130 135
 ccc aag cac act cgc att tcc gag ctg aag gct gag gct gtg aag aag 846
 Pro Lys His Thr Arg Ile Ser Glu Leu Lys Ala Glu Ala Val Lys Lys
 140 145 150
 gac cgc aga aag aag ctg acc cag tcc aag ttt gtg ggg ggt gca gag 894
 Asp Arg Arg Lys Lys Leu Thr Gln Ser Lys Phe Val Gly Gly Ala Glu
 155 160 165
 aac act gcc cac ccc aga gtc atc cct gca cct gag atg aga cag gaa 942
 Asn Thr Ala His Pro Arg Val Ile Pro Ala Pro Glu Met Arg Gln Glu
 170 175 180 185
 tcc gaa caa ggc ccc tgc cgc aga cac atg gaa gct tcc ctc cag gag 990
 Ser Glu Gln Gly Pro Cys Arg Arg His Met Glu Ala Ser Leu Gln Glu
 190 195 200
 ttc aaa gcc agc cca cgc atg gtg ccc cgt gct gtg tac ctg ccc aac 1038
 Phe Lys Ala Ser Pro Arg Met Val Pro Arg Ala Val Tyr Leu Pro Asn
 205 210 215
 tgt gac cgc aaa gga ttc tac aag aga aag cag tgt aag ccc tcc cgt 1086
 Cys Asp Arg Lys Gly Phe Tyr Lys Arg Lys Gln Cys Lys Pro Ser Arg
 220 225 230
 ggc cgc aaa cgt ggc atc tgc tgg tgt gtg gac aag tac gga atg aag 1134
 Gly Arg Lys Arg Gly Ile Cys Trp Cys Val Asp Lys Tyr Gly Met Lys
 235 240 245
 ctg ccg ggc atg gag tac gtg gat ggg gac ttt cag tgc cac gcc ttc 1182
 Leu Pro Gly Met Glu Tyr Val Asp Gly Asp Phe Gln Cys His Ala Phe
 250 255 260 265
 gac agc agt aac gtt gag tga cgcgtcccct ccttcctcc ccctatccta 1233
 Asp Ser Ser Asn Val Glu
 270

ccccccagc cccaaticca gccagcgcc cctccaccc caggacgtca ctcatattcat 1293
ctcatattagg ggaaatatat atacatatat atttgaggaa actgaggacc tcggaatctc 1353
tagcaagggc taaggagaca ctccccacca tgaccccgga aatgtattcc tttttgaagc 1413
aagttgaacg gacagagaag ggaaggagag aagaagcaag agggagcgag agatggaaag 1473
aaagcaaagc gttagaatag aggaaaagag ggaaggacag ataggattag agagagaaga 1533
gagaaacagc aaggcagaaa ggactccaca accaaggctg aatctgccct tttgctttca 1593
gctctagcct ggggtcagaa aaagtgtggc attcagtgac acccagtita gattggticaa 1653
ggggagaaaa gaaacaaggt gtgtcagtg ctcctgggtc tgtccctcc tgcagccagc 1713
agtgtggatg gctagacccc tcacctcct ctcctctac ccaagtgcag ggtgatttca 1773
tccccaaatt tacaagact aaaatgcatt ccatccctct gaaaataaac aaaagtgagt 1833
gattgaagat aggittttccc ccagcagaca agtgaactca gaatgtgtgc aaattttact 1893
cttgittaag atttttttta gaagtcagta cgcaccccca acactggaaa gacttgattc 1953
tcagggtga caagcaattc agaagcgct ggcttcggcc cttagattica ctagactcaa 2013
agctggcccg gcagcctctg tggaggagga tgagaggtag agaaaaccaa ggggcttgta 2073
ctcaccaca agactccatg tagactttat aggcatataa atctattttc tttacctttt 2133
tttccctttc cttttctttc gaagttttgc attacctctt taaagtagtt ttttttagga 2193
cactgaagat cttcctcatt ctgggaaaaa tccataattc acaaatacaa ccagaacgc 2253
cagcttgcc tgcgtccagg cagcctttct cgtgagctac aagtgtggct cttttgtggg 2313
gcaccgattt ggatcttctc atgattccaa acgigtgttg aagtgaatcc accaagccag 2373
gtaactgcca gcaccaagg gtgcatcaag tgcatagecc aggtcacccc atttcagcct 2433
tccaaccgc agaaagtaac tgtctcacac cacaccacat aaacctgcca gatccatctg 2493
taaccactg gcctgcccag acctttttt ccatctgca ttttttttt tgaactgcat 2553
tttgaaagcc tccctcagat gccaggctga cagatcagag agaaactaac atgagagatg 2613
acagaggagg aggaagtga gggtaggggc agagacttcc acagagagac atagaagatg 2673
gagcagaggt ctgggggttg ggaggacaag aaagagacag agagaggaaa ataccaatag 2733
aattttcctt ggtgtctccc atctaataa ctccttgaga tttagagga aaaagaaggc 2793
aggggaagaa cttaggtag aaatgaggtc agttcaagtc acaggccca gatgggtgggt 2853
aactgaggca ggatccagac ttgagacaca cggttggaaa caaggctggt tagcctgact 2913
gggtattgaa gggtagaagag gatgccttg aaagacagca caacttcagt tcaacttcag 2973

gcccccaagg aggaactgag gccaaagaat ccttcaagtg cttcatgagt ctctcttgcc 3033
cgactcaaac atccttccct gtgatggagg atggtagaaa gcccaggaca actcaggccc 3093
ggatcttcac gactgttgtc atttgccagc ctgattttga tccaagagaa gcattctcatt 3153
gcccactggc ttcttcaaca aagagggtgct taacaaaagg ctccaggacta tctttgaaga 3213
ctgaagataa ccttccagga gaggagactc ggacattggt acaggaggcc ctttttgccg 3273
ggggacacag ctctttgccc tctcttgatg gcatggcata gttagaggccc cctccaaccc 3333
ggaacatgga gcaacacaaa gggagagcaa agaaactgac gtgcgtcgac tcataggaca 3393
tgggtggctg cgggcacaga aagggaigcc tcctgttgcc tggacaggac agttggctgg 3453
gaaggaaaga gaaaattgat cttcataaga caaagggcct gatgggatgg caatagaagg 3513
acttaccaga cctgcagggt cagtataccc atcacccgc acaacatccc cagcccccaa 3573
ctcaaacttc aatatatctt aggccagtat cctagacctt agtctctcct ttctgcccatt 3633
atttctccgc atcttgagca gtcatctgac tgagatttgc caagtggata ctgggggtacc 3693
actgcccccc aagaaaagac tgagccagga actgcctact cgctccccct cccgagcctg 3753
gagctaactc ctgtgagggg tgctctcttc accccacaac ttactagacc ttgagtgage 3813
ctctgtccct tatgtgggt cttgcgtgtg agccacagat ggaggtcatt gtatagacag 3873
ttagccttcc ccaggtcagc ctacctccc caaacttgtg agtctccccg ctgctcatai 3933
ggagaggcat gtctaagaca gcaagtcttc tagaggaagc ttgcctttta cagacagatg 3993
gaactaaacc ttccaaatgg gagatctggc tgaaccagg atacagagac catggacatg 4053
gatggggta tcaagagaag agggatgtcc ttctccaggt tagggagaga gaaggcaagt 4113
ttgcaacgat cccatcatgc cctgagcaag aagcttttgg cccaggctag cctttaactc 4173
cattagaggc ctctctgttg ggtttatcca cagcagtagg cccaagtatg gcctgtcccc 4233
accttacta tcccgtggaa ggtttcttcc caccctttt tgacaaatgc ctactcgag 4293
cagtggaaag atagctctct tccccctctt ctgccaggta acaaagagac ctaaccagga 4353
cctattctcc accccagcca gtcttgacca gccagaacaa agcagggaac ctggagaata 4413
aaagacteta cgttcctctg acaaagactc tacgtttctc tgacggccag gcctaaacag 4473
acaaggcttg ggaacatctg ccccacagga tacggaggag gtcagctgtg ctactcctc 4533
ttctccttcc aagaccctct tccgaccatg acttatctcc atggtaacat cctcaccatc 4593
attctccac taccaagggt tgccatggca acctcccaac cacttgcca tccaggcag 4653
gcagctgtcc ttctgtcag aacctagag gactctaggt gaaattttac agcttaagag 4713

aggagt gaggc caaggagaag agaccctgta gtcctctggc tttcaagaga aagaaggcta 4773
 tgattt aaaa cacagtagaa gggaaagagg tctcgtcgag gtcgacctct cccggggagc 4833
 ttaggggttg tactgtcttt attttttaaa ccactaaagt gcaatntttc ctgcactctt 4893
 gttacccgc ctccttcccc tgtaggttt tcatctctt gagcagactt tcttggtttt 4953
 ttaatggagt atagactttc accacttcac agactctggc ctccctctcca agtctctctg 5013
 gatggggaaa aggaaggtag aggtcagag gggaagggt cctcgtcac cccgcatcca 5073
 ttcaccccca ctctcttggt ccctagtcac cggcttcacc ccatctccg acaccatcac 5133
 tgtcacacag tagcctgtca cacgtagt acagttcaga caagactcct tcagattccg 5193
 agacgcctac cggttgtttt tggttttgt tttgtttct tttgtttgtt tgtttgtttg 5253
 ttttttacia cagcaataac cacatcacat attactgtag ctctctatag tgttacgttc 5313
 agacaccgta gctctgtcct ctcttatttt gttaggtttg acttaaaaaa aaatacttat 5373
 gctttttact ggtgaaacag attgaaaaaa aaatigaaca acaaaccagt ttgtgaaaaa 5433
 aaaaaaaaaat gtgaaaaaaaa atcacccga tgtggaagag ctgggtcct ctttagcatt 5493
 ttgtacttaa ggaaataaaa aagaaaaacc tggaagatct cacattttat taaaagtga 5553
 aaaaaaaaaa 5561

<210> 33

<211> 271

<212> PRT

<213> Mus musculus

<400> 33

Met Val Ile Ser Val Val Leu Leu Leu Leu Ala Ala Tyr Ala Val Pro

1

5

10

15

Ala Gln Gly Leu Gly Ser Phe Val His Cys Glu Pro Cys Asp Glu Lys

20

25

30

Ala Leu Ser Met Cys Pro Pro Ser Pro Leu Gly Cys Glu Leu Val Lys

35

40

45

Glu Pro Gly Cys Gly Cys Cys Met Thr Cys Ala Leu Ala Glu Gly Gln

50	55	60
Ser Cys Gly Val Tyr Thr Glu Arg Cys Ala Gln Gly Leu Arg Cys Leu		
65	70	75
Pro Arg Gln Asp Glu Glu Lys Pro Leu His Ala Leu Leu His Gly Arg		
85	90	95
Gly Val Cys Leu Asn Glu Lys Ser Tyr Gly Glu Gln Thr Lys Ile Glu		
100	105	110
Arg Asp Ser Arg Glu His Glu Glu Pro Thr Thr Ser Glu Met Ala Glu		
115	120	125
Glu Thr Tyr Ser Pro Lys Val Phe Arg Pro Lys His Thr Arg Ile Ser		
130	135	140
Glu Leu Lys Ala Glu Ala Val Lys Lys Asp Arg Arg Lys Lys Leu Thr		
145	150	155
Gln Ser Lys Phe Val Gly Gly Ala Glu Asn Thr Ala His Pro Arg Val		
165	170	175
Ile Pro Ala Pro Glu Met Arg Gln Glu Ser Glu Gln Gly Pro Cys Arg		
180	185	190
Arg His Met Glu Ala Ser Leu Gln Glu Phe Lys Ala Ser Pro Arg Met		
195	200	205
Val Pro Arg Ala Val Tyr Leu Pro Asn Cys Asp Arg Lys Gly Phe Tyr		
210	215	220
Lys Arg Lys Gln Cys Lys Pro Ser Arg Gly Arg Lys Arg Gly Ile Cys		
225	230	235
Trp Cys Val Asp Lys Tyr Gly Met Lys Leu Pro Gly Met Glu Tyr Val		
245	250	255
Asp Gly Asp Phe Gln Cys His Ala Phe Asp Ser Ser Asn Val Glu		
260	265	270

<210> 34

<211> 1714

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (227).. (889)

<400> 34

gaattccggg gcagcggagg agccgagccg ggcigcgtc gctcgccgcc cccagcctc 60
 ttctttctcc gccgggtgca ctgccctgcg ccgtccctc gccgtgcgc cccttgacaa 120
 agaggacaga aagtttgcgc gggggagcgg gccaggtgag gaggggcgtg cccggcgccc 180
 cagtcgcgc cccagcagcc ggaccaggc cccagcgcg cccgcc atg ggc gcc 235

Met Gly Ala

1

gcg gcc cgc agc ctc cgg ctg gcg ctc ggc ctc ctg ctg tta gcc tcg 283
 Ala Ala Arg Ser Leu Arg Leu Ala Leu Gly Leu Leu Leu Leu Ala Ser

5

10

15

ctc gtg cgc ccg gcc gac gcc tgc agc tgc tcc ccg gtg cac ccg caa 331
 Leu Val Arg Pro Ala Asp Ala Cys Ser Cys Ser Pro Val His Pro Gln

20

25

30

35

cag gcg ttt tgc aat gca gac gta gtg atc aga gcc aaa gca gtg agc 379
 Gln Ala Phe Cys Asn Ala Asp Val Val Ile Arg Ala Lys Ala Val Ser

40

45

50

gag aag gag gtg gat tcc ggg aat gac atc tat ggc aac ccc atc aag 427
 Glu Lys Glu Val Asp Ser Gly Asn Asp Ile Tyr Gly Asn Pro Ile Lys

55

60

65

agg att cag tat gag atc aag cag ata aag atg ttc aaa gga cct gac 475
 Arg Ile Gln Tyr Glu Ile Lys Gln Ile Lys Met Phe Lys Gly Pro Asp

70	75	80	
aaa gac atc gag ttt atc tac acg gcc ccc tct tca gca gtg tgc ggg	523		
Lys Asp Ile Glu Phe Ile Tyr Thr Ala Pro Ser Ser Ala Val Cys Gly			
85	90	95	
gtc tcg ctg gac gtt gga gga aag aag gag tat cta att gca gga aag	571		
Val Ser Leu Asp Val Gly Gly Lys Lys Glu Tyr Leu Ile Ala Gly Lys			
100	105	110	115
gca gaa gga gat ggc aag atg cac att acc ctc tgt gac ttc att gtg	619		
Ala Glu Gly Asp Gly Lys Met His Ile Thr Leu Cys Asp Phe Ile Val			
120	125	130	
ccc tgg gac acg ctt agc atc acc cag aag aag agc ctg aac cac agg	667		
Pro Trp Asp Thr Leu Ser Ile Thr Gln Lys Lys Ser Leu Asn His Arg			
135	140	145	
tac cag atg ggc tgt gag tgc aag atc act cgc tgt ccc atg atc cct	715		
Tyr Gln Met Gly Cys Glu Cys Lys Ile Thr Arg Cys Pro Met Ile Pro			
150	155	160	
tgc tac atc tcc tcc ccg gat gag tgc ctc tgg atg gac tgg gtc aca	763		
Cys Tyr Ile Ser Ser Pro Asp Glu Cys Leu Trp Met Asp Trp Val Thr			
165	170	175	
gag aag agc atc aat ggg cac cag gcc aag ttc ttc gcc tgc atc aag	811		
Glu Lys Ser Ile Asn Gly His Gln Ala Lys Phe Phe Ala Cys Ile Lys			
180	185	190	195
aga agt gat ggt tct tgc gcg tgg tac cgc ggg gcg gca ccc ccc aag	859		
Arg Ser Asp Gly Ser Cys Ala Trp Tyr Arg Gly Ala Ala Pro Pro Lys			
200	205	210	
caa gag ttt ctt gac atc gag gac ccg taa gaaggctgac agagcccctg	909		
Gln Glu Phe Leu Asp Ile Glu Asp Pro			
215	220		
tggccaattg aaaagcctct gagggtttag actgggtccag ctttgacatc ccttcctgga	969		

aacagcatga ataaaacatc aatcatccaa gtgggttcac gctaggttga ttctgcccc 1029
 tcccctatit tccctagaca tggtagtggg tctggaggga caggcgggcc aggttccctg 1089
 ccataccctt tccctctgcc agcctgagca ctgtgtgtct cagtctttga tccctgtctac 1149
 aggcaggagt ggagcacaga cttgtttacca ggtctctctg gcactgtcac atgcagcaga 1209
 caggcagcat taagggtacc ctagctctgt tagggcagag ctgggaatgt gcattttgca 1269
 gaaactcttg aaggttgtg taagacigtg tagccggcct accaggctct tttcctctg 1329
 agagtacat gtccctcggt ttctgcagtg gccacctctc tctctggccc ttgcaaatgc 1389
 ttcccatccc tctgtcatct ggtatggact ttcaggacct tggctctcct cgggtctaaag 1449
 aatcacctc caaccagtgg ttcatTTTT taggagctcc agtcagcccc atgaatccac 1509
 agacttcagc gaatggaagc cctccctgag ccgtgtttct ggcttcaacc aagtcattgc 1569
 tgccttctc tcccctgtct ctacacacac cctcagtggg gtctgtgagg tctcatgtctg 1629
 ggggcaggga tctgtggtga ggggtgcttg gcagtccttg ttgccactct caagcttccc 1689
 aagccattct tcaccccccg gaatt 1714

<210> 35

<211> 220

<212> PRT

<213> Mus musculus

<400> 35

Met Gly Ala Ala Ala Arg Ser Leu Arg Leu Ala Leu Gly Leu Leu Leu

1 5 10 15

Leu Ala Ser Leu Val Arg Pro Ala Asp Ala Cys Ser Cys Ser Pro Val

20 25 30

His Pro Gln Gln Ala Phe Cys Asn Ala Asp Val Val Ile Arg Ala Lys

35 40 45

Ala Val Ser Glu Lys Glu Val Asp Ser Gly Asn Asp Ile Tyr Gly Asn

50 55 60

Pro Ile Lys Arg Ile Gln Tyr Glu Ile Lys Gln Ile Lys Met Phe Lys

65	70	75	80
Gly Pro Asp Lys Asp Ile Glu Phe Ile Tyr Thr Ala Pro Ser Ser Ala			
	85	90	95
Val Cys Gly Val Ser Leu Asp Val Gly Gly Lys Lys Glu Tyr Leu Ile			
	100	105	110
Ala Gly Lys Ala Glu Gly Asp Gly Lys Met His Ile Thr Leu Cys Asp			
	115	120	125
Phe Ile Val Pro Trp Asp Thr Leu Ser Ile Thr Gln Lys Lys Ser Leu			
	130	135	140
Asn His Arg Tyr Gln Met Gly Cys Glu Cys Lys Ile Thr Arg Cys Pro			
145	150	155	160
Met Ile Pro Cys Tyr Ile Ser Ser Pro Asp Glu Cys Leu Trp Met Asp			
	165	170	175
Trp Val Thr Glu Lys Ser Ile Asn Gly His Gln Ala Lys Phe Phe Ala			
	180	185	190
Cys Ile Lys Arg Ser Asp Gly Ser Cys Ala Trp Tyr Arg Gly Ala Ala			
	195	200	205
Pro Pro Lys Gln Glu Phe Leu Asp Ile Glu Asp Pro			
	210	215	220

<210> 36

<211> 4591

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (317).. (952)

<400> 36

agccctggac tctcgctcac agtgggcagc gggcagccgc cagcgccaag aatcttcttc 60
 tcccgtttct ccgcttcccg atccttctcc gggaggccac tcgttggctc cgcggactcg 120
 tgttccagcg acccttggcc acttagtctt gtcccgcgg gctacttggga aggcacttcc 180
 ccggagctca tcgttggcca ccgtgcacag tgcccggtta aaccagcga gtgagctcgg 240
 actgtagcat cagcgctagc ctcggaact ttgaagaaaa gagcggcagt ccccgagcg 300
 gaccacaaca gctacc atg act ccc tgg ctt ggg ctt gtc gtg ctc ctg agc 352

Met Thr Pro Trp Leu Gly Leu Val Val Leu Leu Ser

1

5

10

tgt tgg agc ctt ggg cac tgg ggc gcg gaa gcg tgc aca tgc tct ccc 400
 Cys Trp Ser Leu Gly His Trp Gly Ala Glu Ala Cys Thr Cys Ser Pro

15

20

25

agc cat ccc cag gat gcc ttc tgc aac tcc gac atc gtg atc cgg gcc 448
 Ser His Pro Gln Asp Ala Phe Cys Asn Ser Asp Ile Val Ile Arg Ala

30

35

40

aaa gtg gtg gga aag aag ctg gtg aag gag ggg ccc ttt ggc act ctg 496
 Lys Val Val Gly Lys Lys Leu Val Lys Glu Gly Pro Phe Gly Thr Leu

45

50

55

60

gtc tac act att aag cag atg aag atg tac cga ggc ttc agt aag atg 544
 Val Tyr Thr Ile Lys Gln Met Lys Met Tyr Arg Gly Phe Ser Lys Met

65

70

75

ccc cac gtg cag tac att cac acg gaa gcc tct gaa agt ctt tgt ggc 592
 Pro His Val Gln Tyr Ile His Thr Glu Ala Ser Glu Ser Leu Cys Gly

80

85

90

ctc aag cta gaa gtc aac aaa tac cag tac ctg ctg aca ggg cgc gtg 640
 Leu Lys Leu Glu Val Asn Lys Tyr Gln Tyr Leu Leu Thr Gly Arg Val

95

100

105

tat gaa ggc aag atg tac aca gga ctg tgc aac ttt gtg gag agg tgg 688
 Tyr Glu Gly Lys Met Tyr Thr Gly Leu Cys Asn Phe Val Glu Arg Trp

110	115	120	
gac cac ctc aca ctg tcc cag cgc aag ggc ctc aat tac cgc tac cac			736
Asp His Leu Thr Leu Ser Gln Arg Lys Gly Leu Asn Tyr Arg Tyr His			
125	130	135	140
ctg ggt tgc aat tgc aag atc aag tcc tgc tac tac ttg cct tgt ttt			784
Leu Gly Cys Asn Cys Lys Ile Lys Ser Cys Tyr Tyr Leu Pro Cys Phe			
	145	150	155
gtg acc tcc aag aat gag tgt ctc tgg acc gac atg ctc tcc aat ttt			832
Val Thr Ser Lys Asn Glu Cys Leu Trp Thr Asp Met Leu Ser Asn Phe			
	160	165	170
ggg tac cct ggc tat cag tcc aaa cac tac gcc tgc atc cgg cag aag			880
Gly Tyr Pro Gly Tyr Gln Ser Lys His Tyr Ala Cys Ile Arg Gln Lys			
	175	180	185
ggt ggc tac tgc agc tgg tac cga gga tgg gct ccc cca gac aag agc			928
Gly Gly Tyr Cys Ser Trp Tyr Arg Gly Trp Ala Pro Pro Asp Lys Ser			
	190	195	200
atc agc aac gcc aca gat ccc tga acccagacct gccccacctc acctccttcc			982
Ile Ser Asn Ala Thr Asp Pro			
205	210		
catcccgccg agcgtccag acactaactc ttcccagatg atgacaatga aattagtgcc			1042
tgttttcttg caaatttagc actggggaca cttaaagtct ctgctgtcta tggagtigat			1102
ttggaaatac cticctggcc cgcacctac ccttctttt ttggtttgac atcaccatt			1162
tccaactggg gatctctggt gccaaagccag aaagaacgga ggcattgtata cacctcttct			1222
tcatgatata taatctatat ttttttagga aaacagaaat tgaaaaattt atccattgg			1282
ggcatttaat agctactctt ctttcttctt cctctcttga ccacatccta gaccagttc			1342
catatacact tcttcatccc aatacacagg aaacatggat aaggaagttg gcagaagtcc			1402
aactgtttcc caatcagtca aaggcagcaa gcagacagac gccaggtatt tgaaaggtct			1462
tctacacaga ggatatacaa ctgtatgtct gggtcagaca gtctgtctat gtgtgcatgt			1522
cagagggaaa gaagagacag actgtaggag tgggtctcac agttatccag ccctgtgata			1582

cttgggttga ccccatgttt cagatcctgg aacaagcatc caagagtaac agaactttct 1642
gagctggcaa aggccttaaac atctgcctgg gttcagcagg caacctgccc gtctgtacaa 1702
aaaactcaaa gggctgagat gaacgtcttt cctctcctgc ctcccatgag acagtcctct 1762
aggaattctt ggggaagtgt ggctggaagc ttgccaactg taagttggag aaacacacac 1822
ctgacactat ccacagatat agtcaagtag atttgatag agaatactat tccaaagtag 1882
tgttagctc atctaggggg atgtgtttat atatacatc gcataatccc acgggggatt 1942
atgagctaata tttttttata ggacacagaa ttctattcaa tgcgtttaa taigcaaata 2002
gtttaatctt ttttttctt ttgtgtttga tgggaaattg tgacattcca agttgacttt 2062
tttttattat ctgaattaaa atttgaaact ctgaccacac tcagtacct actgtcccta 2122
taactggggt tatctgacca tccatctccc ttctttgttc tgctttctgt tcggggtgcc 2182
cttcacttaa ttgccttact ggctggctga cggcagggga gtgtgagagt taggttaggg 2242
ccttctcatg aaaggggcag ttgcacagtg gaatgactcc tctcctggat ctggggacag 2302
catacacttc tccccagct cagtaatggg tgaagtcact tccggaggtg gtcacctcat 2362
agaatgaaca tgattggta ctgagggagc caggctctgc cgtccaaatg taggcctttt 2422
gttgtgtgt atttttgtt ttaaataaaa gtacagtata aattttccta ttaaataaga 2482
ttatittaaag ttttagtgt aacattgcaa tgccaatagt aggtgagagt gtattgcaca 2542
gagttggaga tagtaagggt gtgacattta acacagttac tctgtctttt ttcagattat 2602
gggtatttat cctctattag tatcatatcg ttctattcc actttagaaa cacagttacc 2662
agttgagaga gagagagaga gagagagaga gagagaacaa gtcttagtct gtccccacc 2722
cacacatacc actgccttgt ccagggtgtt gatagaagag caggacagga agacagttca 2782
ggagatgggt gtcaagtttt ctcttggtt atttcattcc ctgcatctt tcccctgtgc 2842
tgacaggggg cagaaggcac aaccatttcc atgggtgtcc gagagaagga gctgaggtca 2902
gcaagccagt ggttcttaag agctgaacct ctggctttac tgttgaagt tgtctatttc 2962
aacctcagag tttcctaata tggcgctcct gatctatctt actcaagtgc cctcccatat 3022
gtatacccca acatctttc catcttaatc cagcatcggg ccattctcaa tccctggtaa 3082
tcacctcct tttacatgga cagacttgag gtgaggccta agtatgaggc acctgaagat 3142
aaaaccaatg ggcagaacca atggccccag tcggcttttg aggtcttggt gagaagtact 3202
ggccacgaaa gggctttgtg taaagttaca tcatcggaga gcggtttttg agctttcaat 3262
aagctatagc ttgttttatt tcacctgtc acttactgta taatttaaaa tcatttatgt 3322

```

agctgagaca ctttgatact tcaattatat cgtgaatggt ttatittgct aaatcatgtg 3382
ccatgtgtag gctgttgtgt gtacactgtg tctaagagaa gaagaaaaga aaaaaaaaaag 3442
aaagaaaccc acatgccatt ttttttttct gattcaaatt ctacagtaga atggagggca 3502
gaattactgg gacacaatca ccactcagct agaatggaga ttcaaggaaa tggaaggtag 3562
tagaaacaga ctctccagc ctctctctca tagaatccta agggtaggaa gaagaagaag 3622
aaaaaaagca aaagcaaac aaaacagaaa tcaaagtag actcaagttc ttgtcctgta 3682
tcaaataacc ctaggtcacc tgccaccac ttccaagac ctttctcta ctcaaccagg 3742
aagtcattgt ttctgcagtc cagagccatg gcaactgaga ttctaagctc tctttgtctc 3802
atccaggcaa cttttctgtc tcccaaccaa ggaattctc tgctcaggct cctgttgccc 3862
aggatagctc tcttctatag ccaggatgtg gagcttaagg agactccaat gtttactttc 3922
tccagtccta gctctgccat ataaacactg tctcatgttg tgcttcttaa acgacaaaaga 3982
acatagtac ttttggggat agatctgtct gggagataat gtgagtcag gaggcattac 4042
tcttccctgc ctacatcaa ggtgccattc aggtagttag cttccagcta cttaacgata 4102
aaaatatcac ttctgtattt gtatcagaga aacttaaaaa aaaaaataa agtctgatgg 4162
tagaaatcca atgaaatggg agaaggcagg agagagaggt cttagtagat ctaagtcagc 4222
tgtttgggtt gaggaggaga gaacccgagg aaatgaccat gctctgggga caggggtacc 4282
ttagattctc tgtctatttt tctcttagca agccagctgt gctgaagccc agtagagatg 4342
aagagacacc agccagagaa aacccccctc agaaggaatg tatttgttgc taaattttgt 4402
agcactgttt acagitttcc tccatgttat ttatgaattt tatattccgt gaatgtatat 4462
tgtcttgtaa tgttgcatag tgttcacttt ttatagctgt cctttattct aaacagtaaa 4522
gtggttttat ttctatcaca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4582
aaaaaaaaa                                     4591

```

<210> 37

<211> 211

<212> PRT

<213> Mus musculus

<400> 37

Met Thr Pro Trp Leu Gly Leu Val Val Leu Leu Ser Cys Trp Ser Leu
 1 5 10 15
 Gly His Trp Gly Ala Glu Ala Cys Thr Cys Ser Pro Ser His Pro Gln
 20 25 30
 Asp Ala Phe Cys Asn Ser Asp Ile Val Ile Arg Ala Lys Val Val Gly
 35 40 45
 Lys Lys Leu Val Lys Glu Gly Pro Phe Gly Thr Leu Val Tyr Thr Ile
 50 55 60
 Lys Gln Met Lys Met Tyr Arg Gly Phe Ser Lys Met Pro His Val Gln
 65 70 75 80
 Tyr Ile His Thr Glu Ala Ser Glu Ser Leu Cys Gly Leu Lys Leu Glu
 85 90 95
 Val Asn Lys Tyr Gln Tyr Leu Leu Thr Gly Arg Val Tyr Glu Gly Lys
 100 105 110
 Met Tyr Thr Gly Leu Cys Asn Phe Val Glu Arg Trp Asp His Leu Thr
 115 120 125
 Leu Ser Gln Arg Lys Gly Leu Asn Tyr Arg Tyr His Leu Gly Cys Asn
 130 135 140
 Cys Lys Ile Lys Ser Cys Tyr Tyr Leu Pro Cys Phe Val Thr Ser Lys
 145 150 155 160
 Asn Glu Cys Leu Trp Thr Asp Met Leu Ser Asn Phe Gly Tyr Pro Gly
 165 170 175
 Tyr Gln Ser Lys His Tyr Ala Cys Ile Arg Gln Lys Gly Gly Tyr Cys
 180 185 190
 Ser Trp Tyr Arg Gly Trp Ala Pro Pro Asp Lys Ser Ile Ser Asn Ala
 195 200 205
 Thr Asp Pro
 210

<210> 38

<211> 1827

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (198).. (1169)

<400> 38

```

cggtctctgc tgcccagctg ctccggagct cccgccgccg gtccgtcccg gtccgggtccc 60
cgcggtcccg gcgtctgcagg gctgccccct gagcggcagc caagcctgac ggaggcgcct 120
gccggcacgc cgggctcgac gcttccttc gctgcacit cticctgccg cagcgcggtg 180
ccggctgggc gggcggg atg gcg gcc gcg gcc cgg ggg agc ggc cgg gcg 230
      Met Ala Ala Ala Ala Arg Gly Ser Gly Arg Ala
              1              5              10
ccg acg cga agg ctg ctc gtg ctc ttg ctg ctt cag ttg ctc tgg gcc 278
Pro Thr Arg Arg Leu Leu Val Leu Leu Leu Leu Gln Leu Leu Trp Ala
              15              20              25
ccg gcc ggg gtc cgc gcc ggc ccg gag gaa gac ctg agc cat cgg aac 326
Pro Ala Gly Val Arg Ala Gly Pro Glu Glu Asp Leu Ser His Arg Asn
              30              35              40
cag gag ccg ccg gcg ccg ccc agc agc tgc agc ccg cag ccc gcg gcg 374
Gln Glu Pro Pro Ala Pro Pro Ser Ser Cys Ser Pro Gln Pro Ala Ala
              45              50              55
gtg cag ggc ctc gag ccg gcc cgg gcc gag aaa gga ttg aca cca gtc 422
Val Gln Gly Leu Glu Pro Ala Arg Ala Glu Lys Gly Leu Thr Pro Val
              60              65              70              75
gcc cca gtt cat acc aac aaa gaa gat gca gct gcc cag acg aat ctg 470

```

Ala Pro Val His Thr Asn Lys Glu Asp Ala Ala Ala Gln Thr Asn Leu
80 85 90
gga ttt atc cat gcg ttt gtg gct gcc ata tca gtc atc ata gtg tcc 518
Gly Phe Ile His Ala Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser
95 100 105
gaa ctc ggc gac aag acg ttt ttc ata gct gcc atc atg gcg atg cgc 566
Glu Leu Gly Asp Lys Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg
110 115 120
tat aac cgg ctg act gtg ctg gcc ggg gcc atg ctg gcc ttg gcc ttg 614
Tyr Asn Arg Leu Thr Val Leu Ala Gly Ala Met Leu Ala Leu Ala Leu
125 130 135
atg aca tgc ttg tcg gtt ttg ttt ggc tat gcc aca aca gtc atc ccc 662
Met Thr Cys Leu Ser Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro
140 145 150 155
agg gtg tat aca tac tat gtt tca act gca ctc ttc gcc att ttt ggc 710
Arg Val Tyr Thr Tyr Tyr Val Ser Thr Ala Leu Phe Ala Ile Phe Gly
160 165 170
att aga atg ctt cgg gaa ggt ttg aag atg agc cca gat gag ggt cag 758
Ile Arg Met Leu Arg Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln
175 180 185
gag gag cta gaa gaa gtc caa gca gag tta aag aag aag gat gaa gaa 806
Glu Glu Leu Glu Glu Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu
190 195 200
ttc caa cga acc aaa ctc tta aat ggg cca gat gtt gaa act ggt aca 854
Phe Gln Arg Thr Lys Leu Leu Asn Gly Pro Asp Val Glu Thr Gly Thr
205 210 215
agc aca gca ata cct cag aaa aag tgg tta cat ttt att tca ccc att 902
Ser Thr Ala Ile Pro Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile
220 225 230 235

ttt gtt caa gcg ctc aca tta acg ttc ttg gca gaa tgg ggc gat cgc 950
 Phe Val Gln Ala Leu Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg
 240 245 250
 tct caa ctc act acc att gtc ctg gca gct aga gag gac cct tat ggt 998
 Ser Gln Leu Thr Thr Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly
 255 260 265
 gta gcg gtg ggt ggc aca gtg gga cac tgc tta tgt act gga ttg gca 1046
 Val Ala Val Gly Gly Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala
 270 275 280
 gta att gga gga agg atg ata gcg caa aag atc tct gtc cga act gtg 1094
 Val Ile Gly Gly Arg Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val
 285 290 295
 aca atc atc gga ggc atc gta ttt ttg gcg ttt gca ttt tct gcc ctg 1142
 Thr Ile Ile Gly Gly Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu
 300 305 310 315
 ttt ata agt cca gag tct ggt ttt taa caagctgttc ttcagtattc 1189
 Phe Ile Ser Pro Glu Ser Gly Phe
 320
 agcttaagat aggcaactct tttctgtaca tagtgtacat tacaactaaa agtaatggga 1249
 aacactgtat ttgttagcat tgatttgtaa gtttgacca cttaattatt atgccccaaa 1309
 gatataatca ttgattttat ttgtaaagat ttttaaaaag gtttgactcc taagtgtggg 1369
 ttctctctag cttaattatg ttgacacctc agcctccact tctgcttgat atacgcgtcc 1429
 actgaagtga ggcigaccat tgagttttct tgtagcatga ccccttata aacacgtttt 1489
 ctctttggtc actgggggtt taatgtatac cttaagcatt tccttgggga aaagaatgaa 1549
 tgacttcac ttttaaaacc atattcciga gccagtaatc agcaatttta tcttgtcitt 1609
 gggaattagg attgtatcaa taacaaatga taagagtgc tggctaggcc cattctccct 1669
 cttatttttt ttaattgggt aggacacca atataaaaat agtcaatatt tgacaacatg 1729
 gacttaccaa attaaaagag aatactatga atgtattcat attttctat attgaataag 1789
 cattgtaaca aacaatgtaa ataaaaggta taactagt 1827

<210> 39

<211> 323

<212> PRT

<213> Mus musculus

<400> 39

Met Ala Ala Ala Ala Arg Gly Ser Gly Arg Ala Pro Thr Arg Arg Leu
 1 5 10 15
 Leu Val Leu Leu Leu Leu Gln Leu Leu Trp Ala Pro Ala Gly Val Arg
 20 25 30
 Ala Gly Pro Glu Glu Asp Leu Ser His Arg Asn Gln Glu Pro Pro Ala
 35 40 45
 Pro Pro Ser Ser Cys Ser Pro Gln Pro Ala Ala Val Gln Gly Leu Glu
 50 55 60
 Pro Ala Arg Ala Glu Lys Gly Leu Thr Pro Val Ala Pro Val His Thr
 65 70 75 80
 Asn Lys Glu Asp Ala Ala Ala Gln Thr Asn Leu Gly Phe Ile His Ala
 85 90 95
 Phe Val Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys
 100 105 110
 Thr Phe Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr
 115 120 125
 Val Leu Ala Gly Ala Met Leu Ala Leu Ala Leu Met Thr Cys Leu Ser
 130 135 140
 Val Leu Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr
 145 150 155 160
 Tyr Val Ser Thr Ala Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg
 165 170 175

Glu Gly Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu
 180 185 190
 Val Gln Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys
 195 200 205
 Leu Leu Asn Gly Pro Asp Val Glu Thr Gly Thr Ser Thr Ala Ile Pro
 210 215 220
 Gln Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu
 225 230 235 240
 Thr Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr
 245 250 255
 Ile Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly
 260 265 270
 Thr Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg
 275 280 285
 Met Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly
 290 295 300
 Ile Val Phe Leu Ala Phe Ala Phe Ser Ala Leu Phe Ile Ser Pro Glu
 305 310 315 320
 Ser Gly Phe

<210> 40

<211> 2519

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (94).. (1773)

<400> 40

gaattccctc aagagctcag cgtcaaggag aggcccctgc aagagtggga aagaagcaag 60
 cactctcggg acacagaaga aacggggagc aaa atg aag aga gag ctg ctg tgt 114

Met Lys Arg Glu Leu Leu Cys

1

5

gta ctg ctg ctt tgt gga ctg gct ttc cca ttg cct gac cag gga ata 162
 Val Leu Leu Leu Cys Gly Leu Ala Phe Pro Leu Pro Asp Gln Gly Ile

10

15

20

cat ggg agg ttc aga aga gga gcc cgg tcc tac aga gcg acc tgc aga 210
 His Gly Arg Phe Arg Arg Gly Ala Arg Ser Tyr Arg Ala Thr Cys Arg

25

30

35

gat gag cca acg cag aca act tac caa cag cac cag tcg tgg ctc cga 258
 Asp Glu Pro Thr Gln Thr Thr Tyr Gln Gln His Gln Ser Trp Leu Arg

40

45

50

55

ccc atg ctc aga agc agc cgg gtg gaa tat tgc cgg tgc aac agc ggc 306
 Pro Met Leu Arg Ser Ser Arg Val Glu Tyr Cys Arg Cys Asn Ser Gly

60

65

70

ctg gta caa tgc cac tca gtg cct gtc cga agt tgc agc gaa cca aga 354
 Leu Val Gln Cys His Ser Val Pro Val Arg Ser Cys Ser Glu Pro Arg

75

80

85

tgc ttc aat ggg ggg acg tgt cag cag gcc ctg tat ttc tct gac ttt 402
 Cys Phe Asn Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe

90

95

100

gtc tgc cag tgc cct gat gga ttt gta ggg aaa cgc tgt gac ata gat 450
 Val Cys Gln Cys Pro Asp Gly Phe Val Gly Lys Arg Cys Asp Ile Asp

105

110

115

acc aga gca aca tgc ttt gag gag cag ggc atc acc tac aga ggc acg 498
 Thr Arg Ala Thr Cys Phe Glu Glu Gln Gly Ile Thr Tyr Arg Gly Thr

120

125

130

135

tgg agc aca gca gaa agt ggg gct gag tgc atc aac tgg aat agc agt	546
Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys Ile Asn Trp Asn Ser Ser	
140 145 150	
gtt ctg tgc ctg aag ccc tac aat gca agg agg cca aat gcc atc aag	594
Val Leu Ser Leu Lys Pro Tyr Asn Ala Arg Arg Pro Asn Ala Ile Lys	
155 160 165	
ctg ggc ctt ggc aat cac aat tac tgc aga aac cca gac cga gac ttg	642
Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp Leu	
170 175 180	
aag ccc tgg tgc tat gtc ttt aag gca ggg aag tat acc acg gag ttc	690
Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Thr Thr Glu Phe	
185 190 195	
tgt agc aca cca gct tgc cct aag gga aaa agc gag gac tgc tat gtt	738
Cys Ser Thr Pro Ala Cys Pro Lys Gly Lys Ser Glu Asp Cys Tyr Val	
200 205 210 215	
ggg aaa ggt gtg act tac cgt ggc acc cac agc ctc acc aca tcc cag	786
Gly Lys Gly Val Thr Tyr Arg Gly Thr His Ser Leu Thr Thr Ser Gln	
220 225 230	
gcc tcc tgc ctc ccc tgg aat tcc ata gtc ctc atg ggc aag agt tac	834
Ala Ser Cys Leu Pro Trp Asn Ser Ile Val Leu Met Gly Lys Ser Tyr	
235 240 245	
aca gcg tgg agg acc aac tcc cag gca ctc ggc ctg gca cga cac aat	882
Thr Ala Trp Arg Thr Asn Ser Gln Ala Leu Gly Leu Ala Arg His Asn	
250 255 260	
tat tgt cgg aat cca gat ggt gat gcc aga cct tgg tgc cat gtg atg	930
Tyr Cys Arg Asn Pro Asp Gly Asp Ala Arg Pro Trp Cys His Val Met	
265 270 275	
aag gac cga aag ctg acg tgg gaa tac tgt gac atg tcc cca tgc tcc	978
Lys Asp Arg Lys Leu Thr Trp Glu Tyr Cys Asp Met Ser Pro Cys Ser	

280	285	290	295	
acc tgt ggc ctg agg cag tac aaa cgg cct cag ttt aga att aaa gga	1026			
Thr Cys Gly Leu Arg Gln Tyr Lys Arg Pro Gln Phe Arg Ile Lys Gly				
	300	305	310	
gga ctc tac aca gac atc acc tca cac cct tgg cag gct gcc atc ttt	1074			
Gly Leu Tyr Thr Asp Ile Thr Ser His Pro Trp Gln Ala Ala Ile Phe				
	315	320	325	
gtc aag aac aag agg tct cct gga gag aga ttc ctt tgt gga ggg gtg	1122			
Val Lys Asn Lys Arg Ser Pro Gly Glu Arg Phe Leu Cys Gly Gly Val				
	330	335	340	
ctg atc agt tcc tgc tgg gtg ctg tca gct gcc cac tgc ttt cta gag	1170			
Leu Ile Ser Ser Cys Trp Val Leu Ser Ala Ala His Cys Phe Leu Glu				
	345	350	355	
agg ttc ccc ccc aat cat ctt aaa gtg gtc ttg ggc aga aca tac agg	1218			
Arg Phe Pro Pro Asn His Leu Lys Val Val Leu Gly Arg Thr Tyr Arg				
	360	365	370	375
gtg gtc ccc gga gag gaa gaa cag aca ttt gag att gaa aaa tac ata	1266			
Val Val Pro Gly Glu Glu Glu Gln Thr Phe Glu Ile Glu Lys Tyr Ile				
	380	385	390	
gtc cat gag gaa ttt gat gac gat act tat gac aac gac atc gca tta	1314			
Val His Glu Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu				
	395	400	405	
ctg cag ctg agg tca cag tcc aag caa tgt gcc caa gag agc agc tct	1362			
Leu Gln Leu Arg Ser Gln Ser Lys Gln Cys Ala Gln Glu Ser Ser Ser				
	410	415	420	
gtt ggc act gcc tgc ctc cct gac ccc aac ctg cag ctc cct gac tgg	1410			
Val Gly Thr Ala Cys Leu Pro Asp Pro Asn Leu Gln Leu Pro Asp Trp				
	425	430	435	
aca gag tgt gag ctt tct ggc tac ggc aag cat gag gca tcg tct cca	1458			

Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys His Glu Ala Ser Ser Pro
 440 445 450 455
 ttc ttc tct gac cgg ctg aag gag gct cac gtc aga ctg tac ccg tcc 1506
 Phe Phe Ser Asp Arg Leu Lys Glu Ala His Val Arg Leu Tyr Pro Ser
 460 465 470
 agc cgc tgc acc tca cag cat ctg ttt aat aaa acc gtc acg aac aac 1554
 Ser Arg Cys Thr Ser Gln His Leu Phe Asn Lys Thr Val Thr Asn Asn
 475 480 485
 atg ctg tgc gct gga gac acc cgg agc gga ggc aac caa gac ctc cac 1602
 Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Asn Gln Asp Leu His
 490 495 500
 gat gca tgc cag ggt gac tgc gga ggc cct ctg gtg tgc atg atc aat 1650
 Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Met Ile Asn
 505 510 515
 aaa cag atg aca ttg act ggc att atc agc tgg ggc ctc ggc tgt ggg 1698
 Lys Gln Met Thr Leu Thr Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
 520 525 530 535
 cag aag gat gtg cct ggg gtc tac aca aag gtt acg aat tac cta gac 1746
 Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp
 540 545 550
 tgg att cac gac aac atg aag caa tga caaagaaagc ccagctcctt 1793
 Trp Ile His Asp Asn Met Lys Gln
 555 560
 caatccagag gaggacctgc ctctctcttc ctcttctaca gaagatgcgc ctaaaaggcc 1853
 aagcattctt tacaccatca tcttcgtgag ctgccactcg ggagagggga ggggggtctt 1913
 tgggagcaga tgtagcattt acctgtgaca ggtacttcac aacttgtaag ttttaaggat 1973
 gaaggtctgg ctttgggaata aatcctgtca gatgagatga caggagatg ccaaccttcc 2033
 ataactctag gattttaaaa agaggagtag accaaagtct gccctcctgg tccactatgt 2093
 tgtacactga accacaagat catgtctcaa cagcaaaaaa tacaacttga tctttcagga 2153

gtgaaagttt gcactgggga caagaatgtg tttttatagt tacacagggc cacagggcct 2213
 ccacgagaag gaaggggtat ctggccgaat cacagcacca taaaatcctt gagatcatgc 2273
 actccccatc cctccacact cctcaactct tgggacatat cccttgtata cagtgtaaat 2333
 gtctttttct ttataaactc tatagatggg tgggagaact gtatgatatt aataatigat 2393
 gaataacact agtatattta tattttaate tatttagat ttactttgt tactataact 2453
 ttgtattata ctgtacttaa ataataaatt cagaggtatt ttccacactt taaaaaaaaa 2513
 aaaaaa 2519

<210> 41

<211> 559

<212> PRT

<213> Mus musculus

<400> 41

Met Lys Arg Glu Leu Leu Cys Val Leu Leu Leu Cys Gly Leu Ala Phe
 1 5 10 15
 Pro Leu Pro Asp Gln Gly Ile His Gly Arg Phe Arg Arg Gly Ala Arg
 20 25 30
 Ser Tyr Arg Ala Thr Cys Arg Asp Glu Pro Thr Gln Thr Thr Tyr Gln
 35 40 45
 Gln His Gln Ser Trp Leu Arg Pro Met Leu Arg Ser Ser Arg Val Glu
 50 55 60
 Tyr Cys Arg Cys Asn Ser Gly Leu Val Gln Cys His Ser Val Pro Val
 65 70 75 80
 Arg Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
 85 90 95
 Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Asp Gly Phe Val
 100 105 110
 Gly Lys Arg Cys Asp Ile Asp Thr Arg Ala Thr Cys Phe Glu Glu Gln

115	120	125
Gly Ile Thr Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu		
130	135	140
Cys Ile Asn Trp Asn Ser Ser Val Leu Ser Leu Lys Pro Tyr Asn Ala		
145	150	155
Arg Arg Pro Asn Ala Ile Lys Leu Gly Leu Gly Asn His Asn Tyr Cys		
165	170	175
Arg Asn Pro Asp Arg Asp Leu Lys Pro Trp Cys Tyr Val Phe Lys Ala		
180	185	190
Gly Lys Tyr Thr Thr Glu Phe Cys Ser Thr Pro Ala Cys Pro Lys Gly		
195	200	205
Lys Ser Glu Asp Cys Tyr Val Gly Lys Gly Val Thr Tyr Arg Gly Thr		
210	215	220
His Ser Leu Thr Thr Ser Gln Ala Ser Cys Leu Pro Trp Asn Ser Ile		
225	230	235
Val Leu Met Gly Lys Ser Tyr Thr Ala Trp Arg Thr Asn Ser Gln Ala		
245	250	255
Leu Gly Leu Ala Arg His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala		
260	265	270
Arg Pro Trp Cys His Val Met Lys Asp Arg Lys Leu Thr Trp Glu Tyr		
275	280	285
Cys Asp Met Ser Pro Cys Ser Thr Cys Gly Leu Arg Gln Tyr Lys Arg		
290	295	300
Pro Gln Phe Arg Ile Lys Gly Gly Leu Tyr Thr Asp Ile Thr Ser His		
305	310	315
Pro Trp Gln Ala Ala Ile Phe Val Lys Asn Lys Arg Ser Pro Gly Glu		
325	330	335
Arg Phe Leu Cys Gly Gly Val Leu Ile Ser Ser Cys Trp Val Leu Ser		
340	345	350

Ala Ala His Cys Phe Leu Glu Arg Phe Pro Pro Asn His Leu Lys Val
 355 360 365
 Val Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Thr
 370 375 380
 Phe Glu Ile Glu Lys Tyr Ile Val His Glu Glu Phe Asp Asp Asp Thr
 385 390 395 400
 Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Arg Ser Gln Ser Lys Gln
 405 410 415
 Cys Ala Gln Glu Ser Ser Ser Val Gly Thr Ala Cys Leu Pro Asp Pro
 420 425 430
 Asn Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly
 435 440 445
 Lys His Glu Ala Ser Ser Pro Phe Phe Ser Asp Arg Leu Lys Glu Ala
 450 455 460
 His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Phe
 465 470 475 480
 Asn Lys Thr Val Thr Asn Asn Met Leu Cys Ala Gly Asp Thr Arg Ser
 485 490 495
 Gly Gly Asn Gln Asp Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
 500 505 510
 Pro Leu Val Cys Met Ile Asn Lys Gln Met Thr Leu Thr Gly Ile Ile
 515 520 525
 Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
 530 535 540
 Lys Val Thr Asn Tyr Leu Asp Trp Ile His Asp Asn Met Lys Gln
 545 550 555

<210> 42

<211> 1391

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (271).. (1311)

<400> 42

gccggtttga gttgtgcgct cgggtgtccc tttctcttcc cctcccgca gggcttgcgg 60
 ccaccatggc gtattagagg cagcagtgcc tgcggcagcg ttggcctttg cagcggcggc 120
 agcagcacca ggctctgcag cggcaacccc caccggccta agccatggcg ctcttcacga 180
 aatccagcag cagtgttgct gtaacggaca aagatacctt cgagttaagc acattcctgg 240
 aatccagcaa agccccacaa catgaccgag atg agc ttc ctg aac agc gaa gtg 294

Met Ser Phe Leu Asn Ser Glu Val

1

5

ttg gcg ggg gac ttg atg tcc ccc ttc gac cag tcg ggt ttg ggg gct 342
 Leu Ala Gly Asp Leu Met Ser Pro Phe Asp Gln Ser Gly Leu Gly Ala

10

15

20

gaa gaa agc cta ggt ctc tta gat gac tat ctg gag gtg gcc aag cac 390
 Glu Glu Ser Leu Gly Leu Leu Asp Asp Tyr Leu Glu Val Ala Lys His

25

30

35

40

ttg aaa cct cat ggg ttc tcc agc gac aag gcg ggc tcc tcg gaa tgg 438
 Leu Lys Pro His Gly Phe Ser Ser Asp Lys Ala Gly Ser Ser Glu Trp

45

50

55

ccg gct atg gat gat ggc ttg gcc agt gcc tca gac acc ggc aag gag 486
 Pro Ala Met Asp Asp Gly Leu Ala Ser Ala Ser Asp Thr Gly Lys Glu

60

65

70

gat gcc ttt tcc ggg aca gat tgg atg ttg gag aaa atg gat ctg aaa 534
 Asp Ala Phe Ser Gly Thr Asp Trp Met Leu Glu Lys Met Asp Leu Lys

75	80	85	
gag ttt gac ttc gat gct ctg ttt cga atg gat gac ctg gaa acc atg			582
Glu Phe Asp Phe Asp Ala Leu Phe Arg Met Asp Asp Leu Glu Thr Met			
90	95	100	
cca gat gag ctc ttg acc acg ttg gat gac aca tgt gat ctt ttt gcc			630
Pro Asp Glu Leu Leu Thr Thr Leu Asp Asp Thr Cys Asp Leu Phe Ala			
105	110	115	120
cct cta gtc caa gag act aat aag gag ccc cct cag aca gtg aac cca			678
Pro Leu Val Gln Glu Thr Asn Lys Glu Pro Pro Gln Thr Val Asn Pro			
125	130	135	
att ggc cat ctc cca gaa agt tta ata aaa gtc gac cag gtt gcc ccc			726
Ile Gly His Leu Pro Glu Ser Leu Ile Lys Val Asp Gln Val Ala Pro			
140	145	150	
ttt aca ttc ttg cag cct ttc ccc tgt tcc cca ggg gtt ctg tct tcc			774
Phe Thr Phe Leu Gln Pro Phe Pro Cys Ser Pro Gly Val Leu Ser Ser			
155	160	165	
act cca gag cat tcc ttt agt tta gag cta ggc agt gaa gtt gat atc			822
Thr Pro Glu His Ser Phe Ser Leu Glu Leu Gly Ser Glu Val Asp Ile			
170	175	180	
tct gaa gga gac agg aag cct gac tct gct gct tac att act cta atc			870
Ser Glu Gly Asp Arg Lys Pro Asp Ser Ala Ala Tyr Ile Thr Leu Ile			
185	190	195	200
cct cca tgt gta aag gag gaa gac act ccc tct gac aat gac agt ggc			918
Pro Pro Cys Val Lys Glu Glu Asp Thr Pro Ser Asp Asn Asp Ser Gly			
205	210	215	
atc tgt atg agc ccg gag tcc tac ctg ggc tct ccc cag cat agc ccc			966
Ile Cys Met Ser Pro Glu Ser Tyr Leu Gly Ser Pro Gln His Ser Pro			
220	225	230	
tcc acc tcc agg gcc cca cca gac aat ctg cct tct cca ggt ggt tcc			1014

Ser Thr Ser Arg Ala Pro Pro Asp Asn Leu Pro Ser Pro Gly Gly Ser
 235 240 245
 cgt ggg tct cct cgg ccc aaa cct tat gac cca cct gga gtt agt ttg 1062
 Arg Gly Ser Pro Arg Pro Lys Pro Tyr Asp Pro Pro Gly Val Ser Leu
 250 255 260
 . aca gct aaa gtg aag act gag aaa ttg gat aag aag ctg aaa aag atg 1110
 Thr Ala Lys Val Lys Thr Glu Lys Leu Asp Lys Lys Leu Lys Lys Met
 265 270 275 280
 gag caa aac aag aca gca gcc act agg tac cgc cag aag aag cgg gct 1158
 Glu Gln Asn Lys Thr Ala Ala Thr Arg Tyr Arg Gln Lys Lys Arg Ala
 285 290 295
 gag cag gag gcc ctc act ggc gag tgt aag gag cta gaa aaa aag aat 1206
 Glu Gln Glu Ala Leu Thr Gly Glu Cys Lys Glu Leu Glu Lys Lys Asn
 300 305 310
 gag gct ctg aaa gag aag gca gat tct ctg gcc aag gag atc cag tat 1254
 Glu Ala Leu Lys Glu Lys Ala Asp Ser Leu Ala Lys Glu Ile Gln Tyr
 315 320 325
 ctg aaa gac ctg ata gaa gag gtc cgt aag gca agg ggg aag aag aga 1302
 Leu Lys Asp Leu Ile Glu Glu Val Arg Lys Ala Arg Gly Lys Lys Arg
 330 335 340
 gtt ccg taa tagggtagtc aggtgctttg tgcttgtaca tagtcttgtg 1351
 Val Pro
 345
 ttgctgtgtt tgctgtaata aattattttg tagtgaaagt 1391

<210> 43

<211> 346

<212> PRT

<213> Mus musculus

<400> 43

Met	Ser	Phe	Leu	Asn	Ser	Glu	Val	Leu	Ala	Gly	Asp	Leu	Met	Ser	Pro
1				5					10					15	
Phe	Asp	Gln	Ser	Gly	Leu	Gly	Ala	Glu	Glu	Ser	Leu	Gly	Leu	Leu	Asp
				20				25					30		
Asp	Tyr	Leu	Glu	Val	Ala	Lys	His	Leu	Lys	Pro	His	Gly	Phe	Ser	Ser
				35				40					45		
Asp	Lys	Ala	Gly	Ser	Ser	Glu	Trp	Pro	Ala	Met	Asp	Asp	Gly	Leu	Ala
				50				55					60		
Ser	Ala	Ser	Asp	Thr	Gly	Lys	Glu	Asp	Ala	Phe	Ser	Gly	Thr	Asp	Trp
				65				70					75		80
Met	Leu	Glu	Lys	Met	Asp	Leu	Lys	Glu	Phe	Asp	Phe	Asp	Ala	Leu	Phe
				85				90					95		
Arg	Met	Asp	Asp	Leu	Glu	Thr	Met	Pro	Asp	Glu	Leu	Leu	Thr	Thr	Leu
				100				105					110		
Asp	Asp	Thr	Cys	Asp	Leu	Phe	Ala	Pro	Leu	Val	Gln	Glu	Thr	Asn	Lys
				115				120					125		
Glu	Pro	Pro	Gln	Thr	Val	Asn	Pro	Ile	Gly	His	Leu	Pro	Glu	Ser	Leu
				130				135					140		
Ile	Lys	Val	Asp	Gln	Val	Ala	Pro	Phe	Thr	Phe	Leu	Gln	Pro	Phe	Pro
				145				150					155		160
Cys	Ser	Pro	Gly	Val	Leu	Ser	Ser	Thr	Pro	Glu	His	Ser	Phe	Ser	Leu
				165				170					175		
Glu	Leu	Gly	Ser	Glu	Val	Asp	Ile	Ser	Glu	Gly	Asp	Arg	Lys	Pro	Asp
				180				185					190		
Ser	Ala	Ala	Tyr	Ile	Thr	Leu	Ile	Pro	Pro	Cys	Val	Lys	Glu	Glu	Asp
				195				200					205		
Thr	Pro	Ser	Asp	Asn	Asp	Ser	Gly	Ile	Cys	Met	Ser	Pro	Glu	Ser	Tyr

210 215 220
 Leu Gly Ser Pro Gln His Ser Pro Ser Thr Ser Arg Ala Pro Pro Asp
 225 230 235 240
 Asn Leu Pro Ser Pro Gly Gly Ser Arg Gly Ser Pro Arg Pro Lys Pro
 245 250 255
 Tyr Asp Pro Pro Gly Val Ser Leu Thr Ala Lys Val Lys Thr Glu Lys
 260 265 270
 Leu Asp Lys Lys Leu Lys Lys Met Glu Gln Asn Lys Thr Ala Ala Thr
 275 280 285
 Arg Tyr Arg Gln Lys Lys Arg Ala Glu Gln Glu Ala Leu Thr Gly Glu
 290 295 300
 Cys Lys Glu Leu Glu Lys Lys Asn Glu Ala Leu Lys Glu Lys Ala Asp
 305 310 315 320
 Ser Leu Ala Lys Glu Ile Gln Tyr Leu Lys Asp Leu Ile Glu Glu Val
 325 330 335
 Arg Lys Ala Arg Gly Lys Lys Arg Val Pro
 340 345

<210> 44

<211> 3161

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (662).. (3013)

<400> 44

ccgggcgctg ttccttccca gactccagga ccggctgcgg cggctgtagc ggcgccagggg 60
 tgagtagcgg cgcgggggtt cggagcaggg ttacggcgc ccctgaagaa tcgcggtgg 120

cggcacgctg ctgccgcgga gcagtcctgc tccacacgga gctgagggcg gtggaggcgg 180
 caggcctggc ggcccccgga gccggccctt gcctcaggtt tgcgtgactg aaccctcaga 240
 agtgggaccc cgccccggag tcccgcgctt gacagtgcac ctigatctta cctgtcaccc 300
 aggcctcccc gcgtccctgga gctttctcat acaacctttt gacacctaag gcagagtgtg 360
 ttgagtgcga ggcactgaaa tgacctggat ggtctttcat cctagaacag taccgttacg 420
 tggatgatga tggttgcgtt ttacggaaaa cactgaggta aactaagtta cccaaaacct 480
 tacaggaatg acagaaacga cagtgtattc aggcagaatc ctcccgacct accgggacct 540
 actctgaaac actaacgatt agacttaagt gttcggaaaa gacagaccga cagaccgacc 600
 gtagctttct gtgtcccgag gttgcttgaa ttgttttct ttttgcaagt ttttaactca 660
 a atg ggt gat gaa aag gac tct tgg aaa gtg aaa acg tta gat gaa att 709

Met Gly Asp Glu Lys Asp Ser Trp Lys Val Lys Thr Leu Asp Glu Ile

1 5 10 15
 ctc cag gaa aag aaa cga agg aaa gaa caa gag gag aaa gca gag ata 757
 Leu Gln Glu Lys Lys Arg Arg Lys Glu Gln Glu Glu Lys Ala Glu Ile

20 25 30
 aaa cgc tta aaa aat tct gat gac cgc gat tcc aaa agg gat tcc ctt 805
 Lys Arg Leu Lys Asn Ser Asp Asp Arg Asp Ser Lys Arg Asp Ser Leu

35 40 45
 gag gag ggg gag ctg aga gat cac cga atg gag atc aca atc agg aac 853
 Glu Glu Gly Glu Leu Arg Asp His Arg Met Glu Ile Thr Ile Arg Asn

50 55 60
 tca cca tat aga aga gag gat tct atg gaa gac aga gga gag gag gat 901
 Ser Pro Tyr Arg Arg Glu Asp Ser Met Glu Asp Arg Gly Glu Glu Asp

65 70 75 80
 gat tct ctg gcc atc aaa cca ccc cag caa atg tct cgg aaa gaa aag 949
 Asp Ser Leu Ala Ile Lys Pro Pro Gln Gln Met Ser Arg Lys Glu Lys

85 90 95
 gct cat cac aga aaa gac gag aaa aga aaa gag aaa cgt cga cat cgt 997
 Ala His His Arg Lys Asp Glu Lys Arg Lys Glu Lys Arg Arg His Arg

100	105	110	
agc cat tca gca gag gga ggg aaa cat gcc aga gtg aaa gag aaa gaa			1045
Ser His Ser Ala Glu Gly Gly Lys His Ala Arg Val Lys Glu Lys Glu			
115	120	125	
agg gag cac gaa cgc cgg aaa cgc cac cga gaa gaa caa gat aaa gct			1093
Arg Glu His Glu Arg Arg Lys Arg His Arg Glu Glu Gln Asp Lys Ala			
130	135	140	
cga agg gag tgg gaa aga cag aag agg agg gaa atg gcg aga gaa cat			1141
Arg Arg Glu Trp Glu Arg Gln Lys Arg Arg Glu Met Ala Arg Glu His			
145	150	155	160
tcc aga aga gag agg gac cgc ctg gag cag tta gaa agg aag agg gag			1189
Ser Arg Arg Glu Arg Asp Arg Leu Glu Gln Leu Glu Arg Lys Arg Glu			
165	170	175	
cgg gag cgc aag ctg agg gag cag cag aag gag cag cgg gag cag aag			1237
Arg Glu Arg Lys Leu Arg Glu Gln Gln Lys Glu Gln Arg Glu Gln Lys			
180	185	190	
gag cgg gaa cgg agg gca gag gag cgc cgc aaa gag aga gaa gcg cgt			1285
Glu Arg Glu Arg Arg Ala Glu Glu Arg Arg Lys Glu Arg Glu Ala Arg			
195	200	205	
agg gaa gtc tct gca cat cac cgt acc atg agg gag gag tac agt gat			1333
Arg Glu Val Ser Ala His His Arg Thr Met Arg Glu Glu Tyr Ser Asp			
210	215	220	
aag ggg aag gtt ggc cac tgg agc cgc agc cct ctg agg cca cca aga			1381
Lys Gly Lys Val Gly His Trp Ser Arg Ser Pro Leu Arg Pro Pro Arg			
225	230	235	240
gag cgc ttt gag atg gga gac aac cgg aag cca gta aaa gaa gag aag			1429
Glu Arg Phe Glu Met Gly Asp Asn Arg Lys Pro Val Lys Glu Glu Lys			
245	250	255	
gtg gaa gag aga gac ttg ttg tca gac ctc caa gac atc agt gac agc			1477

Val Glu Glu Arg Asp Leu Leu Ser Asp Leu Gln Asp Ile Ser Asp Ser
 260 265 270
 gag agg aaa acc agc tca gct gag tct tca tca gaa tca ggc tca ggt 1525
 Glu Arg Lys Thr Ser Ser Ala Glu Ser Ser Ser Glu Ser Gly Ser Gly
 275 280 285
 tct gaa gag gag gag gag gaa gaa gaa gag gaa gaa gaa gaa gaa ggg 1573
 Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly
 290 295 300
 agc acc agt gaa gaa tca gag gaa gaa gag gaa gaa gaa gag gag gag 1621
 Ser Thr Ser Glu Glu Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu
 305 310 315 320
 gaa gaa gag gag act ggg agc aac tct gag gag gcc tct gaa cag tcc 1669
 Glu Glu Glu Glu Thr Gly Ser Asn Ser Glu Glu Ala Ser Glu Gln Ser
 325 330 335
 gca gaa gaa gtc agt gat gag gaa atg agt gaa gat gaa gac aga gaa 1717
 Ala Glu Glu Val Ser Asp Glu Glu Met Ser Glu Asp Glu Asp Arg Glu
 340 345 350
 aac gag aac cac atc ttg gtt gtt cca gag tca cga ttt gac cga gat 1765
 Asn Glu Asn His Ile Leu Val Val Pro Glu Ser Arg Phe Asp Arg Asp
 355 360 365
 tct ggg gac agt gaa gaa ggg gag gaa gaa gtt ggt gaa ggg act cca 1813
 Ser Gly Asp Ser Glu Glu Gly Glu Glu Glu Val Gly Glu Gly Thr Pro
 370 375 380
 cag agc agt gcc ccc acc gaa gga gac tat gtt cct gac tct cca gca 1861
 Gln Ser Ser Ala Pro Thr Glu Gly Asp Tyr Val Pro Asp Ser Pro Ala
 385 390 395 400
 ctg tca cct att gag cta aaa caa gaa ctg ccc aaa tac ctg cca gcc 1909
 Leu Ser Pro Ile Glu Leu Lys Gln Glu Leu Pro Lys Tyr Leu Pro Ala
 405 410 415

ctg cag gga tgc agg agt gta gag gag ttt cag tgt ctg aac agg att	1957
Leu Gln Gly Cys Arg Ser Val Glu Glu Phe Gln Cys Leu Asn Arg Ile	
420 425 430	
gaa gaa ggc acc tat ggg gtg gtc tac aga gca aag gac aag aaa aca	2005
Glu Glu Gly Thr Tyr Gly Val Val Tyr Arg Ala Lys Asp Lys Lys Thr	
435 440 445	
gat gaa att gtg gct ctg aag cgg tta aag atg gag aag gag aag gaa	2053
Asp Glu Ile Val Ala Leu Lys Arg Leu Lys Met Glu Lys Glu Lys Glu	
450 455 460	
ggc ttc cca atc acg tcg ctg agg gaa atc aac acc atc ctc aag gcc	2101
Gly Phe Pro Ile Thr Ser Leu Arg Glu Ile Asn Thr Ile Leu Lys Ala	
465 470 475 480	
cag cac ccc aac atc gtc acc gtc agg gaa att gtt gtg gga agt aac	2149
Gln His Pro Asn Ile Val Thr Val Arg Glu Ile Val Val Gly Ser Asn	
485 490 495	
atg gac aag atc tac att gtg atg aac tac gtg gaa cat gac ctc aag	2197
Met Asp Lys Ile Tyr Ile Val Met Asn Tyr Val Glu His Asp Leu Lys	
500 505 510	
agc cta atg gag acc atg aag cag ccc ttc ctg cca ggg gag gtg aag	2245
Ser Leu Met Glu Thr Met Lys Gln Pro Phe Leu Pro Gly Glu Val Lys	
515 520 525	
acc ctg atg att cag ctg ctg agt ggg gta aag cac ctc cat gac aat	2293
Thr Leu Met Ile Gln Leu Leu Ser Gly Val Lys His Leu His Asp Asn	
530 535 540	
tgg atc cta cac cgt gac ctg aag acc tct aac ctc ctg ctg agc cat	2341
Trp Ile Leu His Arg Asp Leu Lys Thr Ser Asn Leu Leu Leu Ser His	
545 550 555 560	
gct ggc att ctc aag gtg ggc gac ttt ggg ctg gct cgg gag tat ggt	2389
Ala Gly Ile Leu Lys Val Gly Asp Phe Gly Leu Ala Arg Glu Tyr Gly	

565	570	575	
tca ccc cta aag gcc tac act cca gtt gtt gta acc ctg tgg tat cgt	2437		
Ser Pro Leu Lys Ala Tyr Thr Pro Val Val Val Thr Leu Trp Tyr Arg			
580	585	590	
gcc cca gaa cta ctg ctt ggt gct aag gaa tac tcc aca gct gtg gac	2485		
Ala Pro Glu Leu Leu Leu Gly Ala Lys Glu Tyr Ser Thr Ala Val Asp			
595	600	605	
atg tgg tcg gta ggc tgc ata ttt gga gaa ctg ctg aca cag aaa cct	2533		
Met Trp Ser Val Gly Cys Ile Phe Gly Glu Leu Leu Thr Gln Lys Pro			
610	615	620	
ctg ttc cct ggg aag tca gat att gat cag att aac aag att ttc aag	2581		
Leu Phe Pro Gly Lys Ser Asp Ile Asp Gln Ile Asn Lys Ile Phe Lys			
625	630	635	640
gac ctg ggt act cct agt gag aaa atc tgg cct ggc tat aat gac ctc	2629		
Asp Leu Gly Thr Pro Ser Glu Lys Ile Trp Pro Gly Tyr Asn Asp Leu			
645	650	655	
cca gcc gtc aag aag atg acc ttc agc gag tat ccc tat aac aac ctc	2677		
Pro Ala Val Lys Lys Met Thr Phe Ser Glu Tyr Pro Tyr Asn Asn Leu			
660	665	670	
cgc aag aga ttt ggg gct ttg tta tca gat caa ggc ttt gat ctc atg	2725		
Arg Lys Arg Phe Gly Ala Leu Leu Ser Asp Gln Gly Phe Asp Leu Met			
675	680	685	
aac aag ttc ctg aca tac tac cct ggc agg agg atc aac gca gaa gat	2773		
Asn Lys Phe Leu Thr Tyr Tyr Pro Gly Arg Arg Ile Asn Ala Glu Asp			
690	695	700	
ggc ctc aag cac gaa tat ttc cga gag act ccc ctc ccc atc gac cca	2821		
Gly Leu Lys His Glu Tyr Phe Arg Glu Thr Pro Leu Pro Ile Asp Pro			
705	710	715	720
tcc atg ttc ccc acg tgg cct gcc aag agt gag cag cag aga gtg aag	2869		

Ser Met Phe Pro Thr Trp Pro Ala Lys Ser Glu Gln Gln Arg Val Lys
 725 730 735
 cga ggc acg agt cca cgg cct cct gag ggc ggc ctg ggc tac agc cag 2917
 Arg Gly Thr Ser Pro Arg Pro Pro Glu Gly Gly Leu Gly Tyr Ser Gln
 740 745 750
 ctg ggt gat gat gac ctg aag gag acg ggc ttc cac ctc acc acc acc 2965
 Leu Gly Asp Asp Asp Leu Lys Glu Thr Gly Phe His Leu Thr Thr Thr
 755 760 765
 aac cag gga gcc tca gct gca ggc cct ggc ttc agc ctc aag ttc tga 3013
 Asn Gln Gly Ala Ser Ala Ala Gly Pro Gly Phe Ser Leu Lys Phe
 770 775 780
 ggtaggcttg atggacgtgg cccgactagg tggtagacagc cagacctgct gatgctgaat 3073
 cagggcaact tggttgtttt ttccacgttg ttgtttttgg ggcaggttgt aaattttag 3133
 aattaaatga aattttcctt ttggaggg 3161

<210> 45

<211> 783

<212> PRT

<213> Mus musculus

<400> 45

Met Gly Asp Glu Lys Asp Ser Trp Lys Val Lys Thr Leu Asp Glu Ile
 1 5 10 15
 Leu Gln Glu Lys Lys Arg Arg Lys Glu Gln Glu Glu Lys Ala Glu Ile
 20 25 30
 Lys Arg Leu Lys Asn Ser Asp Asp Arg Asp Ser Lys Arg Asp Ser Leu
 35 40 45
 Glu Glu Gly Glu Leu Arg Asp His Arg Met Glu Ile Thr Ile Arg Asn
 50 55 60

Ser Pro Tyr Arg Arg Glu Asp Ser Met Glu Asp Arg Gly Glu Glu Asp
 65 70 75 80
 Asp Ser Leu Ala Ile Lys Pro Pro Gln Gln Met Ser Arg Lys Glu Lys
 85 90 95
 Ala His His Arg Lys Asp Glu Lys Arg Lys Glu Lys Arg Arg His Arg
 100 105 110
 Ser His Ser Ala Glu Gly Gly Lys His Ala Arg Val Lys Glu Lys Glu
 115 120 125
 Arg Glu His Glu Arg Arg Lys Arg His Arg Glu Glu Gln Asp Lys Ala
 130 135 140
 Arg Arg Glu Trp Glu Arg Gln Lys Arg Arg Glu Met Ala Arg Glu His
 145 150 155 160
 Ser Arg Arg Glu Arg Asp Arg Leu Glu Gln Leu Glu Arg Lys Arg Glu
 165 170 175
 Arg Glu Arg Lys Leu Arg Glu Gln Gln Lys Glu Gln Arg Glu Gln Lys
 180 185 190
 Glu Arg Glu Arg Arg Ala Glu Glu Arg Arg Lys Glu Arg Glu Ala Arg
 195 200 205
 Arg Glu Val Ser Ala His His Arg Thr Met Arg Glu Glu Tyr Ser Asp
 210 215 220
 Lys Gly Lys Val Gly His Trp Ser Arg Ser Pro Leu Arg Pro Pro Arg
 225 230 235 240
 Glu Arg Phe Glu Met Gly Asp Asn Arg Lys Pro Val Lys Glu Glu Lys
 245 250 255
 Val Glu Glu Arg Asp Leu Leu Ser Asp Leu Gln Asp Ile Ser Asp Ser
 260 265 270
 Glu Arg Lys Thr Ser Ser Ala Glu Ser Ser Ser Glu Ser Gly Ser Gly
 275 280 285
 Ser Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Gly

290	295	300
Ser Thr Ser Glu Glu	Ser Glu Glu Glu Glu Glu Glu Glu Glu	
305	310	315
Glu Glu Glu Glu Thr Gly Ser Asn Ser Glu Glu Ala Ser Glu Gln Ser		320
325	330	335
Ala Glu Glu Val Ser Asp Glu Glu Met Ser Glu Asp Glu Asp Arg Glu		
340	345	350
Asn Glu Asn His Ile Leu Val Val Pro Glu Ser Arg Phe Asp Arg Asp		
355	360	365
Ser Gly Asp Ser Glu Glu Gly Glu Glu Glu Val Gly Glu Gly Thr Pro		
370	375	380
Gln Ser Ser Ala Pro Thr Glu Gly Asp Tyr Val Pro Asp Ser Pro Ala		
385	390	395
Leu Ser Pro Ile Glu Leu Lys Gln Glu Leu Pro Lys Tyr Leu Pro Ala		400
405	410	415
Leu Gln Gly Cys Arg Ser Val Glu Glu Phe Gln Cys Leu Asn Arg Ile		
420	425	430
Glu Glu Gly Thr Tyr Gly Val Val Tyr Arg Ala Lys Asp Lys Lys Thr		
435	440	445
Asp Glu Ile Val Ala Leu Lys Arg Leu Lys Met Glu Lys Glu Lys Glu		
450	455	460
Gly Phe Pro Ile Thr Ser Leu Arg Glu Ile Asn Thr Ile Leu Lys Ala		
465	470	475
Gln His Pro Asn Ile Val Thr Val Arg Glu Ile Val Val Gly Ser Asn		480
485	490	495
Met Asp Lys Ile Tyr Ile Val Met Asn Tyr Val Glu His Asp Leu Lys		
500	505	510
Ser Leu Met Glu Thr Met Lys Gln Pro Phe Leu Pro Gly Glu Val Lys		
515	520	525

Thr Leu Met Ile Gln Leu Leu Ser Gly Val Lys His Leu His Asp Asn
 530 535 540
 Trp Ile Leu His Arg Asp Leu Lys Thr Ser Asn Leu Leu Leu Ser His
 545 550 555 560
 Ala Gly Ile Leu Lys Val Gly Asp Phe Gly Leu Ala Arg Glu Tyr Gly
 565 570 575
 Ser Pro Leu Lys Ala Tyr Thr Pro Val Val Val Thr Leu Trp Tyr Arg
 580 585 590
 Ala Pro Glu Leu Leu Leu Gly Ala Lys Glu Tyr Ser Thr Ala Val Asp
 595 600 605
 Met Trp Ser Val Gly Cys Ile Phe Gly Glu Leu Leu Thr Gln Lys Pro
 610 615 620
 Leu Phe Pro Gly Lys Ser Asp Ile Asp Gln Ile Asn Lys Ile Phe Lys
 625 630 635 640
 Asp Leu Gly Thr Pro Ser Glu Lys Ile Trp Pro Gly Tyr Asn Asp Leu
 645 650 655
 Pro Ala Val Lys Lys Met Thr Phe Ser Glu Tyr Pro Tyr Asn Asn Leu
 660 665 670
 Arg Lys Arg Phe Gly Ala Leu Leu Ser Asp Gln Gly Phe Asp Leu Met
 675 680 685
 Asn Lys Phe Leu Thr Tyr Tyr Pro Gly Arg Arg Ile Asn Ala Glu Asp
 690 695 700
 Gly Leu Lys His Glu Tyr Phe Arg Glu Thr Pro Leu Pro Ile Asp Pro
 705 710 715 720
 Ser Met Phe Pro Thr Trp Pro Ala Lys Ser Glu Gln Gln Arg Val Lys
 725 730 735
 Arg Gly Thr Ser Pro Arg Pro Pro Glu Gly Gly Leu Gly Tyr Ser Gln
 740 745 750
 Leu Gly Asp Asp Asp Leu Lys Glu Thr Gly Phe His Leu Thr Thr Thr

114/2644

```

gat gcc cag gag aaa ctg gag ctg gcg gag aaa aag gcc aca gat gct 297
Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp Ala
      70              75              80
gaa gct gac gta gct tct ctg aac aga cgc atc cag ctg gtt gag gag 345
Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu Glu
      85              90              95
gag ttg gat cgt gct cag gag cgt ctg gcc aca gct ctg cag aag ctg 393
Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys Leu
     100             105             110
gag gag gcc gag aag gct gca gat gag agt gag aga ggc atg aaa gtc 441
Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys Val
     115             120             125
att gaa agc cga gcc caa aaa gat gaa gaa aag atg gag att cag gag 489
Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln Glu
    130             135             140             145
atc cag ctg aaa gag gcc aag cac att gct gaa gat gct gac cgg aag 537
Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg Lys
     150             155             160
tat gaa gag gtg gcc cgt aag ctg gtc atc atc gag agc gac ctg gaa 585
Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu Glu
     165             170             175
cgt gca gag gag cgg gct gag ctc tca gaa ggc aaa tgt gcc gag ctt 633
Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu Leu
     180             185             190
gaa gaa gaa ttg aaa acg gtg acg aac aac ttg aag tca ctg gag gct 681
Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu Ala
     195             200             205
cag gct gag aag tac tct cag aag gaa gac aaa tat gaa gag gag atc 729
Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Lys Tyr Glu Glu Glu Ile

```

210	215	220	225	
aag gtt ctc tct gac aag ctg aag gag gct gaa act cgg gct gag ttt				777
Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu Phe				
	230	235	240	
	gca gag aga tca gtg acc aaa ttg gag aaa agc att gat gac tta gaa			825
	Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu Glu			
	245	250	255	
	gag aaa gtg gcc cat gcc aaa gaa gaa aac ctt agt atg cac cag atg			873
	Glu Lys Val Ala His Ala Lys Glu Glu Asn Leu Ser Met His Gln Met			
	260	265	270	
	ctg gat cag act tta ctg gag cta aac aac atg tga aaccctcctt			919
	Leu Asp Gln Thr Leu Leu Glu Leu Asn Asn Met			
275	280	285		
agctgcggcc agattctctc cccctccccc catgtttaat ttgtcttta aacacatgct				979
taccgtgaaa ccccttcaat gcgttttttt ttatatatac ttttaccact gtcactgaaa				1039
catctgccga gagccagcta gggcaggagt tggggaaaga cgcgagaaa ggcaagcccg				1099
agtcagggca cttgttatit aaatgtgcc a tttccaggt tgccaccctt catagagttt				1159
aggcatgcag ttgtccttagc cagtgttaga agcctcatga gaacagaacc attaacagcc				1219
agagtgccaa tgggtgggac agcaggaaga ctgatgttg agacaatcgg gtgcggattg				1279
gtgctaattt aaacaaaagg gcctctgggg tcttttgttc aatattttac aatttagact				1339
tctgtccaac actaatitat ttgtcttga gttgtactgc gagagaagaa tatggggitt				1399
tgtatgcccg tgttccttaa agccaagggt ttgaaagcca cgctggtctt ctgagattcc				1459
aagtccttcc ccagctcaca tgcccgtagc cccctccgac tcagtggggc gagcgctcaa				1519
cacggatcgc ccccccttc ccagttctcc atatcagggt agaagatcta ggcactacat				1579
atgtaattgg taaagaaaag gcattttctt aagagttata actatgtaaa cattgtataa				1639
tgatatgaaa taaaacgcac atttaggaca ttttct				1675

<210> 47

<211> 284

<212> PRT

<213> Mus musculus

<400> 47

```

Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
  1             5             10             15
Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
      20             25             30
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
      35             40             45
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
      50             55             60
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
      65             70             75             80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
      85             90             95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys
      100            105            110
Leu Glu Glu Ala Glu Lys Ala Ala Asp Glu Ser Glu Arg Gly Met Lys
      115            120            125
Val Ile Glu Ser Arg Ala Gln Lys Asp Glu Glu Lys Met Glu Ile Gln
      130            135            140
Glu Ile Gln Leu Lys Glu Ala Lys His Ile Ala Glu Asp Ala Asp Arg
      145            150            155            160
Lys Tyr Glu Glu Val Ala Arg Lys Leu Val Ile Ile Glu Ser Asp Leu
      165            170            175
Glu Arg Ala Glu Glu Arg Ala Glu Leu Ser Glu Gly Lys Cys Ala Glu
      180            185            190
Leu Glu Glu Glu Leu Lys Thr Val Thr Asn Asn Leu Lys Ser Leu Glu

```

195	200	205
Ala Gln Ala Glu Lys Tyr Ser Gln Lys Glu Asp Lys Tyr Glu Glu Glu		
210	215	220
Ile Lys Val Leu Ser Asp Lys Leu Lys Glu Ala Glu Thr Arg Ala Glu		
225	230	235
Phe Ala Glu Arg Ser Val Thr Lys Leu Glu Lys Ser Ile Asp Asp Leu		
245	250	255
Glu Glu Lys Val Ala His Ala Lys Glu Glu Asn Leu Ser Met His Gln		
260	265	270
Met Leu Asp Gln Thr Leu Leu Glu Leu Asn Asn Met		
275	280	

<210> 48

<211> 949

<212> DNA

<213> Mus musculus

<400> 48

gacggcaaca gcaaggggtg cgcctttgtg aagtactcct cccatgccga ggcacaagcc 60
gccatcaacg ctctacatgg cagccagacc atgcctggag cctcctccag cctgggtggtc 120
aagtttgcag acactgacaa ggagcgcaca atgcgacgga tgcagcagat ggctggccag 180
atgggcatgt tcaaccccat ggccatcccc ttcggagcct atggcgcccta tgctcaggca 240
ctgatgcagc agcaagcagc cctcatggca tcggtcgcgc aaggaggcta cctgaatccc 300
atggctgcct tcgctgccgc ccaaatgcag cagatggcgg ccctcaacat gaatggcctg 360
gcagccgcac ctatgacccc aacctcaggt ggcagcacc ctcaggcat cactgcacca 420
gctgtgccta gcatcccatc ccccatgtgg gtgaacggct tcacgggcct cccctcagg 480
ccaatgggca gcgtgctgcg gaacgtgtgt ntgccaatgn gcattcaccg tacgcagcac 540
agagccccac ggcagccgac cccgtgcagc aggcctacgc tggagtigca gattatcgag 600
gacgtgccta gcctgctgcc tatggtcaga ttagccaggc ctttctcag cgacggcgaa 660

tgattccag canagagaga agggccgtag gtgttatitt tgcggcgcgt cgcgggagtt 720
 gtggacgacg tggaagagct gcctgtggtt ggggttgaag atgagacgaa acgatctcga 780
 tagggttaca ttctgaggcg agggcggttg ggtaagagtt ccgaatttgg tgtgctgggc 840
 acgatggaga caggcgagaa taacattcta tatggagggg ttaacaagag aaaggittgtg 900
 ttatagaggg ggagtaaatg aaaaacatat ggggagcctc ttcttcctc 949

<210> 49

<211> 980

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (87).. (659)

<400> 49

caagcgcgca agagagcggg ctgcctcgca gtccgagccg gagagaggga gcgcgacgcg 60
 cgcggccccg gacgccctcc gaaacc atg aac ttt ctg ctc tct tgg gtg cac 113

Met Asn Phe Leu Leu Ser Trp Val His

1

5

tgg acc ctg gct tta ctg ctg tac ctc cac cat gcc aag tgg tcc cag 161

Trp Thr Leu Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln

10

15

20

25

gct gca ccc acg aca gaa gga gag cag aag tcc cat gaa gtg atc aag 209

Ala Ala Pro Thr Thr Glu Gly Glu Gln Lys Ser His Glu Val Ile Lys

30

35

40

ttc atg gac gtc tac cag cga agc tac tgc cgt cca att gag acc ctg 257

Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys Arg Pro Ile Glu Thr Leu

45

50

55

gtg gac atc ttc cag gag tac ccc gac gag ata gag tac atc ttc aag 305
 Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys
 60 65 70
 ccg tcc tgt gtg ccg ctg atg cgc tgt gca ggc tgc tgt aac gat gaa 353
 Pro Ser Cys Val Pro Leu Met Arg Cys Ala Gly Cys Cys Asn Asp Glu
 75 80 85
 gcc ctg gag tgc gtg ccc acg tca gag agc aac atc acc atg cag atc 401
 Ala Leu Glu Cys Val Pro Thr Ser Glu Ser Asn Ile Thr Met Gln Ile
 90 95 100 105
 atg cgg atc aaa cct cac caa agc cag cac ata gag aga atg agc ttc 449
 Met Arg Ile Lys Pro His Gln Ser Gln His Ile Glu Arg Met Ser Phe
 110 115 120
 cta cag cac agc aga tgt gaa tgc aga cca aag aaa gac aga aca aag 497
 Leu Gln His Ser Arg Cys Glu Cys Arg Pro Lys Lys Asp Arg Thr Lys
 125 130 135
 cca gaa aat cac tgt gag cct tgt tca gag cgg aga aag cat ttg ttt 545
 Pro Glu Asn His Cys Glu Pro Cys Ser Glu Arg Arg Lys His Leu Phe
 140 145 150
 gtc caa gat ccg cag acg tgt aaa tgt tcc tgc aaa aac aca gac tgc 593
 Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser
 155 160 165
 cgt tgc aag gcg agg cag ctt gag tta aac gaa cgt act tgc aga tgt 641
 Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys
 170 175 180 185
 gac aag cca agg cgg tga gccaggctgg caggaaggag cctcctcagg 689
 Asp Lys Pro Arg Arg
 190
 gtttcgggaa ccagacctct caccggaaag accgattaac catgtcacca ccatgccatc 749
 atcgtcaccg ttgacagaac agtccttaat ccagaaagcc tgatatgaag gaagaggaga 809

tccttcgagg agcacttttg gtccggaggg cgagactccg gcagacgcat tcccgggcag 869
 gtgaccaagc acgtgcctcg tgggactgga ttgccattt tcttataatct gctgctaaat 929
 cgccaagccc ggaagattag ggttgtttct gggattcctg tagagctcgt g 980

<210> 50

<211> 190

<212> PRT

<213> Mus musculus

<400> 50

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Thr	Leu	Ala	Leu	Leu	Leu
1					5					10					15
Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Thr	Thr	Glu	Gly
				20					25					30	
Glu	Gln	Lys	Ser	His	Glu	Val	Ile	Lys	Phe	Met	Asp	Val	Tyr	Gln	Arg
				35					40					45	
Ser	Tyr	Cys	Arg	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu	Tyr
				50					55					60	
Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu	Met
				65					70					75	
Arg	Cys	Ala	Gly	Cys	Cys	Asn	Asp	Glu	Ala	Leu	Glu	Cys	Val	Pro	Thr
				85					90					95	
Ser	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	Gln
				100					105					110	
Ser	Gln	His	Ile	Glu	Arg	Met	Ser	Phe	Leu	Gln	His	Ser	Arg	Cys	Glu
				115					120					125	
Cys	Arg	Pro	Lys	Lys	Asp	Arg	Thr	Lys	Pro	Glu	Asn	His	Cys	Glu	Pro
				130					135					140	
Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys

145	150	155	160
Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu			
	165	170	175
Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg			
	180	185	190

<210> 51

<211> 1469

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (121).. (1089)

<400> 51

```

ggaattccgg agagatccca gagagccctg agagcccacc gccgccgccg gcctagtcac 60
catcacaccc gggaggagcc gcagccgtcg ccgccggccc cagtcacat caccgcaacc 120
atg agc agc gag gcc gag acc cag cag ccg ccc gcc gcc ccc gcc gcc 168
Met Ser Ser Glu Ala Glu Thr Gln Gln Pro Pro Ala Ala Pro Ala Ala
      1           5           10           15
gcc ctc agc gcc gcc gac acc aag ccc ggc tcc acg gcg agc ggc gcg 216
Ala Leu Ser Ala Ala Asp Thr Lys Pro Gly Ser Thr Ala Ser Gly Ala
           20           25           30
ggc agt ggc ggc ccg ggt ggc ctc aca tcg gcg gcg ccg gcg ggc ggc 264
Gly Ser Gly Gly Pro Gly Gly Leu Thr Ser Ala Ala Pro Ala Gly Gly
           35           40           45
gac aag aag gtc atc gca acg aag gtt ttg gga aca gtc aaa tgg ttc 312
Asp Lys Lys Val Ile Ala Thr Lys Val Leu Gly Thr Val Lys Trp Phe

```

50	55	60	
aat gta agg aac gga tac ggt ttc atc aac agg aat gac acc aag gaa	360		
Asn Val Arg Asn Gly Tyr Gly Phe Ile Asn Arg Asn Asp Thr Lys Glu			
65	70	75	80
gac gta ttt gta cac cag act gcc ata aag aag aat aac ccc agg aag	408		
Asp Val Phe Val His Gln Thr Ala Ile Lys Lys Asn Asn Pro Arg Lys			
85	90	95	
tac ctt cgc agt gta ggc gat gga gag act gtg gag ttt gat gtt gtt	456		
Tyr Leu Arg Ser Val Gly Asp Gly Glu Thr Val Glu Phe Asp Val Val			
100	105	110	
gaa gga gaa aag ggt gcg gag gca gca aat gtt aca ggc cct ggt gga	504		
Glu Gly Glu Lys Gly Ala Glu Ala Ala Asn Val Thr Gly Pro Gly Gly			
115	120	125	
gtt cca gtt caa ggc agt aaa tac gca gca gac cgt aac cat tat aga	552		
Val Pro Val Gln Gly Ser Lys Tyr Ala Ala Asp Arg Asn His Tyr Arg			
130	135	140	
cgc tat cca cgt cgt agg ggt cct cca cgc aat tac cag caa aat tac	600		
Arg Tyr Pro Arg Arg Arg Gly Pro Pro Arg Asn Tyr Gln Gln Asn Tyr			
145	150	155	160
cag aat agt gag agt ggg gaa aag aac gag gga tcg gaa agc gct cct	648		
Gln Asn Ser Glu Ser Gly Glu Lys Asn Glu Gly Ser Glu Ser Ala Pro			
165	170	175	
gaa ggc cag gcc caa caa cgc cgg ccc tat cgc agg cga agg ttc cca	696		
Glu Gly Gln Ala Gln Gln Arg Arg Pro Tyr Arg Arg Arg Arg Phe Pro			
180	185	190	
cct tac tac atg cga aga ccc tat gcg cgt cga cca cag tat tcc aac	744		
Pro Tyr Tyr Met Arg Arg Pro Tyr Ala Arg Arg Pro Gln Tyr Ser Asn			
195	200	205	
ccc cct gtg caa gga gaa gtg atg gag ggt gct gac aac cag ggt gca	792		

Pro Pro Val Gln Gly Glu Val Met Glu Gly Ala Asp Asn Gln Gly Ala
 210 215 220
 gga gag caa ggt aga cca gtg aga cag aat atg tat cgg ggt tac aga 840
 Gly Glu Gln Gly Arg Pro Val Arg Gln Asn Met Tyr Arg Gly Tyr Arg
 225 230 235 240
 cca cga ttc cga agg ggc cct cct cgc caa aga cag cct aga gag gat 888
 Pro Arg Phe Arg Arg Gly Pro Pro Arg Gln Arg Gln Pro Arg Glu Asp
 245 250 255
 ggc aat gaa gag gac aaa gaa aat caa gga gat gag acc caa ggt cag 936
 Gly Asn Glu Glu Asp Lys Glu Asn Gln Gly Asp Glu Thr Gln Gly Gln
 260 265 270
 cag cca cct caa cgt cgg tat cgc cga aac ttc aat tac cga cgc aga 984
 Gln Pro Pro Gln Arg Arg Tyr Arg Arg Asn Phe Asn Tyr Arg Arg Arg
 275 280 285
 cgc cca gag aac cct aaa cca caa gat ggc aaa gag aca aaa gca gcc 1032
 Arg Pro Glu Asn Pro Lys Pro Gln Asp Gly Lys Glu Thr Lys Ala Ala
 290 295 300
 gat cca cca gct gag aat tcg tcc gct ccc gag gct gag cag ggc ggg 1080
 Asp Pro Pro Ala Glu Asn Ser Ser Ala Pro Glu Ala Glu Gln Gly Gly
 305 310 315 320
 gct gag taa atgccggctt accatctcta ccatcatcgc gtttggtcat 1129
 Ala Glu
 ccaccaagaa gaaatgaata tgaaattcca gcaataagaa atgaacaaag attggagctg 1189
 aagaccttaa gtgcttgctt ttgcccgcct gaccagatac attagaacta tctgcattat 1249
 cattgcacat ggggttttta ttatttttac ctaaagatgt ctcttttttg taatgacaaa 1309
 cgtgtttttt aagaaaaaaa aaaaaaggc ctggtttttc tcaatacacc tttaacgggt 1369
 tttaaattgt ttcatatctg gtcaagtga gatttttaag aacttcattt ttaatttgta 1429
 ataaagttaa caacttgatt ttttcaaaaa agtcaacagg 1469

<210> 52

<211> 322

<212> PRT

<213> Mus musculus

<400> 52

Met Ser Ser Glu Ala Glu Thr Gln Gln Pro Pro Ala Ala Pro Ala Ala

1

5

10

15

Ala Leu Ser Ala Ala Asp Thr Lys Pro Gly Ser Thr Ala Ser Gly Ala

20

25

30

Gly Ser Gly Gly Pro Gly Gly Leu Thr Ser Ala Ala Pro Ala Gly Gly

35

40

45

Asp Lys Lys Val Ile Ala Thr Lys Val Leu Gly Thr Val Lys Trp Phe

50

55

60

Asn Val Arg Asn Gly Tyr Gly Phe Ile Asn Arg Asn Asp Thr Lys Glu

65

70

75

80

Asp Val Phe Val His Gln Thr Ala Ile Lys Lys Asn Asn Pro Arg Lys

85

90

95

Tyr Leu Arg Ser Val Gly Asp Gly Glu Thr Val Glu Phe Asp Val Val

100

105

110

Glu Gly Glu Lys Gly Ala Glu Ala Ala Asn Val Thr Gly Pro Gly Gly

115

120

125

Val Pro Val Gln Gly Ser Lys Tyr Ala Ala Asp Arg Asn His Tyr Arg

130

135

140

Arg Tyr Pro Arg Arg Arg Gly Pro Pro Arg Asn Tyr Gln Gln Asn Tyr

145

150

155

160

Gln Asn Ser Glu Ser Gly Glu Lys Asn Glu Gly Ser Glu Ser Ala Pro

165

170

175

Glu Gly Gln Ala Gln Gln Arg Arg Pro Tyr Arg Arg Arg Arg Phe Pro

180 185 190
 Pro Tyr Tyr Met Arg Arg Pro Tyr Ala Arg Arg Pro Gln Tyr Ser Asn
 195 200 205
 Pro Pro Val Gln Gly Glu Val Met Glu Gly Ala Asp Asn Gln Gly Ala
 210 215 220
 Gly Glu Gln Gly Arg Pro Val Arg Gln Asn Met Tyr Arg Gly Tyr Arg
 225 230 235 240
 Pro Arg Phe Arg Arg Gly Pro Pro Arg Gln Arg Gln Pro Arg Glu Asp
 245 250 255
 Gly Asn Glu Glu Asp Lys Glu Asn Gln Gly Asp Glu Thr Gln Gly Gln
 260 265 270
 Gln Pro Pro Gln Arg Arg Tyr Arg Arg Asn Phe Asn Tyr Arg Arg Arg
 275 280 285
 Arg Pro Glu Asn Pro Lys Pro Gln Asp Gly Lys Glu Thr Lys Ala Ala
 290 295 300
 Asp Pro Pro Ala Glu Asn Ser Ser Ala Pro Glu Ala Glu Gln Gly Gly
 305 310 315 320
 Ala Glu

<210> 53

<211> 525

<212> DNA

<213> Mus musculus

<400> 53

ggcacgagtg ataaagaaat tgtggctgag gcagaaagac tggatgtaaa agccatgggt 60
 cctcttgttt tgacagaagt tctctttgat gagaagataa gagagcaaat caagaaatac 120
 aggcgccatt ttctaagatt ttgtcataac aacaaaaagg ctcagcggtta ctttcttcat 180
 ggtttiggaat gtgtggtagc aatgcatcaa gctcagctga tctccaagat cccacacatc 240

ctgaaggaga tgtatgatgc cgacctgita gaggaggagg tcattatcag ctggicagaa 300
 aaggcc tcta agaaatatgt cicaaaagaa ctigccaaag agattcgtgt caaagcagag 360
 ccatittatta aatggittgaa ggaagcagag gaagaatctt ctgggtggiga ggaagaagat 420
 gaagacgaaa atattgaggt cgtatatctg aaaactgcca gtgtacccaaa agttgaaact 480
 gtgaagtctg acaacaagga tgatgacatt gatattgacg ccatt 525

<210> 54

<211> 975

<212> DNA

<213> Mus musculus

<400> 54

tgaataggcc agaggcattg atgtgcagca ggtctcctta gtcatcaact atgaccttcc 60
 caccaacagg gaaaactaca tccacaggta agtctaggtc tgacagctag acaaccacta 120
 tgaatgaagtc ccaagttgtt ccatcatact ttttaccccc ctcagaatcg gtcgagggtgg 180
 tctggtttggt cgttaaggtg tggctattaa catggtgacc gaagaagaca agaggactct 240
 tctgagacatt gagactttct acaacacctc cattgaagag atgcccccca acgttgctga 300
 cctcatittag ggggctgtcc tgcgacctgg ccctagccca ggggttcagtc ctgggggtggg 360
 ggctaaggaa gagctggagg ggggagggga gggagccaag ggaatggacat cttgtttttg 420
 ttttggcttt tttttttttt gtttcagttt tttttctatg aataaatgtc actttttgag 480
 gcaaaaagaa ccgtgaacat tttagacacc cttttctttg gggtaggctc tgccccaggc 540
 gctgccccag ggcgcgtctc ctccccccc cccccaacaa ctaatgcatt tccctaacct 600
 agtcacctcg ttcctaaagg ctttccctacc ccagccaaat ctccaaagtg agtcaagggg 660
 ctaaaaaaca aggctggcct cattgctgga ccaaatctac aggagaaacc cctgagtga 720
 ggattgtcca gggaattgac ccctgggtgag gggagcaagg ggaagaaaaa atggtagcca 780
 tttttacatt gttttgtata gtatttattg attcaggaaa caaacacac aaattgtga 840
 ataaaattac ttggaaactg cctgaatttg ggctctgita cttccattc ctctactgtg 900
 ctgtttgggt tcttgtttgt tttccttaag tctactgtag tgtggatagt gacgatatag 960
 ttgataatgat ttgca 975

<210> 55

<211> 1282

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (76).. (984)

<400> 55

cgggttgtgc tggggggggtc cgcgcgccct gcagtcgccga acccgctacg cgctccgtcg 60
 gcccgcgccgc cgcgc atg gag cct ggc ccc gac ggc cca gcc gcg ccc ggc 111

Met Glu Pro Gly Pro Asp Gly Pro Ala Ala Pro Gly

1 5 10

ccc gcc gcc atc cgt gag ggc tgg ttc cga gag acc tgc agc ctg tgg 159
 Pro Ala Ala Ile Arg Glu Gly Trp Phe Arg Glu Thr Cys Ser Leu Trp

15 20 25

ccc ggc cag gcc ctg tgc ctg caa gtg gag cag ctg ctt cac cac cgg 207
 Pro Gly Gln Ala Leu Ser Leu Gln Val Glu Gln Leu Leu His His Arg

30 35 40

cga tgc cgg tac caa gac atc ctc gtc ttc cgc agt aaa acc tac ggc 255
 Arg Ser Arg Tyr Gln Asp Ile Leu Val Phe Arg Ser Lys Thr Tyr Gly

45 50 55 60

aac gtg ctg gtt ctg gat ggc gtc atc cag tgt act gag agg gat gag 303
 Asn Val Leu Val Leu Asp Gly Val Ile Gln Cys Thr Glu Arg Asp Glu

65 70 75

ttc tcc tac cag gag atg atc gcc aac ctg ccg ctc tgc agc cac ccc 351
 Phe Ser Tyr Gln Glu Met Ile Ala Asn Leu Pro Leu Cys Ser His Pro

80	85	90	
aac ccg cgg aag gtg ctg atc atc ggg ggt gga gat ggg ggc gtc cta			399
Asn Pro Arg Lys Val Leu Ile Ile Gly Gly Gly Asp Gly Gly Val Leu			
95	100	105	
cgg gaa gtg gtg aag cac ccc tct gtg gag tcg gtg gtc cag tgc gag			447
Arg Glu Val Val Lys His Pro Ser Val Glu Ser Val Val Gln Cys Glu			
110	115	120	
att gat gag gat gtc att gaa gtc tct aag aag ttc ctg cct ggc atg			495
Ile Asp Glu Asp Val Ile Glu Val Ser Lys Lys Phe Leu Pro Gly Met			
125	130	135	140
gcc gtt ggc ttc tcc agc tca aag ctg act ctc cac gtg ggc gat ggc			543
Ala Val Gly Phe Ser Ser Ser Lys Leu Thr Leu His Val Gly Asp Gly			
145	150	155	
ttt gag ttc atg aaa cag aac caa gat gcc ttt gac gtc atc atc acc			591
Phe Glu Phe Met Lys Gln Asn Gln Asp Ala Phe Asp Val Ile Ile Thr			
160	165	170	
gac tcc tca gac ccc atg ggc cct gct gag agc ctc ttc aag gag tcc			639
Asp Ser Ser Asp Pro Met Gly Pro Ala Glu Ser Leu Phe Lys Glu Ser			
175	180	185	
tat tac cag ctc atg aag aca gca ctc aaa gaa gat ggc atc ctg tgc			687
Tyr Tyr Gln Leu Met Lys Thr Ala Leu Lys Glu Asp Gly Ile Leu Cys			
190	195	200	
tgc cag ggt gag tgc cag tgg ctg cac ctg gac ctc atc aag gag atg			735
Cys Gln Gly Glu Cys Gln Trp Leu His Leu Asp Leu Ile Lys Glu Met			
205	210	215	220
agg cac ttc tgc aaa tct ctc ttc ccc gtg gtg gac tac gcc tac tgt			783
Arg His Phe Cys Lys Ser Leu Phe Pro Val Val Asp Tyr Ala Tyr Cys			
225	230	235	
agc att cct acc tat ccc agc ggc cag atc ggc ttc atg ctg tgt agc			831

Ser Ile Pro Thr Tyr Pro Ser Gly Gln Ile Gly Phe Met Leu Cys Ser
 240 245 250
 aaa aac ccg agc acc aac ttc cgg gag cca gtg cag cag ttg aca cag 879
 Lys Asn Pro Ser Thr Asn Phe Arg Glu Pro Val Gln Gln Leu Thr Gln
 255 260 265
 gcc cag gtg gag cag atg cag ctg aaa tac tat aac tcg gac atg cac 927
 Ala Gln Val Glu Gln Met Gln Leu Lys Tyr Tyr Asn Ser Asp Met His
 270 275 280
 cgt gcc gcc ttc gta ctg cct gag ttc acc cgg aag gcc ctc aat gac 975
 Arg Ala Ala Phe Val Leu Pro Glu Phe Thr Arg Lys Ala Leu Asn Asp
 285 290 295 300
 ata agc tga atccagggtgc cactgtgaca ccacccgaga cctcaatcgg 1024
 Ile Ser
 attggaccaa ggatcttcca agttgtctgg ggaccaccag tcctggacca gactcccaga 1084
 tgactcttgc ccaccaacca agtgttacag gcccctgat gctgcctggc ctggcctggc 1144
 ctggcctggc ctggcctgcc ctgctgggtg gactcagtct ctgtctgict atctctgtgg 1204
 cgttcagccc cagcctata ccagctctgt acagcacgc ctagccctg tgaccaaca 1264
 aaatacatgt gtattccg 1282

<210> 56

<211> 302

<212> PRT

<213> Mus musculus

<400> 56

Met Glu Pro Gly Pro Asp Gly Pro Ala Ala Pro Gly Pro Ala Ala Ile
 1 5 10 15
 Arg Glu Gly Trp Phe Arg Glu Thr Cys Ser Leu Trp Pro Gly Gln Ala
 20 25 30

Leu Ser Leu Gln Val Glu Gln Leu Leu His His Arg Arg Ser Arg Tyr
 35 40 45
 Gln Asp Ile Leu Val Phe Arg Ser Lys Thr Tyr Gly Asn Val Leu Val
 50 55 60
 Leu Asp Gly Val Ile Gln Cys Thr Glu Arg Asp Glu Phe Ser Tyr Gln
 65 70 75 80
 Glu Met Ile Ala Asn Leu Pro Leu Cys Ser His Pro Asn Pro Arg Lys
 85 90 95
 Val Leu Ile Ile Gly Gly Gly Asp Gly Gly Val Leu Arg Glu Val Val
 100 105 110
 Lys His Pro Ser Val Glu Ser Val Val Gln Cys Glu Ile Asp Glu Asp
 115 120 125
 Val Ile Glu Val Ser Lys Lys Phe Leu Pro Gly Met Ala Val Gly Phe
 130 135 140
 Ser Ser Ser Lys Leu Thr Leu His Val Gly Asp Gly Phe Glu Phe Met
 145 150 155 160
 Lys Gln Asn Gln Asp Ala Phe Asp Val Ile Ile Thr Asp Ser Ser Asp
 165 170 175
 Pro Met Gly Pro Ala Glu Ser Leu Phe Lys Glu Ser Tyr Tyr Gln Leu
 180 185 190
 Met Lys Thr Ala Leu Lys Glu Asp Gly Ile Leu Cys Cys Gln Gly Glu
 195 200 205
 Cys Gln Trp Leu His Leu Asp Leu Ile Lys Glu Met Arg His Phe Cys
 210 215 220
 Lys Ser Leu Phe Pro Val Val Asp Tyr Ala Tyr Cys Ser Ile Pro Thr
 225 230 235 240
 Tyr Pro Ser Gly Gln Ile Gly Phe Met Leu Cys Ser Lys Asn Pro Ser
 245 250 255
 Thr Asn Phe Arg Glu Pro Val Gln Gln Leu Thr Gln Ala Gln Val Glu

	260		265		270
Gln Met Gln Leu Lys Tyr Tyr Asn Ser Asp Met His Arg Ala Ala Phe					
275		280		285	
Val Leu Pro Glu Phe Thr Arg Lys Ala Leu Asn Asp Ile Ser					
290		295		300	

<210> 57

<211> 3566

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (55).. (3045)

<400> 57

```

cttttttttt tttttattca cactgataca aaagtagatt ttacttttct agaa atg      57
                                                    Met
                                                    1
ttc cct tgt gct aga ggg aga gag agc tca gag ccg gga agg atg agg      105
Phe Pro Cys Ala Arg Gly Arg Glu Ser Ser Glu Pro Gly Arg Met Arg
           5                10                15
cgc ccg cgg cgg ccc ggg ggc tcc ggg ggc tcc ggg ggc tcc ggg ggc      153
Arg Pro Arg Arg Pro Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly
           20                25                30
ctc cgg ctg ctg gtc tgc ctg ctg ttg ctg agc ggc cgc ccc ggg ggc      201
Leu Arg Leu Leu Val Cys Leu Leu Leu Leu Ser Gly Arg Pro Gly Gly
           35                40                45
tgc agc gcc atc agt gcc cac ggc tgt ctg ttt gac cgc aga ctt tgt      249

```


Cys Ser Ala Ile Ser Ala His Gly Cys Leu Phe Asp Arg Arg Leu Cys
 50 55 60 65
 tgc cat ctg gaa gtc tgt att cag gat ggc ttg ttt gga cag tgc cag 297
 Ser His Leu Glu Val Cys Ile Gln Asp Gly Leu Phe Gly Gln Cys Gln
 70 75 80
 gca gga gtg ggg cag gca cgg ccc ctc tta caa gtc act tcc cca gtt 345
 Ala Gly Val Gly Gln Ala Arg Pro Leu Leu Gln Val Thr Ser Pro Val
 85 90 95
 ctc cag cgc cta caa ggt gtg ctc cgg caa ctc atg tcc caa ggc ttg 393
 Leu Gln Arg Leu Gln Gly Val Leu Arg Gln Leu Met Ser Gln Gly Leu
 100 105 110
 tcc tgg cat gat gac ctt acc cag cat gtg atc tcc cag gag atg gaa 441
 Ser Trp His Asp Asp Leu Thr Gln His Val Ile Ser Gln Glu Met Glu
 115 120 125
 cgc atc ccc agg ctt cgc ccc cca gag ccc cat cca agg gac agg tct 489
 Arg Ile Pro Arg Leu Arg Pro Pro Glu Pro His Pro Arg Asp Arg Ser
 130 135 140 145
 ggt ttg gtg ccc agg aaa cca ggc cct gca ggg gaa ttg cta act cag 537
 Gly Leu Val Pro Arg Lys Pro Gly Pro Ala Gly Glu Leu Leu Thr Gln
 150 155 160
 ggc aat cct act ggc tcc tct cct gct gcc cag ggc ttt cca agg cct 585
 Gly Asn Pro Thr Gly Ser Ser Pro Ala Ala Gln Gly Phe Pro Arg Pro
 165 170 175
 gca ggg ggt ggg gac gga gct ggg gcg ggc tcc cca ctg tcc tct ctg 633
 Ala Gly Gly Gly Asp Gly Ala Gly Ala Gly Ser Pro Leu Ser Ser Leu
 180 185 190
 cag gct gag ttg tta ccc cct ctc ttg gag cat ctg cta atg ccc cca 681
 Gln Ala Glu Leu Leu Pro Pro Leu Leu Glu His Leu Leu Met Pro Pro
 195 200 205

134/2644

355	360	365	
ccg gag cag ttt tct acc ctc ttg acc ctg ctg cag ttg ctg ccc aag	1209		
Pro Glu Gln Phe Ser Thr Leu Leu Thr Leu Leu Gln Leu Leu Pro Lys			
370	375	380	385
ggc aca gga aga aat ctt gaa ggg gct gta aat gtt gga gga gcc gat	1257		
Gly Thr Gly Arg Asn Leu Glu Gly Ala Val Asn Val Gly Gly Ala Asp			
390	395	400	
gtc aag aaa aca ata caa cag atg cag aga gga gac cca gca gaa gct	1305		
Val Lys Lys Thr Ile Gln Gln Met Gln Arg Gly Asp Pro Ala Glu Ala			
405	410	415	
ctg ccc ccc aca ccc tcg ctt cct ggg tac ctc act gcc agc cct gcc	1353		
Leu Pro Pro Thr Pro Ser Leu Pro Gly Tyr Leu Thr Ala Ser Pro Ala			
420	425	430	
tcc agc gaa gtt cag cag gtg ctg agc cct ggt ttc cct gaa cct ccc	1401		
Ser Ser Glu Val Gln Gln Val Leu Ser Pro Gly Phe Pro Glu Pro Pro			
435	440	445	
cac aca ccc agc cct ctg ggc tcc tcc tca gtc ctt ctg gag aag aaa	1449		
His Thr Pro Ser Pro Leu Gly Ser Ser Ser Val Leu Leu Glu Lys Lys			
450	455	460	465
agt ccc ttg ggc cag agc cag ccc aca gtg gtg gga cgg cca tca gct	1497		
Ser Pro Leu Gly Gln Ser Gln Pro Thr Val Val Gly Arg Pro Ser Ala			
470	475	480	
cga cca tcg gcc gag gag tat ggc tat atc gtc act gac cag aaa ccc	1545		
Arg Pro Ser Ala Glu Glu Tyr Gly Tyr Ile Val Thr Asp Gln Lys Pro			
485	490	495	
ctg agc ctg gtg gct gga gtg agg ctg ctg gag att ctg gct gag cac	1593		
Leu Ser Leu Val Ala Gly Val Arg Leu Leu Glu Ile Leu Ala Glu His			
500	505	510	
gtg cat atg tcc tcc ggt agc ttt atc aac atc agt gtg gtg gga cca	1641		

Val His Met Ser Ser Gly Ser Phe Ile Asn Ile Ser Val Val Gly Pro
 515 520 525
 gct gtc acc ttc cga atc cgg cac aat gag cag aac ctg tct ttg gca 1689
 Ala Val Thr Phe Arg Ile Arg His Asn Glu Gln Asn Leu Ser Leu Ala
 530 535 540 545
 gat gtg acc cag caa gct ggg ctg gtg aag tct gaa ctg gaa gcg cag 1737
 Asp Val Thr Gln Gln Ala Gly Leu Val Lys Ser Glu Leu Glu Ala Gln
 550 555 560
 aca ggg ctc cag att ttg cag aca ggg gtg gga cag agg gag gaa gca 1785
 Thr Gly Leu Gln Ile Leu Gln Thr Gly Val Gly Gln Arg Glu Glu Ala
 565 570 575
 gct gaa gtc ctt ccc cga caa gcc cat ggc ata tct ccc atg cgc tca 1833
 Ala Glu Val Leu Pro Arg Gln Ala His Gly Ile Ser Pro Met Arg Ser
 580 585 590
 gtg ctg ctt act cta gtg gcc ctg gca ggc gtc gct ggg ctg cta gtg 1881
 Val Leu Leu Thr Leu Val Ala Leu Ala Gly Val Ala Gly Leu Leu Val
 595 600 605
 gct ttg gca gtg gcc ttg tgt atg cgc cat cat tcg aga cag cgg gat 1929
 Ala Leu Ala Val Ala Leu Cys Met Arg His His Ser Arg Gln Arg Asp
 610 615 620 625
 aag gag cgc ctg gca gcc gtg ggg ccg gag ggg gcc cat ggt gac act 1977
 Lys Glu Arg Leu Ala Ala Val Gly Pro Glu Gly Ala His Gly Asp Thr
 630 635 640
 act ttt gag tac cag gac ctg tgt cgc cag cac atg gcc aca aag tcc 2025
 Thr Phe Glu Tyr Gln Asp Leu Cys Arg Gln His Met Ala Thr Lys Ser
 645 650 655
 ctg ttt aac cgg gcg gag ggt cag cca gag cct tct agg gtg agc agt 2073
 Leu Phe Asn Arg Ala Glu Gly Gln Pro Glu Pro Ser Arg Val Ser Ser
 660 665 670

gtg tcc tcc cag ttc agc gac gcg gcc cag gcc agc ccc agt tcc cac	2121
Val Ser Ser Gln Phe Ser Asp Ala Ala Gln Ala Ser Pro Ser Ser His	
675 : 680 685	
agc agc aca cca tct tgg tgc gag gag ccc gcc cag gcc aac atg gac	2169
Ser Ser Thr Pro Ser Trp Cys Glu Glu Pro Ala Gln Ala Asn Met Asp	
690 695 700 705	
atc tcc aca gga cac atg att ctg gca tac atg gag gat cac ctt cgg	2217
Ile Ser Thr Gly His Met Ile Leu Ala Tyr Met Glu Asp His Leu Arg	
710 715 720	
aac cgg gac cgg ttg gcc aag gag tgg cag gct ctg tgc gcc tac caa	2265
Asn Arg Asp Arg Leu Ala Lys Glu Trp Gln Ala Leu Cys Ala Tyr Gln	
725 730 735	
gca gag cca aac acc tgt gcc gcc gca cag gat gag agc aac atc aag	2313
Ala Glu Pro Asn Thr Cys Ala Ala Ala Gln Asp Glu Ser Asn Ile Lys	
740 745 750	
aag aac cgc cat cct gac ttc cta ccc tat gac cat gcc cga atc aag	2361
Lys Asn Arg His Pro Asp Phe Leu Pro Tyr Asp His Ala Arg Ile Lys	
755 760 765	
ctg aaa gtg gag agc agc cct tct cgg agt gat tac atc aac gcc agc	2409
Leu Lys Val Glu Ser Ser Pro Ser Arg Ser Asp Tyr Ile Asn Ala Ser	
770 775 780 785	
ccc atc atc gag cat gac cct cgg atg ccg gcc tac ata gcc aca cag	2457
Pro Ile Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile Ala Thr Gln	
790 795 800	
gga cca ctg tcc cac acc atc gcg gac ttc tgg cag atg gtg tgg gag	2505
Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met Val Trp Glu	
805 810 815	
agt ggc tgc act gtc atc gtt atg ctg acc ccg ttg gtg gag gac ggt	2553
Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val Glu Asp Gly	

820	825	830	
gtc aaa cag tgt gac cgc tac tgg ccg gat gaa gga tct tcc ctc tac	2601		
Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ser Ser Leu Tyr			
835	840	845	
cac gtc tat gag gtg aac ctg gtg tgc gag cac atc tgg tgc gag gac	2649		
His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp Cys Glu Asp			
850	855	860	865
ttc ctg gtg cgg agc ttc tac ctt aag aac gtg cag acc cag gag acg	2697		
Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr Gln Glu Thr			
870	875	880	
cgc acg ctc act cag ttc cac ttc ctc agc tgg ccg gca gag ggc act	2745		
Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala Glu Gly Thr			
885	890	895	
ccg gcc tcc acc cgg ccg ctg ctg gac ttc cgc agg aaa gtg aac aag	2793		
Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys Val Asn Lys			
900	905	910	
tgc tac aga ggc cgc tcc tgc ccc atc ata gtg cac tgc agt gac ggt	2841		
Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys Ser Asp Gly			
915	920	925	
gca ggg agg aca ggc acc tac atc ctt att gac atg gtc ctg aat cgc	2889		
Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val Leu Asn Arg			
930	935	940	945
atg gcc aaa gga gtg aag gag att gat att gct gcc acc ctg gag cat	2937		
Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr Leu Glu His			
950	955	960	
gtc cgt gac cag cgg cct gga ctt gtc cgt tct aag gac cag ttt gag	2985		
Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp Gln Phe Glu			
965	970	975	
ttt gcg ctg aca gcc gtg gca gag gag gtg aat gct atc ctc aag gcc	3033		

Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile Leu Lys Ala

980

985

990

ctg ccc cag tga gccccctgg gcgcctcagt gggcatcctg gcctcggctc 3085

Leu Pro Gln

995

cttctgcctg tgtgagcatt tgtgcaccca ctcttcagcc cctacccatt tgccaccttg 3145

gtctgacttg gccatgggag cctttcccaa cccagtgttg aaggagtcg ggagggaagg 3205

aaggggtagg ctgcccctgc tttatccatg ctagaacat ggtatccat gggaagcaga 3265

cagcaggcaa ggagaggcgt ggacaccggc cacagggttg cccgagcccc atcctacctg 3325

agtctctgtc tccctctctg gatagtgtcg tccccactcc caccagccta ccacctatag 3385

acaaagcaga acgaggaaac cccagctccc ccaaccctgc taccactggc ctgccacctt 3445

gacctgctc aaccttctcc ctctagcaca agggaacatt tctagaaaag taaaatctac 3505

ttttgtatca gtgtgaataa agttagtgtg ttgtctgtgc agctgcaaaa aaaaaaaaaa 3565

a 3566

<210> 58

<211> 996

<212> PRT

<213> Mus musculus

<400> 58

Met Phe Pro Cys Ala Arg Gly Arg Glu Ser Ser Glu Pro Gly Arg Met

1

5

10

15

Arg Arg Pro Arg Arg Pro Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly

20

25

30

Gly Leu Arg Leu Leu Val Cys Leu Leu Leu Ser Gly Arg Pro Gly

35

40

45

Gly Cys Ser Ala Ile Ser Ala His Gly Cys Leu Phe Asp Arg Arg Leu

50

55

60

Cys Ser His Leu Glu Val Cys Ile Gln Asp Gly Leu Phe Gly Gln Cys
 65 70 75 80
 Gln Ala Gly Val Gly Gln Ala Arg Pro Leu Leu Gln Val Thr Ser Pro
 85 90 95
 Val Leu Gln Arg Leu Gln Gly Val Leu Arg Gln Leu Met Ser Gln Gly
 100 105 110
 Leu Ser Trp His Asp Asp Leu Thr Gln His Val Ile Ser Gln Glu Met
 115 120 125
 Glu Arg Ile Pro Arg Leu Arg Pro Pro Glu Pro His Pro Arg Asp Arg
 130 135 140
 Ser Gly Leu Val Pro Arg Lys Pro Gly Pro Ala Gly Glu Leu Leu Thr
 145 150 155 160
 Gln Gly Asn Pro Thr Gly Ser Ser Pro Ala Ala Gln Gly Phe Pro Arg
 165 170 175
 Pro Ala Gly Gly Gly Asp Gly Ala Gly Ala Gly Ser Pro Leu Ser Ser
 180 185 190
 Leu Gln Ala Glu Leu Leu Pro Pro Leu Leu Glu His Leu Leu Met Pro
 195 200 205
 Pro Gln Pro Pro His Pro Ala Leu Thr Tyr Glu Pro Ala Leu Leu Gln
 210 215 220
 Pro Tyr Leu Phe His Gln Phe Gly Ser Arg Asp Gly Ser Arg Gly Ser
 225 230 235 240
 Glu Ser Ser Ser Gly Val Val Gly Val Gly His Leu Ser Lys Ala Glu
 245 250 255
 Gly Pro Ala Leu Phe Ser Arg Ser Ala Ser Lys Ala Ile Leu Gly Thr
 260 265 270
 His Ser Gly His Ser Phe Gly Asp Leu Thr Gly Pro Ser Pro Ala Gln
 275 280 285
 Leu Phe Gln Asp Ser Gly Leu Leu Tyr Met Ala Gln Glu Leu Pro Val

290	295	300
Pro Gly Arg Ala Arg Ala Pro Arg Leu Pro Glu Asn Gly Gly Asn Arg		
305	310	315
Ala Glu Asp Ser Ser Glu Gly His Glu Glu Glu Val Leu Gly Gly Arg		
	325	330
		335
Gly Glu Lys Ser Pro Pro Gln Ala Ala Gln Pro Glu Leu Ser Leu Gln		
	340	345
		350
Arg Leu Thr Ala Val Leu Ala Gly Tyr Gly Val Glu Leu Arg Gln Leu		
	355	360
		365
Thr Pro Glu Gln Phe Ser Thr Leu Leu Thr Leu Leu Gln Leu Leu Pro		
	370	375
		380
Lys Gly Thr Gly Arg Asn Leu Glu Gly Ala Val Asn Val Gly Gly Ala		
385	390	395
		400
Asp Val Lys Lys Thr Ile Gln Gln Met Gln Arg Gly Asp Pro Ala Glu		
	405	410
		415
Ala Leu Pro Pro Thr Pro Ser Leu Pro Gly Tyr Leu Thr Ala Ser Pro		
	420	425
		430
Ala Ser Ser Glu Val Gln Gln Val Leu Ser Pro Gly Phe Pro Glu Pro		
	435	440
		445
Pro His Thr Pro Ser Pro Leu Gly Ser Ser Ser Val Leu Leu Glu Lys		
	450	455
		460
Lys Ser Pro Leu Gly Gln Ser Gln Pro Thr Val Val Gly Arg Pro Ser		
465	470	475
		480
Ala Arg Pro Ser Ala Glu Glu Tyr Gly Tyr Ile Val Thr Asp Gln Lys		
	485	490
		495
Pro Leu Ser Leu Val Ala Gly Val Arg Leu Leu Glu Ile Leu Ala Glu		
	500	505
		510
His Val His Met Ser Ser Gly Ser Phe Ile Asn Ile Ser Val Val Gly		
	515	520
		525

Pro Ala Val Thr Phe Arg Ile Arg His Asn Glu Gln Asn Leu Ser Leu
 530 535 540
 Ala Asp Val Thr Gln Gln Ala Gly Leu Val Lys Ser Glu Leu Glu Ala
 545 550 555 560
 Gln Thr Gly Leu Gln Ile Leu Gln Thr Gly Val Gly Gln Arg Glu Glu
 565 570 575
 Ala Ala Glu Val Leu Pro Arg Gln Ala His Gly Ile Ser Pro Met Arg
 580 585 590
 Ser Val Leu Leu Thr Leu Val Ala Leu Ala Gly Val Ala Gly Leu Leu
 595 600 605
 Val Ala Leu Ala Val Ala Leu Cys Met Arg His His Ser Arg Gln Arg
 610 615 620
 Asp Lys Glu Arg Leu Ala Ala Val Gly Pro Glu Gly Ala His Gly Asp
 625 630 635 640
 Thr Thr Phe Glu Tyr Gln Asp Leu Cys Arg Gln His Met Ala Thr Lys
 645 650 655
 Ser Leu Phe Asn Arg Ala Glu Gly Gln Pro Glu Pro Ser Arg Val Ser
 660 665 670
 Ser Val Ser Ser Gln Phe Ser Asp Ala Ala Gln Ala Ser Pro Ser Ser
 675 680 685
 His Ser Ser Thr Pro Ser Trp Cys Glu Glu Pro Ala Gln Ala Asn Met
 690 695 700
 Asp Ile Ser Thr Gly His Met Ile Leu Ala Tyr Met Glu Asp His Leu
 705 710 715 720
 Arg Asn Arg Asp Arg Leu Ala Lys Glu Trp Gln Ala Leu Cys Ala Tyr
 725 730 735
 Gln Ala Glu Pro Asn Thr Cys Ala Ala Ala Gln Asp Glu Ser Asn Ile
 740 745 750
 Lys Lys Asn Arg His Pro Asp Phe Leu Pro Tyr Asp His Ala Arg Ile

755	760	765
Lys Leu Lys Val Glu Ser Ser Pro Ser Arg Ser Asp Tyr Ile Asn Ala		
770	775	780
Ser Pro Ile Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile Ala Thr		
785	790	795
Gln Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met Val Trp		
805	810	815
Glu Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val Glu Asp		
820	825	830
Gly Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ser Ser Leu		
835	840	845
Tyr His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp Cys Glu		
850	855	860
Asp Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr Gln Glu		
865	870	875
Thr Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala Glu Gly		
885	890	895
Thr Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys Val Asn		
900	905	910
Lys Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys Ser Asp		
915	920	925
Gly Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val Leu Asn		
930	935	940
Arg Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr Leu Glu		
945	950	955
His Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp Gln Phe		
965	970	975
Glu Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile Leu Lys		
980	985	990

Ala Leu Pro Gln

995

<210> 59

<211> 561

<212> DNA

<213> Mus musculus

<400> 59

```

gccccgcgct tcccttttcc ggtcgcggcg ctgcgcgac gtggagctcg tgcttgtgct 60
cggagctaig ccgccaagg gtcgcgtgca gtccgtgcag gtcttcggac gcaagaaaac 120
agccacggct gtggccccac tgcaaacggg gaaatgggct catcaagggt aacggacgtc 180
ccctggagat gatcgagccg cgcacgctgc agtacaagtt actggagcct gttttgcttc 240
tgggcaagga gcgatttgct ggtgtggata ttcgggtccg tgtgaagggt ggtggacatg 300
tgccccaaat ttatgccatc cgacagtcca tctcaaaggc cctggtagct tattaccaa 360
aatatgtgga tgaagcctcc aagaaggaga tcaaagatat cctcatcaa tacgatcgga 420
ccctgcttgt agctgacccc cgtcgctgcg aatccaaaaa gtttggaggt cctggtgccc 480
gtgcccgata ccagaaatcc taccgataag gcaatctcaa ggatcggggt ttacctttgt 540
aaaaacatcc taggatttta a 561

```

<210> 60

<211> 2947

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (531).. (1874)

<400> 60

agagagagag agagagagag agagagagag agagagagag tgagagagag agagactgag 60
 actagtggag aagtgaggag gggcgcgctg cgcgaggaga cagggcgagc agtggcggct 120
 ctggcgttca cattcctcta tgccacaaat ccgggaagaa gttttattgg gggggctgag 180
 atgttctatg cctttcccg ggcaagcctt gaticgaggc cctctcggca gagactgagc 240
 ggcgagaaag tgagagcccg gcccgcgcg ttcgagcgct ggcgctggag ccgcccttct 300
 accggccggc agtcattctt ctgacctgcc ttggccggg cgggtgccgg tagcgctgg 360
 ccgttgctg ctggctgaga ctctgttagg tgggtcgact cccctccct cctcctcttc 420
 ttctcctct tcttcgcct ccgttcctc ctctcctcc tgatcttccc tcttggcgg 480
 gcgagggtgg gggggcggg ggaggccgg gcttgcccc tgcagccacg atg ctc 536

Met Leu

1

ctg gac gcc gga ccc cag tat ccc gcg att ggt gtg acc acc ttt ggt 584
 Leu Asp Ala Gly Pro Gln Tyr Pro Ala Ile Gly Val Thr Thr Phe Gly

5

10

15

gca tcc cgg cac cac tcg gcg ggc gac gtg gcc gag aga gac gtg ggc 632
 Ala Ser Arg His His Ser Ala Gly Asp Val Ala Glu Arg Asp Val Gly

20

25

30

ctg ggt atc aac ccg ttc gcc gac ggc atg ggc gcc ttc aag ctc aac 680
 Leu Gly Ile Asn Pro Phe Ala Asp Gly Met Gly Ala Phe Lys Leu Asn

35

40

45

50

ccc agt tcg cac gaa ctg gcc tcg gct ggc cag aca gcc ttc acg tcg 728
 Pro Ser Ser His Glu Leu Ala Ser Ala Gly Gln Thr Ala Phe Thr Ser

55

60

65

cag gct ccg ggc tac cgc gct gct gcg gcc ctg ggc cac cat cac cac 776
 Gln Ala Pro Gly Tyr Arg Ala Ala Ala Ala Leu Gly His His His His

70

75

80

ccc ggc cac gtc ggc tcc tac tcc agc gct gct ttc aat tct acc cgg 824
 Pro Gly His Val Gly Ser Tyr Ser Ser Ala Ala Phe Asn Ser Thr Arg

85	90	95	
gac ttt ctg ttc cgc aac cgt ggc ttc ggc gac gcg gcg gcg gca gct	872		
Asp Phe Leu Phe Arg Asn Arg Gly Phe Gly Asp Ala Ala Ala Ala Ala			
100	105	110	
agc gcc cag cac agi ctc ttc gct gct tcg gcc ggc ggc ttt ggg ggc	920		
Ser Ala Gln His Ser Leu Phe Ala Ala Ser Ala Gly Gly Phe Gly Gly			
115	120	125	130
cca cac ggc cat acg gac gcc gcg ggc cac ctc ctt ttt tct ggg ctt	968		
Pro His Gly His Thr Asp Ala Ala Gly His Leu Leu Phe Ser Gly Leu			
	135	140	145
cac gag cag gcg gct ggc cac gct tcg ccc aac gtg gtt aac ggg cag	1016		
His Glu Gln Ala Ala Gly His Ala Ser Pro Asn Val Val Asn Gly Gln			
	150	155	160
atg cgg cta ggt ttc tcc ggg gac atg tac cca cgg ccg gaa cag tac	1064		
Met Arg Leu Gly Phe Ser Gly Asp Met Tyr Pro Arg Pro Glu Gln Tyr			
	165	170	175
ggc cag gtg acc agc ccg cga tcc gag cac tat gct gcc ccg cag ctt	1112		
Gly Gln Val Thr Ser Pro Arg Ser Glu His Tyr Ala Ala Pro Gln Leu			
	180	185	190
cac ggc tat ggg ccc atg aac gtg aac atg gct gca cat cac ggg gct	1160		
His Gly Tyr Gly Pro Met Asn Val Asn Met Ala Ala His His Gly Ala			
195	200	205	210
gga gcc ttc ttc cgc tat atg cgc caa ccc atc aag caa gag ctt atc	1208		
Gly Ala Phe Phe Arg Tyr Met Arg Gln Pro Ile Lys Gln Glu Leu Ile			
	215	220	225
tgt aaa tgg atc gag ccg gag cag ctg gcc aac ccc aaa aag tcg tgc	1256		
Cys Lys Trp Ile Glu Pro Glu Gln Leu Ala Asn Pro Lys Lys Ser Cys			
	230	235	240
aac aaa act ttc agc acc atg cac gag ctg gtc acg cac gtc acg gtg	1304		

Asn Lys Thr Phe Ser Thr Met His Glu Leu Val Thr His Val Thr Val	
245	250
255	
gag cac gtc ggc ggc cca gag cag agc aac cac atc tgc ttc tgg gag	1352
Glu His Val Gly Gly Pro Glu Gln Ser Asn His Ile Cys Phe Trp Glu	
260	265
270	
gag tgt cca cgc gag ggc aag ccc ttc aaa gcc aaa tac aaa ctg gtc	1400
Glu Cys Pro Arg Glu Gly Lys Pro Phe Lys Ala Lys Tyr Lys Leu Val	
275	280
285	290
aac cac atc cga gtg cac aca ggc gaa aag cct ttt ccc tgc ccg ttt	1448
Asn His Ile Arg Val His Thr Gly Glu Lys Pro Phe Pro Cys Pro Phe	
295	300
305	
cct ggc tgc ggc aag gtt ttc gcg cgt tca gag aac ctc aag atc cac	1496
Pro Gly Cys Gly Lys Val Phe Ala Arg Ser Glu Asn Leu Lys Ile His	
310	315
320	
aaa agg aca cac aca ggg gag aag ccc ttc aag tgc gag ttc gag ggc	1544
Lys Arg Thr His Thr Gly Glu Lys Pro Phe Lys Cys Glu Phe Glu Gly	
325	330
335	
tgc gac cgg cgc ttc gcc aac agc agc gac cgc aag aag cac atg cac	1592
Cys Asp Arg Arg Phe Ala Asn Ser Ser Asp Arg Lys Lys His Met His	
340	345
350	
gtg cac acg agc gac aag ccc tac ctt tgc aag atg tgc gat aag tcc	1640
Val His Thr Ser Asp Lys Pro Tyr Leu Cys Lys Met Cys Asp Lys Ser	
355	360
365	370
tac acg cac ccc agc tct ctg cgt aaa cac atg aag gtc cat gag tcc	1688
Tyr Thr His Pro Ser Ser Leu Arg Lys His Met Lys Val His Glu Ser	
375	380
385	
tct tct cag ggc tca cag cct tcg ccc gcc gcc agc tcg ggg tat gag	1736
Ser Ser Gln Gly Ser Gln Pro Ser Pro Ala Ala Ser Ser Gly Tyr Glu	
390	395
400	

tgc tcc acg cca ccc acc atc gtg tct ccc aca aca gac aac ccg acc 1784
 Ser Ser Thr Pro Pro Thr Ile Val Ser Pro Thr Thr Asp Asn Pro Thr
 405 410 415
 acc agc tcc atg tgc ccc tcc tcc tcc gcg gtt cac cac aca gcc ggc 1832
 Thr Ser Ser Met Ser Pro Ser Ser Ser Ala Val His His Thr Ala Gly
 420 425 430
 cac agc gcg ctc tct tcc aat ttt aac gaa tgg tac gtt taa 1874
 His Ser Ala Leu Ser Ser Asn Phe Asn Glu Trp Tyr Val
 435 440 445
 aatcagaaac aaaacatgcc gacccccctat ttaagagact gaacacacac gtatatagc 1934
 cgtattattg aaagaatcct gaaactcgag acacccctcg tcccgattcc cgcaaacgtt 1994
 tttatitttta tttttgttgt tgtttgttgt tgtttgattt tgtttttaaa tctgccggta 2054
 aatccaggac tgagtaaaac agaggaggca gcaagccttt aggttttttc actccaaatt 2114
 tttccitccc ccacccacct ctgaaaaggt ttggtagctg aagggcggaa gggggtggaa 2174
 gagaaggcgg ctgcctgacc gaacaccgcc aaaggcccca gggccaattt ctgtttggat 2234
 cagaacaagc tctctggggc ttcagctttt ctttatcttt ttgttttgtt ttcttgtaaa 2294
 tacagaatta ttagcttaaa tctgttctgt tggattctgt atatagctac acttcggttg 2354
 gagtgggttg gtgggatcgt ggcgttgttg tctttgcctt ggggagggga gggccagagg 2414
 gagggggagg gggaggggag gggcggccga aagccaactg ttgtactga atggcaagaa 2474
 tgttctagta aatgtgtacc aaaatgtgaa ctactttgta cgattacagt ctccacgtcg 2534
 acctaacaga atattattga tattaatgtg cttttttttg tataaagtcg aaacatttcg 2594
 tcccaaagtc tgagtacttt agtgcagtaa aatgttgttt catgtcctgt caagaattcg 2654
 tatagtacga gcctggatct acgtgtcaaa ctgttccatt tgtttatgta aagtgatatt 2714
 aaaaagatat aaactatagc tgtccattgc ttttgcaaa atatacaacc acacaatgta 2774
 tataattcct agtttcata tttatccgca tgtaaagggt ctggtttatt catgttacag 2834
 ctattcaata tttatggcta gtaaaaaaaaa aaaaaaaaaac tcgtatgtac actttagttt 2894
 ccagaactgt ttggtaacct ttcgtacgtt attaaagatt cttaaatttc aaa 2947

<211> 447

<212> PRT

<213> Mus musculus

<400> 61

```

Met Leu Leu Asp Ala Gly Pro Gln Tyr Pro Ala Ile Gly Val Thr Thr
  1             5             10             15
Phe Gly Ala Ser Arg His His Ser Ala Gly Asp Val Ala Glu Arg Asp
      20             25             30
Val Gly Leu Gly Ile Asn Pro Phe Ala Asp Gly Met Gly Ala Phe Lys
      35             40             45
Leu Asn Pro Ser Ser His Glu Leu Ala Ser Ala Gly Gln Thr Ala Phe
      50             55             60
Thr Ser Gln Ala Pro Gly Tyr Arg Ala Ala Ala Ala Leu Gly His His
      65             70             75             80
His His Pro Gly His Val Gly Ser Tyr Ser Ser Ala Ala Phe Asn Ser
      85             90             95
Thr Arg Asp Phe Leu Phe Arg Asn Arg Gly Phe Gly Asp Ala Ala Ala
      100             105             110
Ala Ala Ser Ala Gln His Ser Leu Phe Ala Ala Ser Ala Gly Gly Phe
      115             120             125
Gly Gly Pro His Gly His Thr Asp Ala Ala Gly His Leu Leu Phe Ser
      130             135             140
Gly Leu His Glu Gln Ala Ala Gly His Ala Ser Pro Asn Val Val Asn
      145             150             155             160
Gly Gln Met Arg Leu Gly Phe Ser Gly Asp Met Tyr Pro Arg Pro Glu
      165             170             175
Gln Tyr Gly Gln Val Thr Ser Pro Arg Ser Glu His Tyr Ala Ala Pro
      180             185             190

```

Gln Leu His Gly Tyr Gly Pro Met Asn Val Asn Met Ala Ala His His
 195 200 205
 Gly Ala Gly Ala Phe Phe Arg Tyr Met Arg Gln Pro Ile Lys Gln Glu
 210 215 220
 Leu Ile Cys Lys Trp Ile Glu Pro Glu Gln Leu Ala Asn Pro Lys Lys
 225 230 235 240
 Ser Cys Asn Lys Thr Phe Ser Thr Met His Glu Leu Val Thr His Val
 245 250 255
 Thr Val Glu His Val Gly Gly Pro Glu Gln Ser Asn His Ile Cys Phe
 260 265 270
 Trp Glu Glu Cys Pro Arg Glu Gly Lys Pro Phe Lys Ala Lys Tyr Lys
 275 280 285
 Leu Val Asn His Ile Arg Val His Thr Gly Glu Lys Pro Phe Pro Cys
 290 295 300
 Pro Phe Pro Gly Cys Gly Lys Val Phe Ala Arg Ser Glu Asn Leu Lys
 305 310 315 320
 Ile His Lys Arg Thr His Thr Gly Glu Lys Pro Phe Lys Cys Glu Phe
 325 330 335
 Glu Gly Cys Asp Arg Arg Phe Ala Asn Ser Ser Asp Arg Lys Lys His
 340 345 350
 Met His Val His Thr Ser Asp Lys Pro Tyr Leu Cys Lys Met Cys Asp
 355 360 365
 Lys Ser Tyr Thr His Pro Ser Ser Leu Arg Lys His Met Lys Val His
 370 375 380
 Glu Ser Ser Ser Gln Gly Ser Gln Pro Ser Pro Ala Ala Ser Ser Gly
 385 390 395 400
 Tyr Glu Ser Ser Thr Pro Pro Thr Ile Val Ser Pro Thr Thr Asp Asn
 405 410 415
 Pro Thr Thr Ser Ser Met Ser Pro Ser Ser Ser Ala Val His His Thr

420 425 430
 Ala Gly His Ser Ala Leu Ser Ser Asn Phe Asn Glu Trp Tyr Val
 435 440 445

<210> 62

<211> 2346

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (710).. (2008)

<400> 62

gaattcggga tccttttgcg cattcctagt tagcagtgcg tactcatcag actggagatg 60
 tttaatgaca tcagggaacc aaacggacaa cccatagtag ccgaagacag ggtgaaccag 120
 acaatcgtaa gcttgaatgg gttttccctg actgggtagt tgaagcatct catgaatgtc 180
 agccaaattc cgtacagttc ggtgcggatc cgaacgaaac accctctgta ccaggttccc 240
 gtgtcgctct caatttcaat cagctcatct atttgtttgg gagtcttgat tttatattacc 300
 gtgaagacct tctctggctg gccccgggct ctcatgttgg tgtcatgaat taacttcaga 360
 atcatccagg ctcatcatg ttttcccacc tccagcaaga accgagggtt ttctggcatg 420
 aaggtagagag ccaccacaga ggagacgcat gggagcgcac agacgatgac gaagacgcgc 480
 cacgtgtgga actggttaggc tgaacccatg ctgaagctcc acccgtagtg gggaatgatg 540
 gcccgaggcat ggccggaggct agatgccgcc aatcatccag aacatgcaga agccgctgct 600
 ggggagcttg gggctgcggt ggtggcgggt gacgggcttc gggacgcgga gcgacgcggc 660
 ctagcgcggc ggacggccgt gggaactcgg gcagccgacc cgtcccgcc atg gag atg 718

Met Glu Met

1

gag aag gag ttc gag gag atc gac aag gct ggg aac tgg gcg gct att 766

Glu	Lys	Glu	Phe	Glu	Glu	Ile	Asp	Lys	Ala	Gly	Asn	Trp	Ala	Ala	Ile		
5						10					15						
tac	cag	gac	att	cga	cat	gaa	gcc	agc	gac	ttc	cca	tgc	aaa	gtc	gcg	814	
Tyr	Gln	Asp	Ile	Arg	His	Glu	Ala	Ser	Asp	Phe	Pro	Cys	Lys	Val	Ala		
20						25					30				35		
aag	ctt	cct	aag	aac	aaa	aac	cgg	aac	agg	tac	cga	gat	gtc	agc	cct	862	
Lys	Leu	Pro	Lys	Asn	Lys	Asn	Arg	Asn	Arg	Tyr	Arg	Asp	Val	Ser	Pro		
						40					45				50		
ttt	gac	cac	agt	cgg	att	aaa	ttg	cac	cag	gaa	gat	aat	gac	tat	atc	910	
Phe	Asp	His	Ser	Arg	Ile	Lys	Leu	His	Gln	Glu	Asp	Asn	Asp	Tyr	Ile		
						55									65		
aat	gcc	agc	ttg	ata	aaa	atg	gaa	gaa	gcc	cag	agg	agc	tat	att	ctc	958	
Asn	Ala	Ser	Leu	Ile	Lys	Met	Glu	Glu	Ala	Gln	Arg	Ser	Tyr	Ile	Leu		
						70									80		
acc	cag	ggc	cct	tta	cca	aac	aca	tgt	ggg	cac	ttc	tgg	gag	atg	gtg	1006	
Thr	Gln	Gly	Pro	Leu	Pro	Asn	Thr	Cys	Gly	His	Phe	Trp	Glu	Met	Val		
						85									95		
tgg	gag	cag	aag	agc	agg	ggc	gtg	gtc	atg	ctc	aac	cgc	atc	atg	gag	1054	
Trp	Glu	Gln	Lys	Ser	Arg	Gly	Val	Val	Met	Leu	Asn	Arg	Ile	Met	Glu		
100						105					110				115		
aaa	ggc	tcg	tta	aaa	tgt	gcc	cag	tat	tgg	cca	cag	caa	gaa	gaa	aag	1102	
Lys	Gly	Ser	Leu	Lys	Cys	Ala	Gln	Tyr	Trp	Pro	Gln	Gln	Glu	Glu	Lys		
						120					125				130		
gag	atg	gtc	ttt	gat	gac	aca	ggt	ttg	aag	ttg	aca	cta	atc	tct	gaa	1150	
Glu	Met	Val	Phe	Asp	Asp	Thr	Gly	Leu	Lys	Leu	Thr	Leu	Ile	Ser	Glu		
						135					140				145		
gat	gtc	aag	tca	tat	tac	aca	gta	cga	cag	ttg	gag	ttg	gaa	aac	ctg	1198	
Asp	Val	Lys	Ser	Tyr	Tyr	Thr	Val	Arg	Gln	Leu	Glu	Leu	Glu	Asn	Leu		
						150									160		

act acc aag gag act cga gag atc ctg cat ttc cac tac acc aca tgg 1246
 Thr Thr Lys Glu Thr Arg Glu Ile Leu His Phe His Tyr Thr Thr Trp
 165 170 175
 cct gac ttt gga gtc ccc gag tca ccg gct tct ttc ctc aat ttc ctt 1294
 Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu Asn Phe Leu
 180 185 190 195
 ttc aaa gtc cga gag tca ggc tca ctc agc ctg gag cat ggc ccc att 1342
 Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Leu Glu His Gly Pro Ile
 200 205 210
 gtg gtc cac tgc agc gcc ggc atc ggg agg tca ggg acc ttc tgt ctg 1390
 Val Val His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr Phe Cys Leu
 215 220 225
 gct gac acc tgc ctc tta ctg atg gac aag agg aaa gac cca tct tcc 1438
 Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp Pro Ser Ser
 230 235 240
 gtg gac atc aag aaa gta ctg ctg gag atg cgc agg ttc cgc atg ggg 1486
 Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Arg Phe Arg Met Gly
 245 250 255
 ctc atc cag act gcc gac cag ctg cgc ttc tcc tac ctg gct gtc atc 1534
 Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu Ala Val Ile
 260 265 270 275
 gag ggc gcc aag ttc atc atg ggc gac tcg tca gtg cag gat cag tgg 1582
 Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln Asp Gln Trp
 280 285 290
 aag gag ctc tcc cgg gag gat cta gac ctt cca ccc gag cac gtg ccc 1630
 Lys Glu Leu Ser Arg Glu Asp Leu Asp Leu Pro Pro Glu His Val Pro
 295 300 305
 cca cct ccc cgg cca ccc aaa cgc aca ctg gag cct cac aac ggg aag 1678
 Pro Pro Pro Arg Pro Pro Lys Arg Thr Leu Glu Pro His Asn Gly Lys

310	315	320	
tgc aag gag ctc ttc tcc agc cac cag tgg gtg agc gag gag acc tgt			1726
Cys Lys Glu Leu Phe Ser Ser His Gln Trp Val Ser Glu Glu Thr Cys			
325	330	335	
ggg gat gaa gac agc ctg gcc aga gag gaa ggc aga gcc cag tca agt			1774
Gly Asp Glu Asp Ser Leu Ala Arg Glu Glu Gly Arg Ala Gln Ser Ser			
340	345	350	355
gcc atg cac agc gtg agc agc atg agt cca gac act gaa gtt agg aga			1822
Ala Met His Ser Val Ser Ser Met Ser Pro Asp Thr Glu Val Arg Arg			
	360	365	370
cgg atg gtg ggt gga ggt ctt caa agt gct cag gcg tct gtc ccc acc			1870
Arg Met Val Gly Gly Gly Leu Gln Ser Ala Gln Ala Ser Val Pro Thr			
	375	380	385
gag gaa gag ctg tcc tcc act gag gag gaa cac aag gca cat tgg cca			1918
Glu Glu Glu Leu Ser Ser Thr Glu Glu Glu His Lys Ala His Trp Pro			
	390	395	400
agt cac tgg aag ccc ttc ctg gtc aat gtg tgc atg gcc acg ctc ctg			1966
Ser His Trp Lys Pro Phe Leu Val Asn Val Cys Met Ala Thr Leu Leu			
	405	410	415
gcc acc ggc gcg tac ttg tgc tac cgg gtg tgt ttt cac tga			2008
Ala Thr Gly Ala Tyr Leu Cys Tyr Arg Val Cys Phe His			
420	425	430	
cagactggga ggcactgccca ctgcccagct taggatgcgg tctgcggcgt ctagcctggt			2068
gtagaggga caacaactcg caagcctgct ctggaactgg aagggcctgc cccaggaggg			2128
tattagtgca ctgggctttg aaggagcccc tgggtcccacg aacagagtct aatctcaggg			2188
ccttaacctg ttcaggagaa gtagaggaaa tgccaaatac tcttcttgct ctcacctcac			2248
tcctcccttt tctctgattc atttgTTTTT ggaaaaaaaa aaaaaaagaa ttacaacaca			2308
ttgttgTTTT taacatttat aaaggcaggc ccgaattc			2346

<210> 63

<211> 432

<212> PRT

<213> Mus musculus

<400> 63

Met Glu Met Glu Lys Glu Phe Glu Glu Ile Asp Lys Ala Gly Asn Trp

1 5 10 15

Ala Ala Ile Tyr Gln Asp Ile Arg His Glu Ala Ser Asp Phe Pro Cys

20 25 30

Lys Val Ala Lys Leu Pro Lys Asn Lys Asn Arg Asn Arg Tyr Arg Asp

35 40 45

Val Ser Pro Phe Asp His Ser Arg Ile Lys Leu His Gln Glu Asp Asn

50 55 60

Asp Tyr Ile Asn Ala Ser Leu Ile Lys Met Glu Glu Ala Gln Arg Ser

65 70 75 80

Tyr Ile Leu Thr Gln Gly Pro Leu Pro Asn Thr Cys Gly His Phe Trp

85 90 95

Glu Met Val Trp Glu Gln Lys Ser Arg Gly Val Val Met Leu Asn Arg

100 105 110

Ile Met Glu Lys Gly Ser Leu Lys Cys Ala Gln Tyr Trp Pro Gln Gln

115 120 125

Glu Glu Lys Glu Met Val Phe Asp Asp Thr Gly Leu Lys Leu Thr Leu

130 135 140

Ile Ser Glu Asp Val Lys Ser Tyr Tyr Thr Val Arg Gln Leu Glu Leu

145 150 155 160

Glu Asn Leu Thr Thr Lys Glu Thr Arg Glu Ile Leu His Phe His Tyr

165 170 175

Thr Thr Trp Pro Asp Phe Gly Val Pro Glu Ser Pro Ala Ser Phe Leu

180	185	190
Asn Phe Leu Phe Lys Val Arg Glu Ser Gly Ser Leu Ser Leu Glu His		
195	200	205
Gly Pro Ile Val Val His Cys Ser Ala Gly Ile Gly Arg Ser Gly Thr		
210	215	220
Phe Cys Leu Ala Asp Thr Cys Leu Leu Leu Met Asp Lys Arg Lys Asp		
225	230	235
Pro Ser Ser Val Asp Ile Lys Lys Val Leu Leu Glu Met Arg Arg Phe		
245	250	255
Arg Met Gly Leu Ile Gln Thr Ala Asp Gln Leu Arg Phe Ser Tyr Leu		
260	265	270
Ala Val Ile Glu Gly Ala Lys Phe Ile Met Gly Asp Ser Ser Val Gln		
275	280	285
Asp Gln Trp Lys Glu Leu Ser Arg Glu Asp Leu Asp Leu Pro Pro Glu		
290	295	300
His Val Pro Pro Pro Pro Arg Pro Pro Lys Arg Thr Leu Glu Pro His		
305	310	315
Asn Gly Lys Cys Lys Glu Leu Phe Ser Ser His Gln Trp Val Ser Glu		
325	330	335
Glu Thr Cys Gly Asp Glu Asp Ser Leu Ala Arg Glu Glu Gly Arg Ala		
340	345	350
Gln Ser Ser Ala Met His Ser Val Ser Ser Met Ser Pro Asp Thr Glu		
355	360	365
Val Arg Arg Arg Met Val Gly Gly Gly Leu Gln Ser Ala Gln Ala Ser		
370	375	380
Val Pro Thr Glu Glu Glu Leu Ser Ser Thr Glu Glu Glu His Lys Ala		
385	390	395
His Trp Pro Ser His Trp Lys Pro Phe Leu Val Asn Val Cys Met Ala		
405	410	415

Thr Leu Leu Ala Thr Gly Ala Tyr Leu Cys Tyr Arg Val Cys Phe His

420

425

430

<210> 64

<211> 445

<212> DNA

<213> Mus musculus

<400> 64

```

gcttccctcc cctttcctca gagactgtga accaggaaga gaagagtggc ccaggtgcag 60
gtggcgggtgg cagcggggac tctgacagct tcttcaactc caaggtagca ttgttcgcag 120
ccgtcgggcgc cggctgtgtc atcttcctgc tcatcatcat cttcttgaca gtcctactac 180
tcaagctccg caagcgccat cgcaagcata cacagcagcg ggcggctgcc ctctcgctca 240
gtaccctagc cagccccaaa gggggtagtgt gtacagcggg caccgagccc agcgacatca 300
tcatcccttt acggactaca gagaacaact actgccccca ctatgagaag gtgagtgggg 360
actacgggca tcctgtctac atcgtccagg agatgcccc tcagagcccg gccaacatct 420
actacaaggt ttgaaggccc agtat                                     445

```

<210> 65

<211> 3103

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (109).. (1536)

<400> 65

```

ccgggcgggt ttccagtcgt tggctccgag cggtgccgcg ggagccctcag gaggagcggg 60

```

cgtggcggct gctctggccc gggcggaact cccgggcctc ccgtgcga atg ggc ccg 117
 Met Gly Pro
 1
 gcg ccg ggt caa ggg ctg tac cgc tct ccg atg ccc ggg gcg gcc tat 165
 Ala Pro Gly Gln Gly Leu Tyr Arg Ser Pro Met Pro Gly Ala Ala Tyr
 5 10 15
 ccg aga cca ggt atg ctg cca ggt agc cga atg aca cct cag gga cct 213
 Pro Arg Pro Gly Met Leu Pro Gly Ser Arg Met Thr Pro Gln Gly Pro
 20 25 30 35
 tcc atg gga cct cct ggc tat ggg ggg aac cct tca gtc cga cct ggt 261
 Ser Met Gly Pro Pro Gly Tyr Gly Gly Asn Pro Ser Val Arg Pro Gly
 40 45 50
 ctg gcc cag tca ggg atg gac cag tcc cgc aag aga cct gca cct caa 309
 Leu Ala Gln Ser Gly Met Asp Gln Ser Arg Lys Arg Pro Ala Pro Gln
 55 60 65
 cag atc cag cag gtc cag cag cag gcg gtc caa aat cga aat cac aat 357
 Gln Ile Gln Gln Val Gln Gln Gln Ala Val Gln Asn Arg Asn His Asn
 70 75 80
 gca aag aaa aag aag atg gct gac aaa atc cta cct caa agg att cgg 405
 Ala Lys Lys Lys Lys Met Ala Asp Lys Ile Leu Pro Gln Arg Ile Arg
 85 90 95
 gaa ctg gtc cca gaa tca cag gcc tac atg gat ctc ctg gct ttt gaa 453
 Glu Leu Val Pro Glu Ser Gln Ala Tyr Met Asp Leu Leu Ala Phe Glu
 100 105 110 115
 agg aaa ctg gac cag act att atg agg aag cgg cta gat atc cag gag 501
 Arg Lys Leu Asp Gln Thr Ile Met Arg Lys Arg Leu Asp Ile Gln Glu
 120 125 130
 gcc ttg aaa cgt ccc atc aag caa aaa cgg aag ctg cga att ttc att 549
 Ala Leu Lys Arg Pro Ile Lys Gln Lys Arg Lys Leu Arg Ile Phe Ile

135	140	145	
tct aac acg ttc aat ccg gct aag tcg gac gcg gag gat ggg gaa ggg	597		
Ser Asn Thr Phe Asn Pro Ala Lys Ser Asp Ala Glu Asp Gly Glu Gly			
150	155	160	
acg gtg gct tcc tgg gag ctc cgg gta gaa ggc cgg ctc ctg gag gac	645		
Thr Val Ala Ser Trp Glu Leu Arg Val Glu Gly Arg Leu Leu Glu Asp			
165	170	175	
gcc gcc ttg tcc aaa tat gac gcc acc aag caa aag aga aag ttc tct	693		
Ala Ala Leu Ser Lys Tyr Asp Ala Thr Lys Gln Lys Arg Lys Phe Ser			
180	185	190	195
tcc ttt ttt aag tcc ttg gtg atc gaa ctg gac aaa gac ctc tat ggc	741		
Ser Phe Phe Lys Ser Leu Val Ile Glu Leu Asp Lys Asp Leu Tyr Gly			
200	205	210	
cca gac aac cat ctg gta gaa tgg cac agg acc gcc act acc cag gag	789		
Pro Asp Asn His Leu Val Glu Trp His Arg Thr Ala Thr Thr Gln Glu			
215	220	225	
acc gat ggc ttc cag gtg aag cgg cca gga gat gtg aat gta cgg tgt	837		
Thr Asp Gly Phe Gln Val Lys Arg Pro Gly Asp Val Asn Val Arg Cys			
230	235	240	
act gtc ctg ctg atg ctg gac tac cag ccc ccc cag ttt aaa tta gac	885		
Thr Val Leu Leu Met Leu Asp Tyr Gln Pro Pro Gln Phe Lys Leu Asp			
245	250	255	
cct cgc ctg gct cgg ctc ttg ggc atc cat acc cag aca cgt cca gtg	933		
Pro Arg Leu Ala Arg Leu Leu Gly Ile His Thr Gln Thr Arg Pro Val			
260	265	270	275
atc atc caa gca ctg tgg cag tat att aaa aca cac aag ctc cag gac	981		
Ile Ile Gln Ala Leu Trp Gln Tyr Ile Lys Thr His Lys Leu Gln Asp			
280	285	290	
cct cac gag cga gag ttt gtt ctc tgt gac aag tac ctc cag cag atc	1029		

Pro His Glu Arg Glu Phe Val Leu Cys Asp Lys Tyr Leu Gln Gln Ile
 295 300 305
 ttt gaa tct cag cgg atg aag ttc tca gag atc cct cag cgg ctc cac 1077
 Phe Glu Ser Gln Arg Met Lys Phe Ser Glu Ile Pro Gln Arg Leu His
 310 315 320
 gcc ttg ctt atg cca cca gag ccc atc atc atc aat cat gtc atc agt 1125
 Ala Leu Leu Met Pro Pro Glu Pro Ile Ile Ile Asn His Val Ile Ser
 325 330 335
 gtg gac cca aat gac cag aaa aag acc gcg tgc tat gac att gac gtg 1173
 Val Asp Pro Asn Asp Gln Lys Lys Thr Ala Cys Tyr Asp Ile Asp Val
 340 345 350 355
 gag gtg gat gac act ctg aag acc cag atg aac tct ttc ctg ttg tcc 1221
 Glu Val Asp Asp Thr Leu Lys Thr Gln Met Asn Ser Phe Leu Leu Ser
 360 365 370
 act gcc agc cag cag gag atc gcc act cta gac aac aag atc cat gag 1269
 Thr Ala Ser Gln Gln Glu Ile Ala Thr Leu Asp Asn Lys Ile His Glu
 375 380 385
 acg ata gag acc atc aac cag ctg aag acc cag cga gag ttc atg ttg 1317
 Thr Ile Glu Thr Ile Asn Gln Leu Lys Thr Gln Arg Glu Phe Met Leu
 390 395 400
 agc ttg ccc gag ccc tca ggt ttc atc aat gat tgg ctt cag tcc cag 1365
 Ser Leu Pro Glu Pro Ser Gly Phe Ile Asn Asp Trp Leu Gln Ser Gln
 405 410 415
 tgc agg ggc ctc aag acg atg act gat gtg gtg ggt aac ccg gaa gag 1413
 Cys Arg Gly Leu Lys Thr Met Thr Asp Val Val Gly Asn Pro Glu Glu
 420 425 430 435
 gag cgt cgt gct gag ttc tac ttc cag ccc tgg gct cag gag gct gtg 1461
 Glu Arg Arg Ala Glu Phe Tyr Phe Gln Pro Trp Ala Gln Glu Ala Val
 440 445 450

tgc cga tac ttc tac tcc aag gtg cag cag agg cgg caa gag tta gag 1509
 Cys Arg Tyr Phe Tyr Ser Lys Val Gln Gln Arg Arg Gln Glu Leu Glu

455

460

465

caa gcc ctg gga atc cga aac aca tag ggccctctgtg gcctagcctg 1556
 Gln Ala Leu Gly Ile Arg Asn Thr

470

475

gctgcaccga ttccttgggc cctgtgctgc ctgcctcagt gtacctgtct tggctcttgc 1616
 tgaggcattc caggggacct ggcttcagga cagtgtcaca atgaagaggg tgtcacattt 1676
 ctgtctcaca gtacctgtt atcccgctct gtacccagct cgtcccccgt cccgtcgtgt 1736
 cccccctca cccaccccg cctcagctcc tccccatcag gctcctgtgt gcctctacct 1796
 cccatccta cataggacct ctgatatgtg ttagagaacc acagagtggg gcctcctgag 1856
 gtcaggtagt cttagaggag accagctaca ctgacctgc cctgtcagg agacctaggc 1916
 cttagggagt atccctgtct gagcctcagg cctagggcag tctgtaagct agctgacctt 1976
 ggccctcccg gtaccttgca ctctctccct cccctccgca ggctggggca gaggctcctt 2036
 tacctctggc agtaaaggag cctgggcctc actgagcccc gggttggtcc cctgccctct 2096
 ggacttaacc tgcctgtcga gtgtcctctg acccttaggg gtccatgtca gtattggagt 2156
 gtgtgttgaa ttgttgctcc ctccacaca ctcccgtagc cgcccagttt aggatttccc 2216
 tacacctgcc ctaaccacag cttttgggtt ggggatcttg ctttcccttg tcattcccag 2276
 cagagactgt tccctcctgc tgttagagga gtggcttgtt tattcactcc accctgcccc 2336
 ctctgtaaa tggagaaaca ggctgaaat caaacgggta aagccctagg ccatccctgt 2396
 ctctctgtcc catgtctgcc cagttagaat ccactgggtg ggcttcccg gcactgagga 2456
 gtaaaagcgc ctagggcctg gagaataggt ctgaaatggg tttgtgactc cccacccct 2516
 gccctgccc caaagcttca gacccctcag ggagcagcag gatgtgggat cgaggccct 2576
 tgggacagat gctttagaat tccagggaa gcctccgatt ctccaggtt tgtcaccgg 2636
 agttagcatg tcccaggctc gcagacaaca ctgcagggtg ggagacagct gggcacagg 2696
 ggattctgtt gagcatgggc tctgaacca cagaactgac aaagccctg cttcccacc 2756
 cccacctcag gctcctgcga gcagtgtcc tgcaccttc ccagcctgtt ctgtactggg 2816
 gacagcagtc ttctccctgt cctcccatgt cctatatcca cccctccct tgaaggtcc 2876
 tccccacagt gacactggga cagccctggg gcagctgagc cccagcctgg ctcttggtg 2936

gaagcgcgat gaggagactt agcaatccac agtgcacctg tggtaactgt tcttattaac 2996
 tgatttgttt ttgttttgtt ttgttttgtt ttcatggacc aaaatttttt ttgtactgtc 3056
 tccttaactg atgtcaccca gttttaataa aagacttcta aagagca 3103

<210> 66

<211> 475

<212> PRT

<213> Mus musculus

<400> 66

Met Gly Pro Ala Pro Gly Gln Gly Leu Tyr Arg Ser Pro Met Pro Gly
 1 5 10 15
 Ala Ala Tyr Pro Arg Pro Gly Met Leu Pro Gly Ser Arg Met Thr Pro
 20 25 30
 Gln Gly Pro Ser Met Gly Pro Pro Gly Tyr Gly Gly Asn Pro Ser Val
 35 40 45
 Arg Pro Gly Leu Ala Gln Ser Gly Met Asp Gln Ser Arg Lys Arg Pro
 50 55 60
 Ala Pro Gln Gln Ile Gln Gln Val Gln Gln Gln Ala Val Gln Asn Arg
 65 70 75 80
 Asn His Asn Ala Lys Lys Lys Lys Met Ala Asp Lys Ile Leu Pro Gln
 85 90 95
 Arg Ile Arg Glu Leu Val Pro Glu Ser Gln Ala Tyr Met Asp Leu Leu
 100 105 110
 Ala Phe Glu Arg Lys Leu Asp Gln Thr Ile Met Arg Lys Arg Leu Asp
 115 120 125
 Ile Gln Glu Ala Leu Lys Arg Pro Ile Lys Gln Lys Arg Lys Leu Arg
 130 135 140
 Ile Phe Ile Ser Asn Thr Phe Asn Pro Ala Lys Ser Asp Ala Glu Asp

145	150	155	160
Gly Glu Gly Thr Val	Ala Ser Trp Glu Leu Arg Val	Glu Gly Arg Leu	
	165	170	175
Leu Glu Asp Ala Ala	Leu Ser Lys Tyr Asp Ala Thr	Lys Gln Lys Arg	
	180	185	190
Lys Phe Ser Ser Phe Phe	Lys Ser Leu Val Ile Glu Leu Asp	Lys Asp	
	195	200	205
Leu Tyr Gly Pro Asp Asn His	Leu Val Glu Trp His Arg Thr	Ala Thr	
	210	215	220
Thr Gln Glu Thr Asp Gly Phe	Gln Val Lys Arg Pro Gly Asp	Val Asn	
	225	230	235
Val Arg Cys Thr Val Leu Leu	Met Leu Asp Tyr Gln Pro Pro	Gln Phe	
	245	250	255
Lys Leu Asp Pro Arg Leu Ala	Arg Leu Leu Gly Ile His Thr	Gln Thr	
	260	265	270
Arg Pro Val Ile Ile Gln Ala	Leu Trp Gln Tyr Ile Lys Thr	His Lys	
	275	280	285
Leu Gln Asp Pro His Glu Arg	Glu Phe Val Leu Cys Asp Lys	Tyr Leu	
	290	295	300
Gln Gln Ile Phe Glu Ser Gln	Arg Met Lys Phe Ser Glu Ile	Pro Gln	
	305	310	315
Arg Leu His Ala Leu Leu	Met Pro Pro Glu Pro Ile Ile	Ile Asn His	
	325	330	335
Val Ile Ser Val Asp Pro Asn	Asp Gln Lys Lys Thr Ala Cys	Tyr Asp	
	340	345	350
Ile Asp Val Glu Val Asp Asp	Thr Leu Lys Thr Gln Met Asn	Ser Phe	
	355	360	365
Leu Leu Ser Thr Ala Ser Gln	Gln Glu Ile Ala Thr Leu Asp	Asn Lys	
	370	375	380

Ile His Glu Thr Ile Glu Thr Ile Asn Gln Leu Lys Thr Gln Arg Glu
 385 390 395 400
 Phe Met Leu Ser Leu Pro Glu Pro Ser Gly Phe Ile Asn Asp Trp Leu
 405 410 415
 Gln Ser Gln Cys Arg Gly Leu Lys Thr Met Thr Asp Val Val Gly Asn
 420 425 430
 Pro Glu Glu Glu Arg Arg Ala Glu Phe Tyr Phe Gln Pro Trp Ala Gln
 435 440 445
 Glu Ala Val Cys Arg Tyr Phe Tyr Ser Lys Val Gln Gln Arg Arg Gln
 450 455 460
 Glu Leu Glu Gln Ala Leu Gly Ile Arg Asn Thr
 465 470 475

<210> 67

<211> 2187

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (24).. (2012)

<400> 67

cgatttctcg gtactcttca ggg atg agt cat gtg gca gtg gaa aat gcg ctc 53

Met Ser His Val Ala Val Glu Asn Ala Leu

1

5

10

ggg ctg gac cag cag ttt gct ggc cta gac ctg aac tct tca gat aat 101

Gly Leu Asp Gln Gln Phe Ala Gly Leu Asp Leu Asn Ser Ser Asp Asn

15

20

25

cag agt gga gga agt aca gca agc aaa ggg cgt tat atc cca cct cat 149
 Gln Ser Gly Gly Ser Thr Ala Ser Lys Gly Arg Tyr Ile Pro Pro His
 30 35 40
 tta agg aac aga gaa gct act aaa gga ttc tat gac aaa gac agt tca 197
 Leu Arg Asn Arg Glu Ala Thr Lys Gly Phe Tyr Asp Lys Asp Ser Ser
 45 50 55
 ggg tgg agt tct agt aaa gat aag gat gca tac agc agt ttt gga tca 245
 Gly Trp Ser Ser Ser Lys Asp Lys Asp Ala Tyr Ser Ser Phe Gly Ser
 60 65 70
 cgg ggt gat tca aga ggg aag tct agc ttc ttt gga gat cgt gga agt 293
 Arg Gly Asp Ser Arg Gly Lys Ser Ser Phe Phe Gly Asp Arg Gly Ser
 75 80 85 90
 gga tca agg gga agg ttt gat gat cgt gga cgg gga gac tat gat ggc 341
 Gly Ser Arg Gly Arg Phe Asp Asp Arg Gly Arg Gly Asp Tyr Asp Gly
 95 100 105
 att ggt ggc cgt gga gat aga agt ggc ttt ggc aaa ttt gaa aga ggt 389
 Ile Gly Gly Arg Gly Asp Arg Ser Gly Phe Gly Lys Phe Glu Arg Gly
 110 115 120
 gga aat agt cgc tgg tgt gac aaa tca gat gaa gat gac tgg tca aag 437
 Gly Asn Ser Arg Trp Cys Asp Lys Ser Asp Glu Asp Asp Trp Ser Lys
 125 130 135
 cca ctc cca cca agt gaa cga ttg gaa cag gaa ctc ttt tct gga ggc 485
 Pro Leu Pro Pro Ser Glu Arg Leu Glu Gln Glu Leu Phe Ser Gly Gly
 140 145 150
 aat act ggg att aac ttt gag aaa tat gat gac att cca gtc gaa gca 533
 Asn Thr Gly Ile Asn Phe Glu Lys Tyr Asp Asp Ile Pro Val Glu Ala
 155 160 165 170
 aca ggc aac aac tgt cct cca cac att gaa agt ttc agt gat gtc gag 581
 Thr Gly Asn Asn Cys Pro Pro His Ile Glu Ser Phe Ser Asp Val Glu

175	180	185	
atg gga gaa att att atg gga aac att gag ctt act cgt tat act cgc			629
Met Gly Glu Ile Ile Met Gly Asn Ile Glu Leu Thr Arg Tyr Thr Arg			
190	195	200	
cca act cca gtg cag aag cat gct att cct att atc aaa gag aaa aga			677
Pro Thr Pro Val Gln Lys His Ala Ile Pro Ile Ile Lys Glu Lys Arg			
205	210	215	
gac ttg atg gct tgt gct caa aca ggc tct gga aaa act gca gca ttt			725
Asp Leu Met Ala Cys Ala Gln Thr Gly Ser Gly Lys Thr Ala Ala Phe			
220	225	230	
ctc ttg ccc atc ttg agt cag atc tat gct gat ggt cca gga gaa gct			773
Leu Leu Pro Ile Leu Ser Gln Ile Tyr Ala Asp Gly Pro Gly Glu Ala			
235	240	245	250
ctg agg gct atg aag gaa aat gga aga tat ggc cgt cgt aaa cag tat			821
Leu Arg Ala Met Lys Glu Asn Gly Arg Tyr Gly Arg Arg Lys Gln Tyr			
255	260	265	
cca atc tct ttg gta ctg gca cca acg aga gaa ttg gca gtg cag atc			869
Pro Ile Ser Leu Val Leu Ala Pro Thr Arg Glu Leu Ala Val Gln Ile			
270	275	280	
tat gag gaa gcc aga aaa ttc tca tac cga tct aga gtc cgt cct tgc			917
Tyr Glu Glu Ala Arg Lys Phe Ser Tyr Arg Ser Arg Val Arg Pro Cys			
285	290	295	
gtg gtt tat ggt ggt gct gaa att ggc cag cag att cga gac tta gaa			965
Val Val Tyr Gly Gly Ala Glu Ile Gly Gln Gln Ile Arg Asp Leu Glu			
300	305	310	
cgt gga tgc cac ttg tta gta gcc act cca gga cgt cta gtg gat atg			1013
Arg Gly Cys His Leu Leu Val Ala Thr Pro Gly Arg Leu Val Asp Met			
315	320	325	330
atg gag aga ggg aag atc ggg tta gac ttc tgc aaa tac ctg gtg tta			1061

167/2644

aaa agc cca att cta gtg gct aca gca gta gca gca aga gga ctg gat 1541
 Lys Ser Pro Ile Leu Val Ala Thr Ala Val Ala Ala Arg Gly Leu Asp
 495 500 505
 att tca aat gtg aag cat gtt att aat ttt gac ctg cct agt gat atc 1589
 Ile Ser Asn Val Lys His Val Ile Asn Phe Asp Leu Pro Ser Asp Ile
 510 515 520
 gaa gaa tat gtg cat cgc ata ggc cgt aca ggc cgt gtg gga aac ctt 1637
 Glu Glu Tyr Val His Arg Ile Gly Arg Thr Gly Arg Val Gly Asn Leu
 525 530 535
 ggt ctt gcc acc tca ttc ttt aat gaa agg aat ata aat atc aca aag 1685
 Gly Leu Ala Thr Ser Phe Phe Asn Glu Arg Asn Ile Asn Ile Thr Lys
 540 545 550
 gat tta ctg gat ctt ctt gtt gaa gca aaa caa gaa gtg cct tct tgg 1733
 Asp Leu Leu Asp Leu Leu Val Glu Ala Lys Gln Glu Val Pro Ser Trp
 555 560 565 570
 tta gag aac atg gct ttt gaa cac cac tac aag ggt agc agt cgt gga 1781
 Leu Glu Asn Met Ala Phe Glu His His Tyr Lys Gly Ser Ser Arg Gly
 575 580 585
 cgt tct aag agc agt cga ttt agt gga ggg ttt ggt gcc aga gac tac 1829
 Arg Ser Lys Ser Ser Arg Phe Ser Gly Gly Phe Gly Ala Arg Asp Tyr
 590 595 600
 cga cag agt agc ggt gcc agc agt tcc agc ttc agc agc agc cgt gca 1877
 Arg Gln Ser Ser Gly Ala Ser Ser Ser Ser Phe Ser Ser Ser Arg Ala
 605 610 615
 agc agc agt cga agt ggt gga ggt ggc cat ggc ggc agt cga gga ttt 1925
 Ser Ser Ser Arg Ser Gly Gly Gly Gly His Gly Gly Ser Arg Gly Phe
 620 625 630
 ggt gga ggt ggc tac gga ggc ttt tac aac agt gat gga tat gga ggg 1973
 Gly Gly Gly Gly Tyr Gly Gly Phe Tyr Asn Ser Asp Gly Tyr Gly Gly

635 640 645 650
 aat tat aac tcc cag ggg gtt gac tgg tgg ggt aac tga gcctgctctg 2022
 Asn Tyr Asn Ser Gln Gly Val Asp Trp Trp Gly Asn
 655 660
 tagtaggtca ccctgccaaa caagctaata tggaaccac atgtaactta gccagactat 2082
 acctgtgtga gcttcaagaa ctgcagtac attaccagct gtgattctcc actgaaattt 2142
 tttttaagg gagctcaagg tcacaagtaa agatgaaagg aacaa 2187

<210> 68

<211> 662

<212> PRT

<213> Mus musculus

<400> 68

Met Ser His Val Ala Val Glu Asn Ala Leu Gly Leu Asp Gln Gln Phe
 1 5 10 15
 Ala Gly Leu Asp Leu Asn Ser Ser Asp Asn Gln Ser Gly Gly Ser Thr
 20 25 30
 Ala Ser Lys Gly Arg Tyr Ile Pro Pro His Leu Arg Asn Arg Glu Ala
 35 40 45
 Thr Lys Gly Phe Tyr Asp Lys Asp Ser Ser Gly Trp Ser Ser Ser Lys
 50 55 60
 Asp Lys Asp Ala Tyr Ser Ser Phe Gly Ser Arg Gly Asp Ser Arg Gly
 65 70 75 80
 Lys Ser Ser Phe Phe Gly Asp Arg Gly Ser Gly Ser Arg Gly Arg Phe
 85 90 95
 Asp Asp Arg Gly Arg Gly Asp Tyr Asp Gly Ile Gly Gly Arg Gly Asp
 100 105 110
 Arg Ser Gly Phe Gly Lys Phe Glu Arg Gly Gly Asn Ser Arg Trp Cys

115	120	125
Asp Lys Ser Asp Glu Asp Asp Trp Ser Lys Pro Leu Pro Pro Ser Glu		
130	135	140
Arg Leu Glu Gln Glu Leu Phe Ser Gly Gly Asn Thr Gly Ile Asn Phe		
145	150	155
Glu Lys Tyr Asp Asp Ile Pro Val Glu Ala Thr Gly Asn Asn Cys Pro		
165	170	175
Pro His Ile Glu Ser Phe Ser Asp Val Glu Met Gly Glu Ile Ile Met		
180	185	190
Gly Asn Ile Glu Leu Thr Arg Tyr Thr Arg Pro Thr Pro Val Gln Lys		
195	200	205
His Ala Ile Pro Ile Ile Lys Glu Lys Arg Asp Leu Met Ala Cys Ala		
210	215	220
Gln Thr Gly Ser Gly Lys Thr Ala Ala Phe Leu Leu Pro Ile Leu Ser		
225	230	235
Gln Ile Tyr Ala Asp Gly Pro Gly Glu Ala Leu Arg Ala Met Lys Glu		
245	250	255
Asn Gly Arg Tyr Gly Arg Arg Lys Gln Tyr Pro Ile Ser Leu Val Leu		
260	265	270
Ala Pro Thr Arg Glu Leu Ala Val Gln Ile Tyr Glu Glu Ala Arg Lys		
275	280	285
Phe Ser Tyr Arg Ser Arg Val Arg Pro Cys Val Val Tyr Gly Gly Ala		
290	295	300
Glu Ile Gly Gln Gln Ile Arg Asp Leu Glu Arg Gly Cys His Leu Leu		
305	310	315
Val Ala Thr Pro Gly Arg Leu Val Asp Met Met Glu Arg Gly Lys Ile		
325	330	335
Gly Leu Asp Phe Cys Lys Tyr Leu Val Leu Asp Glu Ala Asp Arg Met		
340	345	350

Leu Asp Met Gly Phe Glu Pro Gln Ile Arg Arg Ile Val Glu Gln Asp
 355 360 365
 Thr Met Pro Pro Lys Gly Val Arg His Thr Met Met Phe Ser Ala Thr
 370 375 380
 Phe Pro Lys Glu Ile Gln Met Leu Ala Arg Asp Phe Leu Asp Glu Tyr
 385 390 395 400
 Ile Phe Leu Ala Val Gly Arg Val Gly Ser Thr Ser Glu Asn Ile Thr
 405 410 415
 Gln Lys Val Val Trp Val Glu Glu Ile Asp Lys Arg Ser Phe Leu Leu
 420 425 430
 Asp Leu Leu Asn Ala Thr Gly Lys Asp Ser Leu Thr Leu Val Phe Val
 435 440 445
 Glu Thr Lys Lys Gly Ala Asp Ser Leu Glu Asp Phe Leu Tyr His Glu
 450 455 460
 Gly Tyr Ala Cys Thr Ser Ile His Gly Asp Arg Ser Gln Arg Asp Arg
 465 470 475 480
 Glu Glu Ala Leu His Gln Phe Arg Ser Gly Lys Ser Pro Ile Leu Val
 485 490 495
 Ala Thr Ala Val Ala Ala Arg Gly Leu Asp Ile Ser Asn Val Lys His
 500 505 510
 Val Ile Asn Phe Asp Leu Pro Ser Asp Ile Glu Glu Tyr Val His Arg
 515 520 525
 Ile Gly Arg Thr Gly Arg Val Gly Asn Leu Gly Leu Ala Thr Ser Phe
 530 535 540
 Phe Asn Glu Arg Asn Ile Asn Ile Thr Lys Asp Leu Leu Asp Leu Leu
 545 550 555 560
 Val Glu Ala Lys Gln Glu Val Pro Ser Trp Leu Glu Asn Met Ala Phe
 565 570 575
 Glu His His Tyr Lys Gly Ser Ser Arg Gly Arg Ser Lys Ser Ser Arg

580 585 590
 Phe Ser Gly Gly Phe Gly Ala Arg Asp Tyr Arg Gln Ser Ser Gly Ala
 595 600 605
 Ser Ser Ser Ser Phe Ser Ser Ser Arg Ala Ser Ser Ser Arg Ser Gly
 610 615 620
 Gly Gly Gly His Gly Gly Ser Arg Gly Phe Gly Gly Gly Gly Tyr Gly
 625 630 635 640
 Gly Phe Tyr Asn Ser Asp Gly Tyr Gly Gly Asn Tyr Asn Ser Gln Gly
 645 650 655
 Val Asp Trp Trp Gly Asn
 660

<210> 69

<211> 2163

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (296).. (1711)

<400> 69

gggtggagta aagctacgcc caggcccgcg tccgctggcg gcgcaggaac ttcagcaccc 60
 gcggggcgga cagcgcttac cgcacctgct cacctgctct gggcgccaga agagcctgca 120
 tcctccitcc agcccgagc aactgcgccc ggaggcgccc agacctctc ccttcccgca 180
 cccaggctcc tgtcccttcc agcttcttaa ctccccctt cattcataac aaaagctaca 240
 gctcaggggc ccagcgccaa gctctttcca gcaaagcaca gaagagcaag aaaga atg 298

Met

1

ggc ttc ctt tgg acc ggc tct tgg ata ctg gtg ttg gtg ctc aac agc 346
 Gly Phe Leu Trp Thr Gly Ser Trp Ile Leu Val Leu Val Leu Asn Ser
 5 10 15
 ggc cca att caa gct ttc ccc aaa ccc gaa ggc agc caa gac aaa tcc 394
 Gly Pro Ile Gln Ala Phe Pro Lys Pro Glu Gly Ser Gln Asp Lys Ser
 20 25 30
 ctg cat aat aga gaa tta agt gca gaa aga cct ttg aat gaa cag atc 442
 Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln Ile
 35 40 45
 gct gag gca gag gca gac aag att aaa aag gca ttc cct tca gaa agc 490
 Ala Glu Ala Glu Ala Asp Lys Ile Lys Lys Ala Phe Pro Ser Glu Ser
 50 55 60 65
 aag ccg agt gaa agc aat tat tct tct gtc gat aac ttg aat ctg ctg 538
 Lys Pro Ser Glu Ser Asn Tyr Ser Ser Val Asp Asn Leu Asn Leu Leu
 70 75 80
 agg gca ata aca gaa aag gaa acc gtt gag aaa gag aga caa tcc ata 586
 Arg Ala Ile Thr Glu Lys Glu Thr Val Glu Lys Glu Arg Gln Ser Ile
 85 90 95
 aga agc ccc ccg ttt gat aac caa ctg aac gtg gaa gac gct gat tca 634
 Arg Ser Pro Pro Phe Asp Asn Gln Leu Asn Val Glu Asp Ala Asp Ser
 100 105 110
 acc aaa aat cgg aaa ctg atc gat gag tac gat tcc acc aag agt gga 682
 Thr Lys Asn Arg Lys Leu Ile Asp Glu Tyr Asp Ser Thr Lys Ser Gly
 115 120 125
 ctg gac cac aag ttt caa gat gac cca gac ggc ctt cat caa ctg gat 730
 Leu Asp His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu Asp
 130 135 140 145
 gga act cct tta act gct gaa gac atc gtc cat aag att gcc acc agg 778
 Gly Thr Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Thr Arg

150	155	160	
att tat gag gag aac gac aga gga gtg ttt gac aaa att gtt tct aaa	826		
Ile Tyr Glu Glu Asn Asp Arg Gly Val Phe Asp Lys Ile Val Ser Lys			
165	170	175	
ctg ctg aat ctt ggc ctg atc act gaa agc cag gca cat act ctg gaa	874		
Leu Leu Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu Glu			
180	185	190	
gat gaa gta gca gaa gct tta caa aaa ctg att tca aaa gag gcc aac	922		
Asp Glu Val Ala Glu Ala Leu Gln Lys Leu Ile Ser Lys Glu Ala Asn			
195	200	205	
aat tat gag gag acc ctg gat aaa ccc aca agc agg acc gag aat cag	970		
Asn Tyr Glu Glu Thr Leu Asp Lys Pro Thr Ser Arg Thr Glu Asn Gln			
210	215	220	225
gat ggg aaa ata cca gag aaa gtg act ccg gtg gca gca gtc caa gat	1018		
Asp Gly Lys Ile Pro Glu Lys Val Thr Pro Val Ala Ala Val Gln Asp			
230	235	240	
ggc ttc act aac cgt gaa aac gat gag acg gtg tct aac acc ttg acc	1066		
Gly Phe Thr Asn Arg Glu Asn Asp Glu Thr Val Ser Asn Thr Leu Thr			
245	250	255	
ttg tcc aat ggc ttg gaa agg aga act aac ccc cac agg gaa gac gac	1114		
Leu Ser Asn Gly Leu Glu Arg Arg Thr Asn Pro His Arg Glu Asp Asp			
260	265	270	
ttt gag gaa ctc cag tat ttc ccc aac ttc tat gca cta ctg aca agc	1162		
Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Thr Ser			
275	280	285	
atc gac tca gaa aaa gaa gca aaa gag aaa gaa acc ctg atc acc atc	1210		
Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr Ile			
290	295	300	305
atg aag aca ttg att gac ttc gtg aaa atg atg gtg aaa tac ggt acg	1258		

Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly Thr	
310 315 320	
ata tct cca gag gaa ggc gtg tcc tac ctt gaa aac ttg gat gaa aca	1306
Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu Thr	
325 330 335	
att gct ctg cag acc aag aac aag cta gaa aaa aat act act gat agc	1354
Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Thr Thr Asp Ser	
340 345 350	
aaa agt aag cta ttc cca gct cca cca gag aag agt cag gaa gaa aca	1402
Lys Ser Lys Leu Phe Pro Ala Pro Pro Glu Lys Ser Gln Glu Glu Thr	
355 360 365	
gac agt acc aag gaa gaa gcc gcc aag atg gaa aag gaa tac gga agc	1450
Asp Ser Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly Ser	
370 375 380 385	
cta aaa gac tct aca aaa gat gat aac tcc aac cta gga gga aag aca	1498
Leu Lys Asp Ser Thr Lys Asp Asp Asn Ser Asn Leu Gly Gly Lys Thr	
390 395 400	
gat gaa gcc aca ggg aag aca gaa gcc tac ttg gaa gcc att aga aaa	1546
Asp Glu Ala Thr Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg Lys	
405 410 415	
aac atc gaa tgg ctg aag aaa cat aac aag aag ggc aac aaa gaa gat	1594
Asn Ile Glu Trp Leu Lys Lys His Asn Lys Lys Gly Asn Lys Glu Asp	
420 425 430	
tac gac ctt tca aag atg agg gac ttt atc aac caa caa gct gac gct	1642
Tyr Asp Leu Ser Lys Met Arg Asp Phe Ile Asn Gln Gln Ala Asp Ala	
435 440 445	
tat gtg gag aag ggc atc ctc gac aag gaa gaa gcc aac gcc atc aaa	1690
Tyr Val Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Asn Ala Ile Lys	
450 455 460 465	

cgc atc tac agc agc ctg tga aaatggcggg cagcttgagc ctccctgttg 1741

Arg Ile Tyr Ser Ser Leu

470

ticcagcaaa aacaatatag cttacaaact aattcggcgg ttaaagggtt accagcccag 1801
 aagtattagg atgtgctgaa tttatagtag ttaatccctt agaaatgagt aaaatagagc 1861
 tctcttgcca taaatacctt atgaaaagca aagctgtaga gaagccgagg ttttctata 1921
 tagaatcctt atttctctt gaatttacat ttgtaatca gagatgtgct gctctggaaa 1981
 agactctaata ggggtgaaca taagtctgaa cctactcccc actgtcctca gccccctgaa 2041
 gctctgagag gccctgtctc ggcatgctag acacctgagc acctcactgg atgtttgtca 2101
 taggatgtcg ttccactag tcgatctctg ttgggcacgg aaataaaccc acgtctcttc 2161
 at 2163

<210> 70

<211> 471

<212> PRT

<213> Mus musculus

<400> 70

Met Gly Phe Leu Trp Thr Gly Ser Trp Ile Leu Val Leu Val Leu Asn

1 5 10 15

Ser Gly Pro Ile Gln Ala Phe Pro Lys Pro Glu Gly Ser Gln Asp Lys

20 25 30

Ser Leu His Asn Arg Glu Leu Ser Ala Glu Arg Pro Leu Asn Glu Gln

35 40 45

Ile Ala Glu Ala Glu Ala Asp Lys Ile Lys Lys Ala Phe Pro Ser Glu

50 55 60

Ser Lys Pro Ser Glu Ser Asn Tyr Ser Ser Val Asp Asn Leu Asn Leu

65 70 75 80

Leu Arg Ala Ile Thr Glu Lys Glu Thr Val Glu Lys Glu Arg Gln Ser

	85		90		95
Ile Arg Ser Pro Pro Phe Asp Asn Gln Leu Asn Val Glu Asp Ala Asp					
	100		105		110
Ser Thr Lys Asn Arg Lys Leu Ile Asp Glu Tyr Asp Ser Thr Lys Ser					
	115		120		125
Gly Leu Asp His Lys Phe Gln Asp Asp Pro Asp Gly Leu His Gln Leu					
	130		135		140
Asp Gly Thr Pro Leu Thr Ala Glu Asp Ile Val His Lys Ile Ala Thr					
145		150		155	160
Arg Ile Tyr Glu Glu Asn Asp Arg Gly Val Phe Asp Lys Ile Val Ser					
	165		170		175
Lys Leu Leu Asn Leu Gly Leu Ile Thr Glu Ser Gln Ala His Thr Leu					
	180		185		190
Glu Asp Glu Val Ala Glu Ala Leu Gln Lys Leu Ile Ser Lys Glu Ala					
	195		200		205
Asn Asn Tyr Glu Glu Thr Leu Asp Lys Pro Thr Ser Arg Thr Glu Asn					
	210		215		220
Gln Asp Gly Lys Ile Pro Glu Lys Val Thr Pro Val Ala Ala Val Gln					
225		230		235	240
Asp Gly Phe Thr Asn Arg Glu Asn Asp Glu Thr Val Ser Asn Thr Leu					
	245		250		255
Thr Leu Ser Asn Gly Leu Glu Arg Arg Thr Asn Pro His Arg Glu Asp					
	260		265		270
Asp Phe Glu Glu Leu Gln Tyr Phe Pro Asn Phe Tyr Ala Leu Leu Thr					
	275		280		285
Ser Ile Asp Ser Glu Lys Glu Ala Lys Glu Lys Glu Thr Leu Ile Thr					
	290		295		300
Ile Met Lys Thr Leu Ile Asp Phe Val Lys Met Met Val Lys Tyr Gly					
305		310		315	320

Thr Ile Ser Pro Glu Glu Gly Val Ser Tyr Leu Glu Asn Leu Asp Glu

325

330

335

Thr Ile Ala Leu Gln Thr Lys Asn Lys Leu Glu Lys Asn Thr Thr Asp

340

345

350

Ser Lys Ser Lys Leu Phe Pro Ala Pro Pro Glu Lys Ser Gln Glu Glu

355

360

365

Thr Asp Ser Thr Lys Glu Glu Ala Ala Lys Met Glu Lys Glu Tyr Gly

370

375

380

Ser Leu Lys Asp Ser Thr Lys Asp Asp Asn Ser Asn Leu Gly Gly Lys

385

390

395

400

Thr Asp Glu Ala Thr Gly Lys Thr Glu Ala Tyr Leu Glu Ala Ile Arg

405

410

415

Lys Asn Ile Glu Trp Leu Lys Lys His Asn Lys Lys Gly Asn Lys Glu

420

425

430

Asp Tyr Asp Leu Ser Lys Met Arg Asp Phe Ile Asn Gln Gln Ala Asp

435

440

445

Ala Tyr Val Glu Lys Gly Ile Leu Asp Lys Glu Glu Ala Asn Ala Ile

450

455

460

Lys Arg Ile Tyr Ser Ser Leu

465

470

<210> 71

<211> 597

<212> DNA

<213> Mus musculus

<400> 71

gtttatctgc ttgaaaatga tgtctctaca ttaggctatg acctcacctt cagcactgag 60

gttcaagaat ttggagtatg tgaagttcgt gacctcaaac ccaatggagc caacatcttg 120

gtaacagagg agaacaagaa ggaatatgta cacctggttt gccagatgag aatgacagga 180
 gccatccgca aacagctggc agccttcctg gagggcttct atgaaatcat tccaaagcgc 240
 ctcatatcca tctttactga gcaggaatta gagctgctca tatcagggtt gcctaccatc 300
 gacattgatg atctaaaatc taacacigag taccacaagt accaatccaa cictattcag 360
 atccagtgtt tttggagagc attgcgttcc ttgaccaag cagaccgtgc caagttcctc 420
 cagtttgta caggtacttc caaggtaccc ctacaaggat ttgctgccct tgaaggatg 480
 aatggcattc agaagtctca gattcatcga gatgacagat ccacagatcg cctgccittca 540
 gctcacacat gttttaatca actggaccct gctgccatg agagcttga gaagctc 597

<210> 72

<211> 2893

<212> DNA

<213> Mus musculus

<400> 72

ccgactttga ggatcgggtg tcggatgaag agaaggtccg catagccgtt aaattcatca 60
 cccatgcacc cccaggggag tttaatgaag tattcaatga tgtccggcta ctgcttaaca 120
 atgacaatct cctcagggaa ggggcagcac atgcatttgc ccagtataac atggatcagt 180
 tcacacccgt gaagatagaa ggctacgatg accaggtctt aattacagag catggtgacc 240
 ttggtaacag cagattttta gatccaagaa accaaatttc cttaagttt gatcatttac 300
 ggaaagaagc aagtgacccg cagccagagg atgtggatgg aggcttgaag tcttggaggg 360
 agtcgtgtga cagtgtctg agagcctatg tgaagatca ttattccaac ggcttctgta 420
 ctgtttacgc taaaactata gatgggcaac agaccattat tgcatgtatt gaaagccacc 480
 agtttcaacc aaaaaacttc tggaatggtc gctggagatc agagtggaag ttcaccatta 540
 caccaccttc agcccagggtg gtggagtac tcaagattca ggttcattat tatgaagatg 600
 gcaatgttca gctggttagt cataaagatg tgcaggacac agtaactgtt tctaataaaa 660
 tccaaactac caaggagttt attaaaatca tagagagtgc agaaaatgag tatcagacag 720
 caattagtga aaattaccaa actatgtcag acaccacgtt caaggccttg cgccggcagc 780
 ttccagttac ccgcaccaa atcgactgga acaagatact cagttacaag attggcaaag 840

aaatgcagaa tgcttaaagg ccgtctctag gagtctccag tacatggaaa gaaaaggatt 900
caacacggtg tggtcataatg aacgaataag tgatttataa acaaacaaga gtgatatttt 960
gctagttaac aaagttaaca gatcttctag ccctatggaa tacigtigaa cctacagcac 1020
tgtcttgatt cttttgtgtg tgttctttgc ttgtlaattt tctgttatca ctatactac 1080
ttgtaaactt ttttttttaa ttctgttaca ttaaatgtcg aagagctata tcttgaagtc 1140
attttactgt ttagaacatt tcttagccat gcagtcctag gactggtttt tacagagtat 1200
ctgttgagta ctttttacc cttgtcttta aagcacttcc agtgcctcag tggcttttag 1260
tgatccacca attgctgaag aggctatgct accaagagct aagtggacaa cacactcctt 1320
ctctgtccga ctgctttggt catttacagc atctcacaat tgtagatttc agacatttgg 1380
attggggctt ttggggctca tgttgggagg caaagtttcc tggaaattcc atggcagcag 1440
cttctctagg gtcttgattt taaatccaaa gacttgaacc acatcccctg ctgcacatga 1500
atgtttgctt actttcattt tctcattgtc tcttcccatc tggttctgtt gtaacatgg 1560
atgtctgtag gaagaacagc ctgagaaaag cactgggaaa ccagggttgt cagtcctatg 1620
ggctctgttc cctcagtgga aggaagtga ggaatgcctga tgactagtat gctggagtgc 1680
tgtgtcaga cagcctgatg agcctctgct cactgtgaag gaccagcctc cactcaatc 1740
tctctcacc acccatgtt ctgagcaatg tttagaccct aatactggcc ttgtctctc 1800
agtgagtaga acttatgccg attcataatc ttctctctg ggccctctg ctaagttctg 1860
tttttcagtc aatagagttc atgtttattg taaaggtcac aggtgcttta ctaccttga 1920
agggacttta gatgtagccg gccctgaagc ttgtttataa gagttgtcac acagagactt 1980
ttcccagag ttctactatg tttaaagtgt tggaaaaatt aaaacatagg atcagagtcc 2040
agaagtcttg atccagtctg accaagtctg gctataccaa gttttcattc ttatccatcc 2100
tgggtccact ttctctgcca gtggcaatac ctgcagaaac gcctcaacag atgttggcat 2160
ttttagaaga gttttgcca ttagtattgc tctttcatag ttgagaactg ctgacatact 2220
atcaatgtag tagaatataa aacttgaaaa cacagacatt gaaggaatca taggtatitt 2280
tgctttatgc tctctggcag gattgttctg taagcagacg aataaatagc tgtgtccctc 2340
acaaagctgg aatgaaccaa agtgaaaagg acggttccca ggcagcatct gtcagtatgt 2400
cagagtgtca gtgttccctt ctaaacagga tgaccaagtc attccagttc atcttttcca 2460
tcatectacc tgcctagaac tcatgtgtaa ctgtgatata gctaccttcc caggtatatt 2520
ggcagggtgt tgtgtgtgtg tgtgatctca gaacacacag gtaatgtgat gtgacctatg 2580

acaactggta atgggtggatt catttacatt gtttacacit ctatgaccag gccttagggg 2640
 aaggtcagtt ttttaaaaac caagtagtgt cttcctacct gtccccaagt acaaggtaaa 2700
 acagaaggct gttggcttca gctttctttt cttttttgct cagtaatact gtcaagcagg 2760
 agtttgtttg caaatgaaag ctgtgtaagc atttttgttt atttcaaata aaatatatatt 2820
 gtattatttg tcattcatac tatccatcca tgccacactg tcttctgtac caggtagccc 2880
 aatagaaata cac 2893

<210> 73

<211> 1690

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (106).. (966)

<400> 73

ggggcccctc ccttggcggg ggcgcgcggc ggaagaccgc tcggaaaggg ggaagtcagg 60
 tggccgcctc tgccaccagc gccacggctc gtcgccagaa ggaag atg gcg gat ctg 117

Met Ala Asp Leu

1

gag gag cag ttg tcc gat gag gag aag gtt cgt ata gca gca aaa ttc 165

Glu Glu Gln Leu Ser Asp Glu Glu Lys Val Arg Ile Ala Ala Lys Phe

5

10

15

20

atc att cac gcc cct cct gga gaa ttt aat gag gtt ttt aat gat gtt 213

Ile Ile His Ala Pro Pro Gly Glu Phe Asn Glu Val Phe Asn Asp Val

25

30

35

cga cta ttg ctt aat aat gat aat ctt ctc agg gaa gga gcc gca cat 261

Arg Leu Leu Leu Asn Asn Asp Asn Leu Leu Arg Glu Gly Ala Ala His

40	45	50	
gca ttt gca cag tat aac ctg gac cag ttt aca cca gta aaa att gaa.			309
Ala Phe Ala Gln Tyr Asn Leu Asp Gln Phe Thr Pro Val Lys Ile Glu			
55	60	65	
ggc tat gaa gat cag gtt ttg ata aca gaa cat gga gac ttg gga aat			357
Gly Tyr Glu Asp Gln Val Leu Ile Thr Glu His Gly Asp Leu Gly Asn			
70	75	80	
gga aaa ttt ttg gat cca aaa aac aga atc tgt ttc aaa ttt gat cat			405
Gly Lys Phe Leu Asp Pro Lys Asn Arg Ile Cys Phe Lys Phe Asp His			
85	90	95	100
tta aga aag gaa gca act gat cca agg ccc tac gaa gca gaa aat gcc			453
Leu Arg Lys Glu Ala Thr Asp Pro Arg Pro Tyr Glu Ala Glu Asn Ala			
105	110	115	
att gaa tcc tgg aga act tca gta gaa act gca ctg cga gct tat gta			501
Ile Glu Ser Trp Arg Thr Ser Val Glu Thr Ala Leu Arg Ala Tyr Val			
120	125	130	
aaa gag cat tat ccg aat ggg gtc tgc act gtg tat ggc aaa aaa gta			549
Lys Glu His Tyr Pro Asn Gly Val Cys Thr Val Tyr Gly Lys Lys Val			
135	140	145	
gat ggg cag caa acc att att gca tgc ata gaa agc cat cag ttt caa			597
Asp Gly Gln Gln Thr Ile Ile Ala Cys Ile Glu Ser His Gln Phe Gln			
150	155	160	
gca aaa aac ttt tgg aat ggt cgt tgg agg tca gag tgg aag ttt aca			645
Ala Lys Asn Phe Trp Asn Gly Arg Trp Arg Ser Glu Trp Lys Phe Thr			
165	170	175	180
gtc act cct tcc acc aca cag gtg gtt ggc att ttg aaa att cag gtt			693
Val Thr Pro Ser Thr Thr Gln Val Val Gly Ile Leu Lys Ile Gln Val			
185	190	195	
cat tat tat gaa gat ggt aat gtt cag cta gtg agt cat aaa gat ata			741

His Tyr Tyr Glu Asp Gly Asn Val Gln Leu Val Ser His Lys Asp Ile
 200 205 210
 caa gat tcc ctc aca gta tct aat gag gtg caa aca gca aaa gaa ttt 789
 Gln Asp Ser Leu Thr Val Ser Asn Glu Val Gln Thr Ala Lys Glu Phe
 215 220 225
 ata aag att gta gaa gct gca gaa aat gaa tac cag act gcc atc agt 837
 Ile Lys Ile Val Glu Ala Ala Glu Asn Glu Tyr Gln Thr Ala Ile Ser
 230 235 240
 gag aat tat cag acg atg tcg gac act acc ttc aaa gcc tta cgt cga 885
 Glu Asn Tyr Gln Thr Met Ser Asp Thr Thr Phe Lys Ala Leu Arg Arg
 245 250 255 260
 cag ttg cca gtg aca cgt act aag atc gac tgg aac aag atc ctt agc 933
 Gln Leu Pro Val Thr Arg Thr Lys Ile Asp Trp Asn Lys Ile Leu Ser
 265 270 275
 tac aag att ggc aaa gag atg cag aat gca taa atgaaaattg catgagcaga 986
 Tyr Lys Ile Gly Lys Glu Met Gln Asn Ala
 280 285
 ttgttttagt gtcttcgct tacaataatt attgcaaaag tattctgagc tgacagctgc 1046
 ccagtgaggt gggctgttgc atctaagatc actgtaatta agtagtgttg ttagagcaca 1106
 gagcttagct aataacctgt tccatttctt ttgttcagag gggttgacat gagtttagat 1166
 aagtaacctt ctctgttctt cctttcgaag tctctctctt tctttctctc tctctctgtt 1226
 ccttctccta caatgaagag gtgatccctc tgggtcatgt cttaaagggt tgaaatatct 1286
 caaaagtacc tcttttactg taacctgaa gtgtctttg gcttgtgaaa ggggcagctt 1346
 ttgatgttag ccaggttagt tttagtgggg tcagtcagta atgggcactc tagttaaggt 1406
 gggtgatgga cttagccatg tatgtgcta aagaaattgt ctacctttc ctttcacctc 1466
 ttccagcatg gaagatggag attagagga gagcatttc taacgagtta cgttaaacct 1526
 tctcagcaag gttatttagc tagcttagtg tctaactaaa cttttttaaa acaaggccaa 1586
 ggctgttgc tgttttgaga ttctgaaatt aaatgagaat acttatttca gaaatgcatt 1646
 taatgctttt ttcttgtgac agttaigcaa attagcttga attc 1690

<210> 74

<211> 286

<212> PRT

<213> Mus musculus

<400> 74

Met Ala Asp Leu Glu Glu Gln Leu Ser Asp Glu Glu Lys Val Arg Ile
 1 5 10 15
 Ala Ala Lys Phe Ile Ile His Ala Pro Pro Gly Glu Phe Asn Glu Val
 20 25 30
 Phe Asn Asp Val Arg Leu Leu Leu Asn Asn Asp Asn Leu Leu Arg Glu
 35 40 45
 Gly Ala Ala His Ala Phe Ala Gln Tyr Asn Leu Asp Gln Phe Thr Pro
 50 55 60
 Val Lys Ile Glu Gly Tyr Glu Asp Gln Val Leu Ile Thr Glu His Gly
 65 70 75 80
 Asp Leu Gly Asn Gly Lys Phe Leu Asp Pro Lys Asn Arg Ile Cys Phe
 85 90 95
 Lys Phe Asp His Leu Arg Lys Glu Ala Thr Asp Pro Arg Pro Tyr Glu
 100 105 110
 Ala Glu Asn Ala Ile Glu Ser Trp Arg Thr Ser Val Glu Thr Ala Leu
 115 120 125
 Arg Ala Tyr Val Lys Glu His Tyr Pro Asn Gly Val Cys Thr Val Tyr
 130 135 140
 Gly Lys Lys Val Asp Gly Gln Gln Thr Ile Ile Ala Cys Ile Glu Ser
 145 150 155 160
 His Gln Phe Gln Ala Lys Asn Phe Trp Asn Gly Arg Trp Arg Ser Glu
 165 170 175

Trp Lys Phe Thr Val Thr Pro Ser Thr Thr Gln Val Val Gly Ile Leu
 180 185 190

Lys Ile Gln Val His Tyr Tyr Glu Asp Gly Asn Val Gln Leu Val Ser
 195 200 205

His Lys Asp Ile Gln Asp Ser Leu Thr Val Ser Asn Glu Val Gln Thr
 210 215 220

Ala Lys Glu Phe Ile Lys Ile Val Glu Ala Ala Glu Asn Glu Tyr Gln
 225 230 235 240

Thr Ala Ile Ser Glu Asn Tyr Gln Thr Met Ser Asp Thr Thr Phe Lys
 245 250 255

Ala Leu Arg Arg Gln Leu Pro Val Thr Arg Thr Lys Ile Asp Trp Asn
 260 265 270

Lys Ile Leu Ser Tyr Lys Ile Gly Lys Glu Met Gln Asn Ala
 275 280 285

<210> 75

<211> 328

<212> DNA

<213> Mus musculus

<400> 75

ccggcttgct agaaagctca ttggagatcc taccgtggag tttgtggcca tgcctgcgcg 60
 tgcgccacct gacgtgggtca tagagccagc tttggcagca cagtacgagc atgattttaga 120
 gggttgctcag acgactgctc tcccagatga ggatgatgag ctgtgagaca gtgaagctgg 180
 agctctgcgt cagaagtcta gttttatagt caactgtcct gtgatgtcag cagttgagcg 240
 cgtgtgcgat ctgagatagc taagcagatg cgtgacacca tatgggatgc tgaaggagat 300
 gcatcgggct cgatctggat gtggcagt 328

<210> 76

<211> 1654

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (183).. (1604)

<400> 76

```

gttgaccgaa cctctgtttt cagaggtag accaatttgt ggtgcctggt gtttctgttt 60
attacactct gacttttctt gccactcaat gttttatgt tttgttttcc ctctgttag 120
ggttccctcc tggcacctct ttctcagtc cgttagacct ggcctaata aagactgagg 180
tt atg aag tcg atc tta gac ggc ctt gca gat acc acc ttc cgt acc 227
Met Lys Ser Ile Leu Asp Gly Leu Ala Asp Thr Thr Phe Arg Thr
      1             5             10             15
atc acc aca gac ctc ctc tac gtg ggc tca aat gac att cag tac gaa 275
Ile Thr Thr Asp Leu Leu Tyr Val Gly Ser Asn Asp Ile Gln Tyr Glu
      20             25             30
gat atc aaa gga gac atg gca tcc aaa tta gga tac ttc cca cag aaa 323
Asp Ile Lys Gly Asp Met Ala Ser Lys Leu Gly Tyr Phe Pro Gln Lys
      35             40             45
ttc cct cta act tcc ttc agg ggt agt ccc ttc caa gaa aag atg acg 371
Phe Pro Leu Thr Ser Phe Arg Gly Ser Pro Phe Gln Glu Lys Met Thr
      50             55             60
gca gga gac aac tcc ccg ttg gtt cca gca gga gac aca acc aac att 419
Ala Gly Asp Asn Ser Pro Leu Val Pro Ala Gly Asp Thr Thr Asn Ile
      65             70             75
aca gag ttc tat aac aag tct ctc tca tcg ttc aag gag aac gag gac 467
Thr Glu Phe Tyr Asn Lys Ser Leu Ser Ser Phe Lys Glu Asn Glu Asp

```

80	85	90	95	
aac atc cag tgt ggg gag aat ttt atg gac atg gag tgc ttc atg att	515			
Asn Ile Gln Cys Gly Glu Asn Phe Met Asp Met Glu Cys Phe Met Ile				
100	105	110		
ctg aat ccc agc cag cag ctg gcc atc gct gtc ctg tcc ctc acc ctg	563			
Leu Asn Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr Leu				
115	120	125		
ggc acc ttc acg gtt ctg gag aac ctg ctg gtg cta tgt gtc atc ctt	611			
Gly Thr Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile Leu				
130	135	140		
cac tcc cgc agt ctc cga tgc agg cct tcc tac cac ttc att ggc agc	659			
His Ser Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly Ser				
145	150	155		
ctg gcg gtg gcc gat ctc ctg gga agt gtc atc ttt gtc tac agc ttt	707			
Leu Ala Val Ala Asp Leu Leu Gly Ser Val Ile Phe Val Tyr Ser Phe				
160	165	170	175	
gtt gac ttc cac gtg ttc cac cgc aaa gat agt ccc aat gtg ttt ctg	755			
Val Asp Phe His Val Phe His Arg Lys Asp Ser Pro Asn Val Phe Leu				
180	185	190		
ttc aaa ctg ggt ggg gtt acc gcc tcc ttc aca gca tct gtg ggc agc	803			
Phe Lys Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly Ser				
195	200	205		
ctg ttc ctc acg gcc atc gac agg tac ata tcc att cac agg cct ctg	851			
Leu Phe Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro Leu				
210	215	220		
gcc tat aag agg atc gtc acc agg ccc aag gcc gta gtg gcc ttt tgc	899			
Ala Tyr Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe Cys				
225	230	235		
ttg atg tgg act att gca ata gta att gct gtg ttg cct ctc ctg ggc	947			

Leu Met Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu Gly
 240 245 250 255
 tgg aac tgc aag aag ctg caa tct gtt tgc tca gac atc ttc cca ctc 995
 Trp Asn Cys Lys Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro Leu
 260 265 270
 att gat gaa acc tac ctg atg ttc tgg atc gga gtc acc agt gtg ctg 1043
 Ile Asp Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val Leu
 275 280 285
 ttg ctg ttc att gtg tat gca tac atg tac att ctc tgg aag gct cac 1091
 Leu Leu Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala His
 290 295 300
 agc cac gca gtt cgc atg atc cag cgt gga acc cag aaa agc atc atc 1139
 Ser His Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile Ile
 305 310 315
 att cac acc tca gaa gat ggc aag gtg cag gtg aca cgg cct gac caa 1187
 Ile His Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp Gln
 320 325 330 335
 gcc cgc atg gac att agg ctg gcc aaa acc ctg gtt ctg atc ctg gtg 1235
 Ala Arg Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu Val
 340 345 350
 gtg ttg atc atc tgc tgg ggc cct ctg ctt gcg atc atg gtg tat gat 1283
 Val Leu Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr Asp
 355 360 365
 gtc ttt ggg aag atg aac aag ctt atc aag acg gtg ttt gcc ttc tgt 1331
 Val Phe Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe Cys
 370 375 380
 agt atg ctc tgc ctg ctg aac tcc acc gtg aac ccc atc atc tat gct 1379
 Ser Met Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr Ala
 385 390 395

ctg agg agc aag gac ctg aga cat gct ttc cgc agc atg ttc cct tca 1427
 Leu Arg Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro Ser
 400 405 410 415
 tgt gaa ggc act gcg cag cct cta gat aac agc atg ggg gac tca gac 1475
 Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser Asp
 420 425 430
 tgc ctg cac aag cac gcc aat aac aca gcc agc atg cac agg gcc gcg 1523
 Cys Leu His Lys His Ala Asn Asn Thr Ala Ser Met His Arg Ala Ala
 435 440 445
 gaa agc tgc atc aag agc act gtt aag atc gcc aag gtg acc atg tct 1571
 Glu Ser Cys Ile Lys Ser Thr Val Lys Ile Ala Lys Val Thr Met Ser
 450 455 460
 gtg tcc aca gac acg tct gcc gag gct ctg tga gctgctgctt ttgtggctgc 1624
 Val Ser Thr Asp Thr Ser Ala Glu Ala Leu
 465 470
 ccagaaaaag aaaatttttt tttttagctt 1654

<210> 77

<211> 473

<212> PRT

<213> Mus musculus

<400> 77

Met Lys Ser Ile Leu Asp Gly Leu Ala Asp Thr Thr Phe Arg Thr Ile
 1 5 10 15
 Thr Thr Asp Leu Leu Tyr Val Gly Ser Asn Asp Ile Gln Tyr Glu Asp
 20 25 30
 Ile Lys Gly Asp Met Ala Ser Lys Leu Gly Tyr Phe Pro Gln Lys Phe
 35 40 45

Pro Leu Thr Ser Phe Arg Gly Ser Pro Phe Gln Glu Lys Met Thr Ala
 50 55 60
 Gly Asp Asn Ser Pro Leu Val Pro Ala Gly Asp Thr Thr Asn Ile Thr
 65 70 75 80
 Glu Phe Tyr Asn Lys Ser Leu Ser Ser Phe Lys Glu Asn Glu Asp Asn
 85 90 95
 Ile Gln Cys Gly Glu Asn Phe Met Asp Met Glu Cys Phe Met Ile Leu
 100 105 110
 Asn Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr Leu Gly
 115 120 125
 Thr Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile Leu His
 130 135 140
 Ser Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly Ser Leu
 145 150 155 160
 Ala Val Ala Asp Leu Leu Gly Ser Val Ile Phe Val Tyr Ser Phe Val
 165 170 175
 Asp Phe His Val Phe His Arg Lys Asp Ser Pro Asn Val Phe Leu Phe
 180 185 190
 Lys Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly Ser Leu
 195 200 205
 Phe Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro Leu Ala
 210 215 220
 Tyr Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe Cys Leu
 225 230 235 240
 Met Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu Gly Trp
 245 250 255
 Asn Cys Lys Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro Leu Ile
 260 265 270
 Asp Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val Leu Leu

275 280 285
 Leu Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala His Ser
 290 295 300
 His Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile Ile Ile
 305 310 315 320
 His Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp Gln Ala
 325 330 335
 Arg Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu Val Val
 340 345 350
 Leu Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr Asp Val
 355 360 365
 Phe Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe Cys Ser
 370 375 380
 Met Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr Ala Leu
 385 390 395 400
 Arg Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro Ser Cys
 405 410 415
 Glu Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser Asp Cys
 420 425 430
 Leu His Lys His Ala Asn Asn Thr Ala Ser Met His Arg Ala Ala Glu
 435 440 445
 Ser Cys Ile Lys Ser Thr Val Lys Ile Ala Lys Val Thr Met Ser Val
 450 455 460
 Ser Thr Asp Thr Ser Ala Glu Ala Leu
 465 470

<210> 78

<211> 3427

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (42).. (2708)

<400> 78

gacagcaggg cccgcctgctc agcacacctg gctccagagc c atg gcc tgc ctc cat 56

Met Ala Cys Leu His

1

5

gaa acc cga aca ccc tcc cct tcc ttt ggg ggc ttt gcg tct act cta 104

Glu Thr Arg Thr Pro Ser Pro Ser Phe Gly Gly Phe Ala Ser Thr Leu

10

15

20

agt gag gct tct atg cga aac gtg gat cca gac act tca gac tgc acc 152

Ser Glu Ala Ser Met Arg Asn Val Asp Pro Asp Thr Ser Asp Cys Thr

25

30

35

ccc gag aaa gac ctg acg ccc acc caa tgt gta ctt cga gat gtt gtg 200

Pro Glu Lys Asp Leu Thr Pro Thr Gln Cys Val Leu Arg Asp Val Val

40

45

50

cct ctc ggt ggg cag ggt gga gga gga ccc agc ccc tcc cca ggt gga 248

Pro Leu Gly Gly Gln Gly Gly Gly Gly Pro Ser Pro Ser Pro Gly Gly

55

60

65

gag cct ccc cca gag cct ttt gcc aat agt gtc ctc cag cta cat gag 296

Glu Pro Pro Pro Glu Pro Phe Ala Asn Ser Val Leu Gln Leu His Glu

70

75

80

85

cag gat aca ggt ggg cca ggg gga gcc act ggg tca cct gag agt cga 344

Gln Asp Thr Gly Gly Pro Gly Gly Ala Thr Gly Ser Pro Glu Ser Arg

90

95

100

gca tct aga gtt cga gct gat gag gta cgt ctg cag tgc cag agt ggc 392

Ala Ser Arg Val Arg Ala Asp Glu Val Arg Leu Gln Cys Gln Ser Gly	
105 110 115	
agt ggc ttc ctt gaa ggt ctt ttt ggc tgc ctg cgc cct gtc tgg aca	440
Ser Gly Phe Leu Glu Gly Leu Phe Gly Cys Leu Arg Pro Val Trp Thr	
120 125 130	
atg att ggc aaa gcc tac tcc aca gaa cac aag caa cag cag gaa gac	488
Met Ile Gly Lys Ala Tyr Ser Thr Glu His Lys Gln Gln Gln Glu Asp	
135 140 145	
ctt tgg gaa gtc ccc ttt gag gaa atc ctg gac ctg cag tgg gta ggc	536
Leu Trp Glu Val Pro Phe Glu Glu Ile Leu Asp Leu Gln Trp Val Gly	
150 155 160 165	
tca ggg gct cag ggt gct gtt ttc ctg gga cgc ttc cac ggg gag gag	584
Ser Gly Ala Gln Gly Ala Val Phe Leu Gly Arg Phe His Gly Glu Glu	
170 175 180	
gta gct gtg aag aag gtt cga gat ctc aag gag act gac atc aag cat	632
Val Ala Val Lys Lys Val Arg Asp Leu Lys Glu Thr Asp Ile Lys His	
185 190 195	
ctt cga aag ctg aag cac ccc aac atc atc act ttc aag ggt gtt tgc	680
Leu Arg Lys Leu Lys His Pro Asn Ile Ile Thr Phe Lys Gly Val Cys	
200 205 210	
aca cag gcc ccc tgc tac tgc atc ctt atg gaa ttc tgc gct caa gga	728
Thr Gln Ala Pro Cys Tyr Cys Ile Leu Met Glu Phe Cys Ala Gln Gly	
215 220 225	
cag cta tat gag gtg ctc aga gcc ggc cgc cct gtc acc ccc tcc ttg	776
Gln Leu Tyr Glu Val Leu Arg Ala Gly Arg Pro Val Thr Pro Ser Leu	
230 235 240 245	
ctg gtt gac tgg tcc atg ggc atc gct ggt ggc atg aat tac ctg cac	824
Leu Val Asp Trp Ser Met Gly Ile Ala Gly Gly Met Asn Tyr Leu His	
250 255 260	

ctg cac aag att atc cac aga gac ctg aag tca ccc aac atg cta atc 872
 Leu His Lys Ile Ile His Arg Asp Leu Lys Ser Pro Asn Met Leu Ile
 265 270 275
 aca tac gac gat gtg gtg aag atc tca gat ttt ggc act tcc aag gag 920
 Thr Tyr Asp Asp Val Val Lys Ile Ser Asp Phe Gly Thr Ser Lys Glu
 280 285 290
 ctg agt gac aag agc acc aag atg tcc ttt gca gga aca gta gcc tgg 968
 Leu Ser Asp Lys Ser Thr Lys Met Ser Phe Ala Gly Thr Val Ala Trp
 295 300 305
 atg gct cct gaa gtg atc aga aat gaa cct gtg tct gag aag gtt gac 1016
 Met Ala Pro Glu Val Ile Arg Asn Glu Pro Val Ser Glu Lys Val Asp
 310 315 320 325
 atc tgg tcc ttt ggg gtg gtg cta tgg gaa cta ctg act gga gag att 1064
 Ile Trp Ser Phe Gly Val Val Leu Trp Glu Leu Leu Thr Gly Glu Ile
 330 335 340
 ccc tac aaa gat gta gat tcc tca gcc atc atc tgg ggt gtg gga agc 1112
 Pro Tyr Lys Asp Val Asp Ser Ser Ala Ile Ile Trp Gly Val Gly Ser
 345 350 355
 aac agt ctc cac ctg cct gta ccc tcc agc tgc cca gat ggt ttt aaa 1160
 Asn Ser Leu His Leu Pro Val Pro Ser Ser Cys Pro Asp Gly Phe Lys
 360 365 370
 att cta ctt cgc cag tgc tgg aac acg aaa cca cga aat cgc cca tca 1208
 Ile Leu Leu Arg Gln Cys Trp Asn Thr Lys Pro Arg Asn Arg Pro Ser
 375 380 385
 ttc cga cag atc ttg ctg cac ctg gac atc gcc tcc gct gat gtg ctc 1256
 Phe Arg Gln Ile Leu Leu His Leu Asp Ile Ala Ser Ala Asp Val Leu
 390 395 400 405
 tct aca ccc cag gag act tac ttt aag tcc cag gca gag tgg cgg gaa 1304
 Ser Thr Pro Gln Glu Thr Tyr Phe Lys Ser Gln Ala Glu Trp Arg Glu

410	415	420	
gaa gta aaa ctg cac ttt gaa aag att aag tca gaa ggg acc tgt ctg			1352
Glu Val Lys Leu His Phe Glu Lys Ile Lys Ser Glu Gly Thr Cys Leu			
425	430	435	
cac cgc cta gaa gag gaa ctg gtg atg cgg aga agg gag gag ctc aga			1400
His Arg Leu Glu Glu Glu Leu Val Met Arg Arg Arg Glu Glu Leu Arg			
440	445	450	
cat gcc ctg gac atc agg gag cac tat gaa cgg aag ttg gag aga gcc			1448
His Ala Leu Asp Ile Arg Glu His Tyr Glu Arg Lys Leu Glu Arg Ala			
455	460	465	
aac aac ctg tac atg gaa ctg aat gcc ctc atg ctg caa cta gaa ctc			1496
Asn Asn Leu Tyr Met Glu Leu Asn Ala Leu Met Leu Gln Leu Glu Leu			
470	475	480	485
aaa gag agg gaa ttg ctc agg cga gac gag gct tta gaa agg cgg tgt			1544
Lys Glu Arg Glu Leu Leu Arg Arg Asp Glu Ala Leu Glu Arg Arg Cys			
490	495	500	
cct ggt cta cta aag tca cac cct tct cgg ggc ctc cta cat gga gac			1592
Pro Gly Leu Leu Lys Ser His Pro Ser Arg Gly Leu Leu His Gly Asp			
505	510	515	
act atg gag aag ctc atc aag aaa agg aac gtg cca cag aaa ctg tcg			1640
Thr Met Glu Lys Leu Ile Lys Lys Arg Asn Val Pro Gln Lys Leu Ser			
520	525	530	
ccc cac agc aaa agg cca gat att ctc aag aca gag tcg ttg cta cct			1688
Pro His Ser Lys Arg Pro Asp Ile Leu Lys Thr Glu Ser Leu Leu Pro			
535	540	545	
aaa cta gat gca gcc cta agt ggg gtg ggg ctt cct ggg tgt cct aag			1736
Lys Leu Asp Ala Ala Leu Ser Gly Val Gly Leu Pro Gly Cys Pro Lys			
550	555	560	565
ggc ccc cct tca cct gga agg agt cgg cgt ggc aag acc cgt cac cga			1784

Gly Pro Pro Ser Pro Gly Arg Ser Arg Arg Gly Lys Thr Arg His Arg
 570 575 580
 aag gcc agt gcc aag ggc agc tgt gga gac ctg cct ggg ctt cgt gca 1832
 Lys Ala Ser Ala Lys Gly Ser Cys Gly Asp Leu Pro Gly Leu Arg Ala
 585 590 595
 gct ttg cca ccc cat gag cct gga gga cta gga agc cca ggg ggc cta 1880
 Ala Leu Pro Pro His Glu Pro Gly Gly Leu Gly Ser Pro Gly Gly Leu
 600 605 610
 gga gtg ggc cct tca gct tgg gat gct tgc ccc cct gct ctc cgt gga 1928
 Gly Val Gly Pro Ser Ala Trp Asp Ala Cys Pro Pro Ala Leu Arg Gly
 615 620 625
 ctc cac cat gac ctt cta ctc cga aag atg tca tca tca tcc cca gac 1976
 Leu His His Asp Leu Leu Leu Arg Lys Met Ser Ser Ser Ser Pro Asp
 630 635 640 645
 ctg cta tca gca gcg ctg gga gcc cga ggc cga ggg gct aca ggg gga 2024
 Leu Leu Ser Ala Ala Leu Gly Ala Arg Gly Arg Gly Ala Thr Gly Gly
 650 655 660
 gct cgg gat cct ggc tca cca cct cca ccc cag ggc gat act cct cca 2072
 Ala Arg Asp Pro Gly Ser Pro Pro Pro Pro Gln Gly Asp Thr Pro Pro
 665 670 675
 agt gag gga tca gct cct ggt tcc acc agc cca gat tcg cct ggg gga 2120
 Ser Glu Gly Ser Ala Pro Gly Ser Thr Ser Pro Asp Ser Pro Gly Gly
 680 685 690
 gct aaa ggg gaa ccc cct cca cca gta ggg cct gga gaa ggt gtg ggg 2168
 Ala Lys Gly Glu Pro Pro Pro Pro Val Gly Pro Gly Glu Gly Val Gly
 695 700 705
 ctg ctg gga act gga agg gaa ggg act gca ggc cgg gga gga aac cgg 2216
 Leu Leu Gly Thr Gly Arg Glu Gly Thr Ala Gly Arg Gly Gly Asn Arg
 710 715 720 725

gct ggg tcc cag cac ttg acc ccc gct gcg ctg ctg tac agg gct gct	2264
Ala Gly Ser Gln His Leu Thr Pro Ala Ala Leu Leu Tyr Arg Ala Ala	
730 735 740	
gtg act cga agt cag aaa cgt ggt atc tca tct gaa gaa gaa gaa gga	2312
Val Thr Arg Ser Gln Lys Arg Gly Ile Ser Ser Glu Glu Glu Glu Gly	
745 750 755	
gag gta gac agt gaa gta gag cta ccc cca agt caa agg tgg cct cag	2360
Glu Val Asp Ser Glu Val Glu Leu Pro Pro Ser Gln Arg Trp Pro Gln	
760 765 770	
ggc ccg aac atg cgt cag tca cta tct aca ttc agc tca gag aac cca	2408
Gly Pro Asn Met Arg Gln Ser Leu Ser Thr Phe Ser Ser Glu Asn Pro	
775 780 785	
tca gat gtg gaa gga ggt aca gct agt gag cct tcc cca agt ggc aca	2456
Ser Asp Val Glu Gly Gly Thr Ala Ser Glu Pro Ser Pro Ser Gly Thr	
790 795 800 805	
cca gaa gtt ggc agt acc aac act gat gag cgg cca gat gaa cga tct	2504
Pro Glu Val Gly Ser Thr Asn Thr Asp Glu Arg Pro Asp Glu Arg Ser	
810 815 820	
gat gac atg tgc tca cag ggc tca gaa att cca ctg gac cta cct act	2552
Asp Asp Met Cys Ser Gln Gly Ser Glu Ile Pro Leu Asp Leu Pro Thr	
825 830 835	
tca gag gtg gtc cct gaa cgt gaa gcc agc tcc ttg ccc atg caa cac	2600
Ser Glu Val Val Pro Glu Arg Glu Ala Ser Ser Leu Pro Met Gln His	
840 845 850	
cag gat ggc cag ggc ccc aat cct gaa gac tca gac tgt gac agc act	2648
Gln Asp Gly Gln Gly Pro Asn Pro Glu Asp Ser Asp Cys Asp Ser Thr	
855 860 865	
gaa ttg gac aac tcc aac agc att gat gcc ttg cgg ccc cca gcc tcc	2696
Glu Leu Asp Asn Ser Asn Ser Ile Asp Ala Leu Arg Pro Pro Ala Ser	

870	875	880	885	
ctt cct cca tga aagacactct tattccttgt acatagagaa atatttatat				2748
Leu Pro Pro				
aaataatata tatgcgccac ataatcaaca gatagatggg gcittcttag ccttaagcca				2808
ggcttigagag tgaacgacgc cccctgacca attaccgaat aagtcttggg gacactggca				2868
gctgtggaaa tgaatgactc cgagtactac cctagagcta taaagaaagg aagctggccc				2928
cttcttgctt caccceattc cttatgttga acaagcaagt aggcaataga aaagccaggc				2988
ttgtctctat actgtctatc cctgaacact ggaggggcag gtagaggatt cacttaaaac				3048
tgcactttta ttttcggtt actgtttaca catittgcac ttgggaggag ggaaactaag				3108
gctgggtcat cctcttgagg tttctcaggt ggcaatgtaa ctcatctctt tgttccctgtt				3168
tccttgccca aaccctggct ttgggccaga cgactaacag catgtgatgg ctccaggctga				3228
agaactgggg tgctgttagt cccactgtt atcttgggtgc ctggtagggg tggggactgt				3288
catattgtaa cccctgtgaa caaccttgaa atataaccac tccatgcagg cccaactgtc				3348
gagggttttc ttgggtgaatg agtagagtgg tataatacat ggtttcaact tggatttaag				3408
attttatctg agaaaaaaaa				3427

<210> 79

<211> 888

<212> PRT

<213> Mus musculus

<400> 79

Met Ala Cys Leu His Glu Thr Arg Thr Pro Ser Pro Ser Phe Gly Gly

1 5 10 15

Phe Ala Ser Thr Leu Ser Glu Ala Ser Met Arg Asn Val Asp Pro Asp

20 25 30

Thr Ser Asp Cys Thr Pro Glu Lys Asp Leu Thr Pro Thr Gln Cys Val

35 40 45

Leu Arg Asp Val Val Pro Leu Gly Gly Gln Gly Gly Gly Gly Pro Ser

50	55	60
Pro Ser Pro Gly Gly Glu Pro Pro Pro Glu Pro Phe Ala Asn Ser Val		
65	70	75
Leu Gln Leu His Glu Gln Asp Thr Gly Gly Pro Gly Gly Ala Thr Gly		80
	85	90
Ser Pro Glu Ser Arg Ala Ser Arg Val Arg Ala Asp Glu Val Arg Leu		95
	100	105
Gln Cys Gln Ser Gly Ser Gly Phe Leu Glu Gly Leu Phe Gly Cys Leu		110
	115	120
Arg Pro Val Trp Thr Met Ile Gly Lys Ala Tyr Ser Thr Glu His Lys		125
	130	135
Gln Gln Gln Glu Asp Leu Trp Glu Val Pro Phe Glu Glu Ile Leu Asp		140
145	150	155
Leu Gln Trp Val Gly Ser Gly Ala Gln Gly Ala Val Phe Leu Gly Arg		160
	165	170
Phe His Gly Glu Glu Val Ala Val Lys Lys Val Arg Asp Leu Lys Glu		175
	180	185
Thr Asp Ile Lys His Leu Arg Lys Leu Lys His Pro Asn Ile Ile Thr		190
	195	200
Phe Lys Gly Val Cys Thr Gln Ala Pro Cys Tyr Cys Ile Leu Met Glu		205
	210	215
Phe Cys Ala Gln Gly Gln Leu Tyr Glu Val Leu Arg Ala Gly Arg Pro		220
225	230	235
Val Thr Pro Ser Leu Leu Val Asp Trp Ser Met Gly Ile Ala Gly Gly		240
	245	250
Met Asn Tyr Leu His Leu His Lys Ile Ile His Arg Asp Leu Lys Ser		255
	260	265
Pro Asn Met Leu Ile Thr Tyr Asp Asp Val Val Lys Ile Ser Asp Phe		270
	275	280
		285

Gly Thr Ser Lys Glu Leu Ser Asp Lys Ser Thr Lys Met Ser Phe Ala
 290 295 300
 Gly Thr Val Ala Trp Met Ala Pro Glu Val Ile Arg Asn Glu Pro Val
 305 310 315 320
 Ser Glu Lys Val Asp Ile Trp Ser Phe Gly Val Val Leu Trp Glu Leu
 325 330 335
 Leu Thr Gly Glu Ile Pro Tyr Lys Asp Val Asp Ser Ser Ala Ile Ile
 340 345 350
 Trp Gly Val Gly Ser Asn Ser Leu His Leu Pro Val Pro Ser Ser Cys
 355 360 365
 Pro Asp Gly Phe Lys Ile Leu Leu Arg Gln Cys Trp Asn Thr Lys Pro
 370 375 380
 Arg Asn Arg Pro Ser Phe Arg Gln Ile Leu Leu His Leu Asp Ile Ala
 385 390 395 400
 Ser Ala Asp Val Leu Ser Thr Pro Gln Glu Thr Tyr Phe Lys Ser Gln
 405 410 415
 Ala Glu Trp Arg Glu Glu Val Lys Leu His Phe Glu Lys Ile Lys Ser
 420 425 430
 Glu Gly Thr Cys Leu His Arg Leu Glu Glu Glu Leu Val Met Arg Arg
 435 440 445
 Arg Glu Glu Leu Arg His Ala Leu Asp Ile Arg Glu His Tyr Glu Arg
 450 455 460
 Lys Leu Glu Arg Ala Asn Asn Leu Tyr Met Glu Leu Asn Ala Leu Met
 465 470 475 480
 Leu Gln Leu Glu Leu Lys Glu Arg Glu Leu Leu Arg Arg Asp Glu Ala
 485 490 495
 Leu Glu Arg Arg Cys Pro Gly Leu Leu Lys Ser His Pro Ser Arg Gly
 500 505 510
 Leu Leu His Gly Asp Thr Met Glu Lys Leu Ile Lys Lys Arg Asn Val

515	520	525
Pro Gln Lys Leu Ser Pro His Ser Lys Arg Pro Asp Ile Leu Lys Thr		
530	535	540
Glu Ser Leu Leu Pro Lys Leu Asp Ala Ala Leu Ser Gly Val Gly Leu		
545	550	555
Pro Gly Cys Pro Lys Gly Pro Pro Ser Pro Gly Arg Ser Arg Arg Gly		
565	570	575
Lys Thr Arg His Arg Lys Ala Ser Ala Lys Gly Ser Cys Gly Asp Leu		
580	585	590
Pro Gly Leu Arg Ala Ala Leu Pro Pro His Glu Pro Gly Gly Leu Gly		
595	600	605
Ser Pro Gly Gly Leu Gly Val Gly Pro Ser Ala Trp Asp Ala Cys Pro		
610	615	620
Pro Ala Leu Arg Gly Leu His His Asp Leu Leu Leu Arg Lys Met Ser		
625	630	635
Ser Ser Ser Pro Asp Leu Leu Ser Ala Ala Leu Gly Ala Arg Gly Arg		
645	650	655
Gly Ala Thr Gly Gly Ala Arg Asp Pro Gly Ser Pro Pro Pro Pro Gln		
660	665	670
Gly Asp Thr Pro Pro Ser Glu Gly Ser Ala Pro Gly Ser Thr Ser Pro		
675	680	685
Asp Ser Pro Gly Gly Ala Lys Gly Glu Pro Pro Pro Pro Val Gly Pro		
690	695	700
Gly Glu Gly Val Gly Leu Leu Gly Thr Gly Arg Glu Gly Thr Ala Gly		
705	710	715
Arg Gly Gly Asn Arg Ala Gly Ser Gln His Leu Thr Pro Ala Ala Leu		
725	730	735
Leu Tyr Arg Ala Ala Val Thr Arg Ser Gln Lys Arg Gly Ile Ser Ser		
740	745	750

Glu Glu Glu Glu Gly Glu Val Asp Ser Glu Val Glu Leu Pro Pro Ser
 755 760 765
 Gln Arg Trp Pro Gln Gly Pro Asn Met Arg Gln Ser Leu Ser Thr Phe
 770 775 780
 Ser Ser Glu Asn Pro Ser Asp Val Glu Gly Gly Thr Ala Ser Glu Pro
 785 790 795 800
 Ser Pro Ser Gly Thr Pro Glu Val Gly Ser Thr Asn Thr Asp Glu Arg
 805 810 815
 Pro Asp Glu Arg Ser Asp Asp Met Cys Ser Gln Gly Ser Glu Ile Pro
 820 825 830
 Leu Asp Leu Pro Thr Ser Glu Val Val Pro Glu Arg Glu Ala Ser Ser
 835 840 845
 Leu Pro Met Gln His Gln Asp Gly Gln Gly Pro Asn Pro Glu Asp Ser
 850 855 860
 Asp Cys Asp Ser Thr Glu Leu Asp Asn Ser Asn Ser Ile Asp Ala Leu
 865 870 875 880
 Arg Pro Pro Ala Ser Leu Pro Pro
 885

<210> 80

<211> 1904

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (596).. (1636)

<400> 80

ggaattccgg ctggaggtag tcatlgagct ttaggaaggt ctgacatgca gcggcgatct 60
 cagcctctgt gtacttgacc gagcagccct tcacgggcca gggcaccgtg aagagtctgg 120
 tgttcaagta ctgttaggtg cagcctgggt ccccgatgag gatgcgagac actgggggtga 180
 gcacatcttt gccittggatc ctcaccacgt cccgaaacaa gcagccaatgc ttatcgagtg 240
 tgagaaaggc ctcgggcacc tccttaigca gctcctctgg tatgctgccg gcctctcgga 300
 aaaccagitt agggatattc agctgccact gctgatagaa ctcatcatct ttgggtgtca 360
 ggtaaggaag ctgggagccc cgggagccac tgctgagcgc caaacacccg ctaagcctgc 420
 tgtgtccttg gacgcccagc tgggtaaaag aacagcttct gggtgctaga gaacacaggg 480
 aagcgagtgc tcgaggaaaa ccaagatgtc acagtagact ctggccccc agagccctgt 540
 gaggcgagag gaagatcctt aggcagcttg gtcttagacg gagtggaaag cagcc atg 598

Met

1

gag atg agc tct gag cag ttg aat ggg agc caa gta tgg gtg tcc tct 646
 Glu Met Ser Ser Glu Gln Leu Asn Gly Ser Gln Val Trp Val Ser Ser

5

10

15

cca ttt gac ctc aac ggt tca ctg ggg cca agc aat ggc tcc aac cag 694
 Pro Phe Asp Leu Asn Gly Ser Leu Gly Pro Ser Asn Gly Ser Asn Gln

20

25

30

acc gag cca tac tac gac atg aca agc aac gcc gtc ctc acg ttc atc 742
 Thr Glu Pro Tyr Tyr Asp Met Thr Ser Asn Ala Val Leu Thr Phe Ile

35

40

45

tac ttc gtg gtg tgc gtc gtc ggg ctg tgc ggc aac acg ctg gtc att 790
 Tyr Phe Val Val Cys Val Val Gly Leu Cys Gly Asn Thr Leu Val Ile

50

55

60

65

tac gtc atc ctc cgc tac gcc aag atg aag acc atc acc aac atc tac 838
 Tyr Val Ile Leu Arg Tyr Ala Lys Met Lys Thr Ile Thr Asn Ile Tyr

70

75

80

atc ctt aac ctg gcc att gca gat gaa ctc ttc atg cta ggg ctg ccc 886
 Ile Leu Asn Leu Ala Ile Ala Asp Glu Leu Phe Met Leu Gly Leu Pro

85	90	95	
ttc ttg gcc atg cag gtg gcg cta gtc cac tgg cct ttt ggc aag gcc			934
Phe Leu Ala Met Gln Val Ala Leu Val His Trp Pro Phe Gly Lys Ala			
100	105	110	
atc tgc cgg gtg gtc atg act gta gat ggc atc aat cag ttc acc agt			982
Ile Cys Arg Val Val Met Thr Val Asp Gly Ile Asn Gln Phe Thr Ser			
115	120	125	
atc ttc tgc ttg acg gtc atg agc atc gac cgc tac ctg gcc gtg gtg			1030
Ile Phe Cys Leu Thr Val Met Ser Ile Asp Arg Tyr Leu Ala Val Val			
130	135	140	145
cac ccc att aag tca gcc aaa tgg agg cga ccc cgg aca gcc aag atg			1078
His Pro Ile Lys Ser Ala Lys Trp Arg Arg Pro Arg Thr Ala Lys Met			
150	155	160	
atc aat gtg gct gtg tgg tgt gtg tct ctg ctc gtc att ttg ccc atc			1126
Ile Asn Val Ala Val Trp Cys Val Ser Leu Leu Val Ile Leu Pro Ile			
165	170	175	
atg tta tac gcc ggc ctc cgg agc aac cag tgg ggc aga agc agc tgt			1174
Met Leu Tyr Ala Gly Leu Arg Ser Asn Gln Trp Gly Arg Ser Ser Cys			
180	185	190	
acc atc aac tgg cca ggc gaa tcc ggg gcg tgg tac aca ggt ttc att			1222
Thr Ile Asn Trp Pro Gly Glu Ser Gly Ala Trp Tyr Thr Gly Phe Ile			
195	200	205	
atc tac gcc ttc atc ctg ggg ttc ctg gta ccc ctt acc atc att tgt			1270
Ile Tyr Ala Phe Ile Leu Gly Phe Leu Val Pro Leu Thr Ile Ile Cys			
210	215	220	225
ctc tgc tac ctg ttc atc atc atc aag gtg aag tcc tct gga atc cga			1318
Leu Cys Tyr Leu Phe Ile Ile Ile Lys Val Lys Ser Ser Gly Ile Arg			
230	235	240	
gtg gga tca tcc aag agg aaa aag tca gag aaa aag gtg acc cgc atg			1366

Val Gly Ser Ser Lys Arg Lys Lys Ser Glu Lys Lys Val Thr Arg Met
 245 250 255
 gtg tcc atc gta gtg gct gtc ttc atc ttc tgc tgg ctc cct ttc tac 1414
 Val Ser Ile Val Val Ala Val Phe Ile Phe Cys Trp Leu Pro Phe Tyr
 260 265 270
 atc ttc aac gtc tct tcc gtg tct gtg gcc atc agt ccc acc cca gcc 1462
 Ile Phe Asn Val Ser Ser Val Ser Val Ala Ile Ser Pro Thr Pro Ala
 275 280 285
 ctg aaa gga atg ttt gac ttt gtg gtg atc ctc acc tat gcc aac acg 1510
 Leu Lys Gly Met Phe Asp Phe Val Val Ile Leu Thr Tyr Ala Asn Thr
 290 295 300 305
 tgc gcc aac ccc atc ctg tac gcc ttc ttg tct gac aac ttc aag aag 1558
 Cys Ala Asn Pro Ile Leu Tyr Ala Phe Leu Ser Asp Asn Phe Lys Lys
 310 315 320
 agc ttc cag aat gtt ctt tgc ttg gtc aag gca gac aat tca caa tcc 1606
 Ser Phe Gln Asn Val Leu Cys Leu Val Lys Ala Asp Asn Ser Gln Ser
 325 330 335
 gga gcg gaa gac atc att gcc tgg gtg tga cctgggtggaa aacagctgcc 1656
 Gly Ala Glu Asp Ile Ile Ala Trp Val
 340 345
 cggcagaaac cggaaaaacc aaaactaaat caaagtcctg tgtgtatgtg tgctaacacg 1716
 ttacgtaaat cttgtgatct gatatttaca ttgtatatt ctcctctccc cggtcacaca 1776
 aacatgtccc gtgtttgtaa gcccaagtag ctagttcgtg tgcgtctagt ataggtggac 1836
 agttaccaca acgctgaacc tgaagaaaag gactcgccac gtcacagtca gtccaatctc 1896
 cggaattc 1904

<210> 81

<211> 346

<212> PRT

<213> Mus musculus

<400> 81

Met	Glu	Met	Ser	Ser	Glu	Gln	Leu	Asn	Gly	Ser	Gln	Val	Trp	Val	Ser
1				5					10					15	
Ser	Pro	Phe	Asp	Leu	Asn	Gly	Ser	Leu	Gly	Pro	Ser	Asn	Gly	Ser	Asn
			20					25					30		
Gln	Thr	Glu	Pro	Tyr	Tyr	Asp	Met	Thr	Ser	Asn	Ala	Val	Leu	Thr	Phe
			35				40					45			
Ile	Tyr	Phe	Val	Val	Cys	Val	Val	Gly	Leu	Cys	Gly	Asn	Thr	Leu	Val
	50					55				60					
Ile	Tyr	Val	Ile	Leu	Arg	Tyr	Ala	Lys	Met	Lys	Thr	Ile	Thr	Asn	Ile
65				70					75					80	
Tyr	Ile	Leu	Asn	Leu	Ala	Ile	Ala	Asp	Glu	Leu	Phe	Met	Leu	Gly	Leu
			85					90					95		
Pro	Phe	Leu	Ala	Met	Gln	Val	Ala	Leu	Val	His	Trp	Pro	Phe	Gly	Lys
		100					105						110		
Ala	Ile	Cys	Arg	Val	Val	Met	Thr	Val	Asp	Gly	Ile	Asn	Gln	Phe	Thr
		115					120					125			
Ser	Ile	Phe	Cys	Leu	Thr	Val	Met	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Val
	130					135					140				
Val	His	Pro	Ile	Lys	Ser	Ala	Lys	Trp	Arg	Arg	Pro	Arg	Thr	Ala	Lys
145				150					155					160	
Met	Ile	Asn	Val	Ala	Val	Trp	Cys	Val	Ser	Leu	Leu	Val	Ile	Leu	Pro
			165					170					175		
Ile	Met	Leu	Tyr	Ala	Gly	Leu	Arg	Ser	Asn	Gln	Trp	Gly	Arg	Ser	Ser
		180					185						190		
Cys	Thr	Ile	Asn	Trp	Pro	Gly	Glu	Ser	Gly	Ala	Trp	Tyr	Thr	Gly	Phe
	195						200						205		

Ile Ile Tyr Ala Phe Ile Leu Gly Phe Leu Val Pro Leu Thr Ile Ile
 210 215 220
 Cys Leu Cys Tyr Leu Phe Ile Ile Ile Lys Val Lys Ser Ser Gly Ile
 225 230 235 240
 Arg Val Gly Ser Ser Lys Arg Lys Lys Ser Glu Lys Lys Val Thr Arg
 245 250 255
 Met Val Ser Ile Val Val Ala Val Phe Ile Phe Cys Trp Leu Pro Phe
 260 265 270
 Tyr Ile Phe Asn Val Ser Ser Val Ser Val Ala Ile Ser Pro Thr Pro
 275 280 285
 Ala Leu Lys Gly Met Phe Asp Phe Val Val Ile Leu Thr Tyr Ala Asn
 290 295 300
 Thr Cys Ala Asn Pro Ile Leu Tyr Ala Phe Leu Ser Asp Asn Phe Lys
 305 310 315 320
 Lys Ser Phe Gln Asn Val Leu Cys Leu Val Lys Ala Asp Asn Ser Gln
 325 330 335
 Ser Gly Ala Glu Asp Ile Ile Ala Trp Val
 340 345

<210> 82

<211> 666

<212> DNA

<213> Mus musculus

<400> 82

ggcggtgcat ctccgacacc atgagcggct tcacagcgag gagccgccgc gccttcaccc 60
 tcgagtaccg cgtcttcctc aaaaatgaga aagggcagta catttctcca tttcatgatg 120
 ttccaattta tgcagacaag gatgtgttcc acatgggtggg tgaggttcca cgctgggtcca 180
 acgccaaaat ggagattgct acaaaggacc ctttaaacc aatcaagcaa gatgtgaaaa 240

aggggaagct ccgctatgtg gcgaaatctgt tccctataa aggttatatt tggaactacg 300
 gcgccatccc tcagacatgg gaaganccag gacacagiga caagcacact ggctgctgtg 360
 gtgacaacga cccaatcgga tgttgtgaaa tcggaagcaa gtgtgtgcca gagtgagata 420
 atcagggtga aagtcctggg catactggcc atgatcgatt gaggcgaaaa cgacctgaag 480
 ggcaatggcc attaaatggg acgatccgga cggcgccatt aataaggata ttccgatgtc 540
 gaccgcctaa aaccgggcta tttagagcta actgtggatt ggtaagagg gaataagttc 600
 ctgttgaaa accggaaatt gggttgccat cattgccgaa tttaaacc aa ggccttgca 660
 ttgacg 666

<210> 83

<211> 3283

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (182).. (2803)

<400> 83

gggaagggt gcccgtcct tgcgtgctct ccgtgctccc ggctcttcac tccttcccc 60
 tcctcctcgt ctctctctc cccgccccca cctcttctt cctctccgtt ggctggtaac 120
 ttgttgtgcg gacgaacggc gacaacgacg gcgcgacgga ggcacatcc gggcgggcag 180
 c atg ggc acg tcc gcg cgc tgg gcg ctg tgg ctg ctg ctc gcg ctg tgc 229
 Met Gly Thr Ser Ala Arg Trp Ala Leu Trp Leu Leu Leu Ala Leu Cys
 1 5 10 15
 tgg gcg ccc cgg gac agc ggc gcc act gca agc ggg aag aaa gcc aaa 277
 Trp Ala Pro Arg Asp Ser Gly Ala Thr Ala Ser Gly Lys Lys Ala Lys
 20 25 30
 tgt gat agc tcc cag ttt cag tgc aca aat ggc cgc tgc att acc ctg 325

Cys Asp Ser Ser Gln Phe Gln Cys Thr Asn Gly Arg Cys Ile Thr Leu	
35 40 45	
ctg tgg aaa tgt gat gga gat gaa gac tgt gcg gat ggc agc gac gag	373
Leu Trp Lys Cys Asp Gly Asp Glu Asp Cys Ala Asp Gly Ser Asp Glu	
50 55 60	
aag aac tgt gta aag aag acg tgt gct gag tct gac ttc gtg tgc aaa	421
Lys Asn Cys Val Lys Lys Thr Cys Ala Glu Ser Asp Phe Val Cys Lys	
65 70 75 80	
aac ggc cag tgt gtt cct aac aga tgg cag tgt gac ggg gat cct gat	469
Asn Gly Gln Cys Val Pro Asn Arg Trp Gln Cys Asp Gly Asp Pro Asp	
85 90 95	
tgc gaa gac ggt tct gat gaa agc cct gaa cag tgc cat atg aga aca	517
Cys Glu Asp Gly Ser Asp Glu Ser Pro Glu Gln Cys His Met Arg Thr	
100 105 110	
tgc cgc ata aat gaa atc agc tgt ggc gcc cgt tct act cag tgt atc	565
Cys Arg Ile Asn Glu Ile Ser Cys Gly Ala Arg Ser Thr Gln Cys Ile	
115 120 125	
ccc gtg tcc tgg aga tgc gat ggt gaa aat gat tgt gac aat gga gaa	613
Pro Val Ser Trp Arg Cys Asp Gly Glu Asn Asp Cys Asp Asn Gly Glu	
130 135 140	
gat gaa gaa aac tgt ggc aac ata aca tgt agt gca gat gag ttc act	661
Asp Glu Glu Asn Cys Gly Asn Ile Thr Cys Ser Ala Asp Glu Phe Thr	
145 150 155 160	
tgc tcc agt ggc cgc tgc gtc tcc aga aac ttt gtg tgc aat ggc cag	709
Cys Ser Ser Gly Arg Cys Val Ser Arg Asn Phe Val Cys Asn Gly Gln	
165 170 175	
gat gac tgt gac gat ggc agt gat gag ctg gac tgt gct cca cca acc	757
Asp Asp Cys Asp Asp Gly Ser Asp Glu Leu Asp Cys Ala Pro Pro Thr	
180 185 190	

tgc gga gcc cac gag ttc cag tgc agc acc tct tcc tgc att ccc ctc	805
Cys Gly Ala His Glu Phe Gln Cys Ser Thr Ser Ser Cys Ile Pro Leu	
195 200 205	
agc tgg gtg tgt gat gat gac gca gac tgt tca gac caa tca gac gag	853
Ser Trp Val Cys Asp Asp Asp Ala Asp Cys Ser Asp Gln Ser Asp Glu	
210 215 220	
tct ctt gag cag tgt ggc cgt cag cct gtg ata cat acc aaa tgt cct	901
Ser Leu Glu Gln Cys Gly Arg Gln Pro Val Ile His Thr Lys Cys Pro	
225 230 235 240	
acc agt gag atc cag tgt ggc tct ggc gag tgc att cac aaa aaa tgg	949
Thr Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp	
245 250 255	
cgg tgt gac gga gac cct gac tgc aag gac ggc agc gat gag gtc aac	997
Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn	
260 265 270	
tgc cct tct cga acc tgc cga cct gac cag ttt gaa tgt gaa gat ggt	1045
Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly	
275 280 285	
agc tgt atc cac ggc agc agg caa tcg aat ggc atc cga gac tgt gtt	1093
Ser Cys Ile His Gly Ser Arg Gln Ser Asn Gly Ile Arg Asp Cys Val	
290 295 300	
gat ggc tct gat gaa gtc aac tgc aaa aac gtc aat cag tgc ctg ggc	1141
Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly	
305 310 315 320	
cct gga aag ttc aag tgc aga agc ggg gaa tgc ata gac atg agc aaa	1189
Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Met Ser Lys	
325 330 335	
gta tgt gac cag gaa caa gac tgc aga gac tgg agt gac gag ccc ctg	1237
Val Cys Asp Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu	

340	345	350	
aag gaa tgc cat atc aac gaa tgc ctg gtc aat aat gga ggc tgt tcc			1285
Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser			
355	360	365	
cat atc tgc aaa gac cta gtt ata ggt tat gag tgt gat tgt gca gct			1333
His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala			
370	375	380	
ggg ttt gaa ctg ata gat agg aaa acc tgt gga gat att gat gaa tgc			1381
Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys			
385	390	395	400
caa aac ccg ggg atc tgc agt caa att tgt atc aac tta aaa ggc ggt			1429
Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly			
405	410	415	
tac aag tgt gaa tgt agt cgt ggc tat caa atg gat ctt gcc act ggc			1477
Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly			
420	425	430	
gtg tgc aag gca gta ggc aaa gag ccg agt ctg atc ttc act aat cga			1525
Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg			
435	440	445	
aga gac atc agg aag att ggc cta gag aga aag gaa tac atc caa ctt			1573
Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu			
450	455	460	
gta gag caa cta agg aac acg gtg gct ctc gat gcg gac att gca gct			1621
Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala			
465	470	475	480
cag aag ctg ttt tgg gct gat ctc agc cag aag gcc atc ttc agt gcc			1669
Gln Lys Leu Phe Trp Ala Asp Leu Ser Gln Lys Ala Ile Phe Ser Ala			
485	490	495	
tca att gat gac aag gtt ggt aga cat ttt aaa atg atc gac aat gtc			1717

Ser Ile Asp Asp Lys Val Gly Arg His Phe Lys Met Ile Asp Asn Val	
500	505
510	
tat aat cct gca gcc att gct gtt gat tgg gtg tac aag acc atc tac	1765
Tyr Asn Pro Ala Ala Ile Ala Val Asp Trp Val Tyr Lys Thr Ile Tyr	
515	520
525	
tgg act gat gcg gct tct aag act att tca gta gct acc cta gac gga	1813
Trp Thr Asp Ala Ala Ser Lys Thr Ile Ser Val Ala Thr Leu Asp Gly	
530	535
540	
gcc aag agg aag ttc ctg ttt aat tct gac ttg cga gag cct gcc tcc	1861
Ala Lys Arg Lys Phe Leu Phe Asn Ser Asp Leu Arg Glu Pro Ala Ser	
545	550
555	560
ata gct gtg gat ccg ttg tcg ggc ttt gtt tac tgg tca gac tgg ggc	1909
Ile Ala Val Asp Pro Leu Ser Gly Phe Val Tyr Trp Ser Asp Trp Gly	
565	570
575	
gag cca gct aaa ata gaa aaa gca gga atg aat gga ttt gat aga cgt	1957
Glu Pro Ala Lys Ile Glu Lys Ala Gly Met Asn Gly Phe Asp Arg Arg	
580	585
590	
cct ctg gtg acg gag gac atc caa tgg cct aat gga att aca ctc gac	2005
Pro Leu Val Thr Glu Asp Ile Gln Trp Pro Asn Gly Ile Thr Leu Asp	
595	600
605	
ctt gtc aaa agc cgc ctc tac tgg ctg gat tcc aag ttg cac atg ctc	2053
Leu Val Lys Ser Arg Leu Tyr Trp Leu Asp Ser Lys Leu His Met Leu	
610	615
620	
tct agc gtg gac ctg aat ggt caa gat cgt agg ata gtg ctc aag tct	2101
Ser Ser Val Asp Leu Asn Gly Gln Asp Arg Arg Ile Val Leu Lys Ser	
625	630
635	640
ctg gag ttc cta gct cat cct ctt gca ctc acc ata ttt gag gat cgc	2149
Leu Glu Phe Leu Ala His Pro Leu Ala Leu Thr Ile Phe Glu Asp Arg	
645	650
655	

gtc tac tgg ata gat gga gaa aat gaa gca gtg tac ggt gcc aat aaa 2197
 Val Tyr Trp Ile Asp Gly Glu Asn Glu Ala Val Tyr Gly Ala Asn Lys
 660 665 670
 ttc act ggg tca gag ctg gcc act cta gtg aat aat ctc aat gat gcc 2245
 Phe Thr Gly Ser Glu Leu Ala Thr Leu Val Asn Asn Leu Asn Asp Ala
 675 680 685
 caa gac atc att gtc tac cat gaa ctc gtc cag ccg tca ggt aaa aac 2293
 Gln Asp Ile Ile Val Tyr His Glu Leu Val Gln Pro Ser Gly Lys Asn
 690 695 700
 tgg tgt gaa gac gat atg gag aat gga gga tgt gaa tat ctc tgc ctg 2341
 Trp Cys Glu Asp Asp Met Glu Asn Gly Gly Cys Glu Tyr Leu Cys Leu
 705 710 715 720
 cca gca cca cag atc aat gac cac tct cca aaa tat acc tgt tcc tgt 2389
 Pro Ala Pro Gln Ile Asn Asp His Ser Pro Lys Tyr Thr Cys Ser Cys
 725 730 735
 ccc aat ggg tac aat ctc gaa gaa aat gga cga gag tgt caa agt act 2437
 Pro Asn Gly Tyr Asn Leu Glu Glu Asn Gly Arg Glu Cys Gln Ser Thr
 740 745 750
 tca act cct gtg act tac agt gag aca aaa gat atc aac aca aca gac 2485
 Ser Thr Pro Val Thr Tyr Ser Glu Thr Lys Asp Ile Asn Thr Thr Asp
 755 760 765
 att cta cga act agt gga ctg gtt cct gga ggg atc aat gtg acc aca 2533
 Ile Leu Arg Thr Ser Gly Leu Val Pro Gly Gly Ile Asn Val Thr Thr
 770 775 780
 gca gta tca gaa gtc agt gtt ccc cca aaa ggg acg tca gct gcc tgg 2581
 Ala Val Ser Glu Val Ser Val Pro Pro Lys Gly Thr Ser Ala Ala Trp
 785 790 795 800
 gcc atc ctt cct ctc ttg ctc tta gtg atg gca gca gta ggt ggc tac 2629
 Ala Ile Leu Pro Leu Leu Leu Leu Val Met Ala Ala Val Gly Gly Tyr

805	810	815	
ttg atg tgg agg aat tgg caa cat aaa aac atg aaa agc atg aac ttt			2677
Leu Met Trp Arg Asn Trp Gln His Lys Asn Met Lys Ser Met Asn Phe			
820	825	830	
gac aat cct gtg tac ttg aag acc act gaa gag gac ctg tgc ata gac			2725
Asp Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp			
835	840	845	
att ggt aga cac agc gct tct gta gga cac aca tac cca gca ata tca			2773
Ile Gly Arg His Ser Ala Ser Val Gly His Thr Tyr Pro Ala Ile Ser			
850	855	860	
gtt gta agc aca gat gat gat ctg gct tga gttctgaaca aatcttggtc			2823
Val Val Ser Thr Asp Asp Asp Leu Ala			
865	870		
tatgaggctc acaccaataa caccctactc tggaatggta acagagccag cgctgaagtc			2883
tcctttcttc ctcccatctg gaagaacatc aagatatctt ttgttggaac aagtttgagt			2943
acttgatcat ttttatatta cttttgtaaa tattcttggc cacattctac ttcagctctg			3003
gatgtgggta ccaagtatct gtaacccttg agcccctaga cagtattgcc atctctggcc			3063
aaatatgcac ttccctaga aagccatatt ccagcaatga acctgtgct atagtgactc			3123
ccacctgtac atacattgta taggccacct gtacatatcc cagagaacaa tcactattct			3183
taagcacttt gttgatattt ctatgtaaat tattgtaaac tttttcaatg gttgggacaa			3243
tggcaatagg ataaaacggg ttactaagat gaaattgcc			3283

<210> 84

<211> 873

<212> PRT

<213> Mus musculus

<400> 84

Met Gly Thr Ser Ala Arg Trp Ala Leu Trp Leu Leu Ala Leu Cys

1	5	10	15												
Trp	Ala	Pro	Arg	Asp	Ser	Gly	Ala	Thr	Ala	Ser	Gly	Lys	Lys	Ala	Lys
	20		25		30										
Cys	Asp	Ser	Ser	Gln	Phe	Gln	Cys	Thr	Asn	Gly	Arg	Cys	Ile	Thr	Leu
	35		40		45										
Leu	Trp	Lys	Cys	Asp	Gly	Asp	Glu	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu
	50		55		60										
Lys	Asn	Cys	Val	Lys	Lys	Thr	Cys	Ala	Glu	Ser	Asp	Phe	Val	Cys	Lys
65			70		75										80
Asn	Gly	Gln	Cys	Val	Pro	Asn	Arg	Trp	Gln	Cys	Asp	Gly	Asp	Pro	Asp
		85			90										95
Cys	Glu	Asp	Gly	Ser	Asp	Glu	Ser	Pro	Glu	Gln	Cys	His	Met	Arg	Thr
	100		105		110										
Cys	Arg	Ile	Asn	Glu	Ile	Ser	Cys	Gly	Ala	Arg	Ser	Thr	Gln	Cys	Ile
	115		120		125										
Pro	Val	Ser	Trp	Arg	Cys	Asp	Gly	Glu	Asn	Asp	Cys	Asp	Asn	Gly	Glu
	130		135		140										
Asp	Glu	Glu	Asn	Cys	Gly	Asn	Ile	Thr	Cys	Ser	Ala	Asp	Glu	Phe	Thr
145			150		155										160
Cys	Ser	Ser	Gly	Arg	Cys	Val	Ser	Arg	Asn	Phe	Val	Cys	Asn	Gly	Gln
	165		170		175										
Asp	Asp	Cys	Asp	Asp	Gly	Ser	Asp	Glu	Leu	Asp	Cys	Ala	Pro	Pro	Thr
	180		185		190										
Cys	Gly	Ala	His	Glu	Phe	Gln	Cys	Ser	Thr	Ser	Ser	Cys	Ile	Pro	Leu
	195		200		205										
Ser	Trp	Val	Cys	Asp	Asp	Asp	Ala	Asp	Cys	Ser	Asp	Gln	Ser	Asp	Glu
	210		215		220										
Ser	Leu	Glu	Gln	Cys	Gly	Arg	Gln	Pro	Val	Ile	His	Thr	Lys	Cys	Pro
225			230		235										240

Thr Ser Glu Ile Gln Cys Gly Ser Gly Glu Cys Ile His Lys Lys Trp
 245 250 255
 Arg Cys Asp Gly Asp Pro Asp Cys Lys Asp Gly Ser Asp Glu Val Asn
 260 265 270
 Cys Pro Ser Arg Thr Cys Arg Pro Asp Gln Phe Glu Cys Glu Asp Gly
 275 280 285
 Ser Cys Ile His Gly Ser Arg Gln Ser Asn Gly Ile Arg Asp Cys Val
 290 295 300
 Asp Gly Ser Asp Glu Val Asn Cys Lys Asn Val Asn Gln Cys Leu Gly
 305 310 315 320
 Pro Gly Lys Phe Lys Cys Arg Ser Gly Glu Cys Ile Asp Met Ser Lys
 325 330 335
 Val Cys Asp Gln Glu Gln Asp Cys Arg Asp Trp Ser Asp Glu Pro Leu
 340 345 350
 Lys Glu Cys His Ile Asn Glu Cys Leu Val Asn Asn Gly Gly Cys Ser
 355 360 365
 His Ile Cys Lys Asp Leu Val Ile Gly Tyr Glu Cys Asp Cys Ala Ala
 370 375 380
 Gly Phe Glu Leu Ile Asp Arg Lys Thr Cys Gly Asp Ile Asp Glu Cys
 385 390 395 400
 Gln Asn Pro Gly Ile Cys Ser Gln Ile Cys Ile Asn Leu Lys Gly Gly
 405 410 415
 Tyr Lys Cys Glu Cys Ser Arg Gly Tyr Gln Met Asp Leu Ala Thr Gly
 420 425 430
 Val Cys Lys Ala Val Gly Lys Glu Pro Ser Leu Ile Phe Thr Asn Arg
 435 440 445
 Arg Asp Ile Arg Lys Ile Gly Leu Glu Arg Lys Glu Tyr Ile Gln Leu
 450 455 460
 Val Glu Gln Leu Arg Asn Thr Val Ala Leu Asp Ala Asp Ile Ala Ala

465	470	475	480
Gln Lys Leu Phe Trp	Ala Asp Leu Ser	Gln Lys Ala Ile Phe	Ser Ala
	485	490	495
Ser Ile Asp Asp Lys	Val Gly Arg His Phe	Lys Met Ile Asp	Asn Val
	500	505	510
Tyr Asn Pro Ala Ala	Ile Ala Val Asp	Trp Val Tyr Lys	Thr Ile Tyr
	515	520	525
Trp Thr Asp Ala Ala	Ser Lys Thr Ile Ser	Val Ala Thr Leu	Asp Gly
	530	535	540
Ala Lys Arg Lys Phe	Leu Phe Asn Ser Asp	Leu Arg Glu Pro	Ala Ser
545	550	555	560
Ile Ala Val Asp Pro	Leu Ser Gly Phe Val	Tyr Trp Ser Asp	Trp Gly
	565	570	575
Glu Pro Ala Lys Ile	Glu Lys Ala Gly Met	Asn Gly Phe Asp	Arg Arg
	580	585	590
Pro Leu Val Thr Glu	Asp Ile Gln Trp Pro	Asn Gly Ile Thr	Leu Asp
	595	600	605
Leu Val Lys Ser Arg	Leu Tyr Trp Leu Asp	Ser Lys Leu His	Met Leu
	610	615	620
Ser Ser Val Asp Leu	Asn Gly Gln Asp Arg	Arg Ile Val Leu	Lys Ser
625	630	635	640
Leu Glu Phe Leu Ala	His Pro Leu Ala Leu	Thr Ile Phe Glu	Asp Arg
	645	650	655
Val Tyr Trp Ile Asp	Gly Glu Asn Glu Ala	Val Tyr Gly Ala	Asn Lys
	660	665	670
Phe Thr Gly Ser Glu	Leu Ala Thr Leu Val	Asn Asn Leu Asn	Asp Ala
	675	680	685
Gln Asp Ile Ile Val	Tyr His Glu Leu Val	Gln Pro Ser Gly	Lys Asn
	690	695	700

Trp Cys Glu Asp Asp Met Glu Asn Gly Gly Cys Glu Tyr Leu Cys Leu
 705 710 715 720
 Pro Ala Pro Gln Ile Asn Asp His Ser Pro Lys Tyr Thr Cys Ser Cys
 725 730 735
 Pro Asn Gly Tyr Asn Leu Glu Glu Asn Gly Arg Glu Cys Gln Ser Thr
 740 745 750
 Ser Thr Pro Val Thr Tyr Ser Glu Thr Lys Asp Ile Asn Thr Thr Asp
 755 760 765
 Ile Leu Arg Thr Ser Gly Leu Val Pro Gly Gly Ile Asn Val Thr Thr
 770 775 780
 Ala Val Ser Glu Val Ser Val Pro Pro Lys Gly Thr Ser Ala Ala Trp
 785 790 795 800
 Ala Ile Leu Pro Leu Leu Leu Leu Val Met Ala Ala Val Gly Gly Tyr
 805 810 815
 Leu Met Trp Arg Asn Trp Gln His Lys Asn Met Lys Ser Met Asn Phe
 820 825 830
 Asp Asn Pro Val Tyr Leu Lys Thr Thr Glu Glu Asp Leu Ser Ile Asp
 835 840 845
 Ile Gly Arg His Ser Ala Ser Val Gly His Thr Tyr Pro Ala Ile Ser
 850 855 860
 Val Val Ser Thr Asp Asp Asp Leu Ala
 865 870

<210> 85

<211> 2404

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (83).. (1573)

<400> 85

```

ggcctcacgt ggaattcccc gccgccacct gaggcggctg aggggcgcgt gcgattgagc 60
tgctgaaact tccgttttca ag atg aag ttt tgc ttg gca atc tcc ttt ttt 112
      Met Lys Phe Ser Leu Ala Ile Ser Phe Phe
                1                5                10
att tta atg tcc ttg ttg ttt gaa gac gct tgt gct aaa gaa aag tct 160
Ile Leu Met Ser Leu Leu Phe Glu Asp Ala Cys Ala Lys Glu Lys Ser
      15                20                25
tcc aag aaa ggg aag ggg aaa aag aag cag tac ttg tgc cca tct cag 208
Ser Lys Lys Gly Lys Gly Lys Lys Lys Gln Tyr Leu Cys Pro Ser Gln
      30                35                40
cag tca ccc gag gac ctg gcc cgt gtg ccc ccc aac tcc acc agc aat 256
Gln Ser Pro Glu Asp Leu Ala Arg Val Pro Pro Asn Ser Thr Ser Asn
      45                50                55
atc ttg aac agg ctg ctg gtc agt tat gat ccc agg atc aga cca aac 304
Ile Leu Asn Arg Leu Leu Val Ser Tyr Asp Pro Arg Ile Arg Pro Asn
      60                65                70
ttc aaa ggc att cct gtt gat gta gta gtc aac att ttt att aat agt 352
Phe Lys Gly Ile Pro Val Asp Val Val Val Asn Ile Phe Ile Asn Ser
      75                80                85                90
ttt gga tcc att caa gag aca aca atg gac tat aga gtt aac att ttc 400
Phe Gly Ser Ile Gln Glu Thr Thr Met Asp Tyr Arg Val Asn Ile Phe
      95                100                105
ttg aga cag aaa tgg aat gac ccc aga ctc aag cta cct agt gac ttc 448
Leu Arg Gln Lys Trp Asn Asp Pro Arg Leu Lys Leu Pro Ser Asp Phe
      110                115                120

```

aga ggc tca gat gca ctg aca gtt gac ccc acc atg tat aag tgc ttg 496
 Arg Gly Ser Asp Ala Leu Thr Val Asp Pro Thr Met Tyr Lys Cys Leu
 125 130 135
 tgg aaa cct gac tta ttc ttt gca aat gaa aaa agt gcc aat ttt cat 544
 Trp Lys Pro Asp Leu Phe Phe Ala Asn Glu Lys Ser Ala Asn Phe His
 140 145 150
 gat gtg acc caa gaa aat atc ctg ttg ttt atc ttt cgg gat gga gac 592
 Asp Val Thr Gln Glu Asn Ile Leu Leu Phe Ile Phe Arg Asp Gly Asp
 155 160 165 170
 gtc ctt gtg agc atg agg ttg tct att aca ctt tca tgt cct ctg gac 640
 Val Leu Val Ser Met Arg Leu Ser Ile Thr Leu Ser Cys Pro Leu Asp
 175 180 185
 tta act ctg ttt ccc atg gac aca caa cgc tgc aaa atg caa ctt gag 688
 Leu Thr Leu Phe Pro Met Asp Thr Gln Arg Cys Lys Met Gln Leu Glu
 190 195 200
 agc ttt gga tat aca acc gat gat tta aga ttc atc tgg cag tca gga 736
 Ser Phe Gly Tyr Thr Thr Asp Asp Leu Arg Phe Ile Trp Gln Ser Gly
 205 210 215
 gat cct gtt cag ttg gaa aaa att gct tta cct caa ttt gat att aaa 784
 Asp Pro Val Gln Leu Glu Lys Ile Ala Leu Pro Gln Phe Asp Ile Lys
 220 225 230
 aag gag gat atc gaa tat ggc aac tgt aca aaa tac tat aaa ggc act 832
 Lys Glu Asp Ile Glu Tyr Gly Asn Cys Thr Lys Tyr Tyr Lys Gly Thr
 235 240 245 250
 ggt tac tac act tgt gtg gag gtc atc ttc acc ctg agg aga cag gtt 880
 Gly Tyr Tyr Thr Cys Val Glu Val Ile Phe Thr Leu Arg Arg Gln Val
 255 260 265
 ggg ttc tac atg atg ggc gta tat gca cca acc ttg ctg att gtg gtt 928
 Gly Phe Tyr Met Met Gly Val Tyr Ala Pro Thr Leu Leu Ile Val Val

270	275	280	
ctc tcc tgg ctc tct ttc tgg atc aac cct gat gct agt gct gcc aga	976		
Leu Ser Trp Leu Ser Phe Trp Ile Asn Pro Asp Ala Ser Ala Ala Arg			
285	290	295	
gta cct ctg ggc atc ttc tcc gtg ctc agt ttg gcc tca gag tgc acc	1024		
Val Pro Leu Gly Ile Phe Ser Val Leu Ser Leu Ala Ser Glu Cys Thr			
300	305	310	
acc ctc gca gcc gag ctt cct aaa gtg tct tat gtg aag gcg ctg gat	1072		
Thr Leu Ala Ala Glu Leu Pro Lys Val Ser Tyr Val Lys Ala Leu Asp			
315	320	325	330
gtg tgg ctc att gcc tgc ctg ctc ttc ggg ttt gcc tcc ctc gtg gag	1120		
Val Trp Leu Ile Ala Cys Leu Leu Phe Gly Phe Ala Ser Leu Val Glu			
335	340	345	
tac gct gtg gtc cag gtg atg ctg aac aat ccc aaa agg gtt gaa gcc	1168		
Tyr Ala Val Val Gln Val Met Leu Asn Asn Pro Lys Arg Val Glu Ala			
350	355	360	
gag aag cgc cga ata gct aag gct gag caa gca gat ggg aaa ggt gga	1216		
Glu Lys Arg Arg Ile Ala Lys Ala Glu Gln Ala Asp Gly Lys Gly Gly			
365	370	375	
aac gca gct aag aag aat act gta aac ggc acg ggg acc cct gtt cat	1264		
Asn Ala Ala Lys Lys Asn Thr Val Asn Gly Thr Gly Thr Pro Val His			
380	385	390	
atc agc act ttg cag gtt ggt gag acc aga tgc aaa aaa gtt tgt act	1312		
Ile Ser Thr Leu Gln Val Gly Glu Thr Arg Cys Lys Lys Val Cys Thr			
395	400	405	410
tcc aag tct gat ttg aga tcc aat gac ttc agc att gtt gga agc tta	1360		
Ser Lys Ser Asp Leu Arg Ser Asn Asp Phe Ser Ile Val Gly Ser Leu			
415	420	425	
cca aga gat ttt gaa tta tcc aat tat gac tgc tat ggg aaa ccc atc	1408		

Pro Arg Asp Phe Glu Leu Ser Asn Tyr Asp Cys Tyr Gly Lys Pro Ile
 430 435 440
 gaa gtc aac aat gga ctt ggg aaa cca cag gca aag aac aag aag cct 1456
 Glu Val Asn Asn Gly Leu Gly Lys Pro Gln Ala Lys Asn Lys Lys Pro
 445 450 455
 ccg cct gcc aag cct gtc atc cca aca gca gcc aag cgc atc gac ctt 1504
 Pro Pro Ala Lys Pro Val Ile Pro Thr Ala Ala Lys Arg Ile Asp Leu
 460 465 470
 tat gca aga gca tta ttt cct ttc tgc ttc ttg ttc ttc aat gtt ata 1552
 Tyr Ala Arg Ala Leu Phe Pro Phe Cys Phe Leu Phe Phe Asn Val Ile
 475 480 485 490
 tat tgg tct ata tat tta tga taaaccattt cccittgtat gaaatacagc 1603
 Tyr Trp Ser Ile Tyr Leu
 495
 accatttcat tgtgaccaat gcaattcata attgctgac tgtggaaact ttgcattttc 1663
 ctagcaatat attgcatttt ggatgccact tgattataat aaaatacagc accttacttt 1723
 tgaatggcag catgaccctg taaagtctct gcaccgactg tgagatagat agatagatgt 1783
 atgtatatig agcatagtgc ttttaagaatc aatgacaaat atgcatacta tgtaatctac 1843
 ataatgltac tgtaactctg taactacaaa tacttccagt aatccagatg aaaacataat 1903
 gtgcacgctg acccctgtca tgttcactgg tccatgtatg cagtatctta catecccttc 1963
 cttgtaagaa agaaagccat cttattaaat aattttcgat agtattattg cagattaagc 2023
 aagattatat ggcatagtgt ttaaagtttt taagagaggt agatcagtaa tagttatgca 2083
 ggctccttaa gaaataaaat cataattata catttattaa gcaagcttat ttttacgtgt 2143
 gcttgtgtcg tcaaaaatgcc agataataga acagtaagca tttctgaaga aaagagaaat 2203
 ctgggctagt ataaatgcat agcaagttct ggcttctggc aaaatacaaa tagtgataga 2263
 tgtattaatt aaatatittg gataaaaata atcctttaat ccaccttaaa tcaaagtcta 2323
 ttttcatgcc tttcattggt tggatggag agcattaagc ataagcctta aaaagagttg 2383
 cacacatttc aaaggaattc c 2404

<210> 86

<211> 496

<212> PRT

<213> Mus musculus

<400> 86

Met Lys Phe Ser Leu Ala Ile Ser Phe Phe Ile Leu Met Ser Leu Leu

1 5 10 15

Phe Glu Asp Ala Cys Ala Lys Glu Lys Ser Ser Lys Lys Gly Lys Gly

20 25 30

Lys Lys Lys Gln Tyr Leu Cys Pro Ser Gln Gln Ser Pro Glu Asp Leu

35 40 45

Ala Arg Val Pro Pro Asn Ser Thr Ser Asn Ile Leu Asn Arg Leu Leu

50 55 60

Val Ser Tyr Asp Pro Arg Ile Arg Pro Asn Phe Lys Gly Ile Pro Val

65 70 75 80

Asp Val Val Val Asn Ile Phe Ile Asn Ser Phe Gly Ser Ile Gln Glu

85 90 95

Thr Thr Met Asp Tyr Arg Val Asn Ile Phe Leu Arg Gln Lys Trp Asn

100 105 110

Asp Pro Arg Leu Lys Leu Pro Ser Asp Phe Arg Gly Ser Asp Ala Leu

115 120 125

Thr Val Asp Pro Thr Met Tyr Lys Cys Leu Trp Lys Pro Asp Leu Phe

130 135 140

Phe Ala Asn Glu Lys Ser Ala Asn Phe His Asp Val Thr Gln Glu Asn

145 150 155 160

Ile Leu Leu Phe Ile Phe Arg Asp Gly Asp Val Leu Val Ser Met Arg

165 170 175

Leu Ser Ile Thr Leu Ser Cys Pro Leu Asp Leu Thr Leu Phe Pro Met

180	185	190
Asp Thr Gln Arg Cys Lys Met Gln Leu Glu Ser Phe Gly Tyr Thr Thr		
195	200	205
Asp Asp Leu Arg Phe Ile Trp Gln Ser Gly Asp Pro Val Gln Leu Glu		
210	215	220
Lys Ile Ala Leu Pro Gln Phe Asp Ile Lys Lys Glu Asp Ile Glu Tyr		
225	230	235
Gly Asn Cys Thr Lys Tyr Tyr Lys Gly Thr Gly Tyr Tyr Thr Cys Val		
245	250	255
Glu Val Ile Phe Thr Leu Arg Arg Gln Val Gly Phe Tyr Met Met Gly		
260	265	270
Val Tyr Ala Pro Thr Leu Leu Ile Val Val Leu Ser Trp Leu Ser Phe		
275	280	285
Trp Ile Asn Pro Asp Ala Ser Ala Ala Arg Val Pro Leu Gly Ile Phe		
290	295	300
Ser Val Leu Ser Leu Ala Ser Glu Cys Thr Thr Leu Ala Ala Glu Leu		
305	310	315
Pro Lys Val Ser Tyr Val Lys Ala Leu Asp Val Trp Leu Ile Ala Cys		
325	330	335
Leu Leu Phe Gly Phe Ala Ser Leu Val Glu Tyr Ala Val Val Gln Val		
340	345	350
Met Leu Asn Asn Pro Lys Arg Val Glu Ala Glu Lys Arg Arg Ile Ala		
355	360	365
Lys Ala Glu Gln Ala Asp Gly Lys Gly Gly Asn Ala Ala Lys Lys Asn		
370	375	380
Thr Val Asn Gly Thr Gly Thr Pro Val His Ile Ser Thr Leu Gln Val		
385	390	395
Gly Glu Thr Arg Cys Lys Lys Val Cys Thr Ser Lys Ser Asp Leu Arg		
405	410	415

Ser Asn Asp Phe Ser Ile Val Gly Ser Leu Pro Arg Asp Phe Glu Leu

420

425

430

Ser Asn Tyr Asp Cys Tyr Gly Lys Pro Ile Glu Val Asn Asn Gly Leu

435

440

445

Gly Lys Pro Gln Ala Lys Asn Lys Lys Pro Pro Pro Ala Lys Pro Val

450

455

460

Ile Pro Thr Ala Ala Lys Arg Ile Asp Leu Tyr Ala Arg Ala Leu Phe

465

470

475

480

Pro Phe Cys Phe Leu Phe Phe Asn Val Ile Tyr Trp Ser Ile Tyr Leu

485

490

495

<210> 87

<211> 1068

<212> DNA

<213> Mus musculus

<400> 87

gaggctgctc aagagctgcg gttgggtcac cgcttcatgt ttctctgccg attctgggga 60
aagatggcaa cgaatgatgc tgttctgaag aggctggagc agaaggggtgc agaggcggat 120
cagatcatcg aatatctcaa gcagcagggtt gctcttctta aggagaaagc aattttgcag 180
gcaacaatga gagaagaaaa gaaacttcga gttgaaaatg ctaaactgaa aaaagaaata 240
gaagagctaa agcaagagct gattctggca gaaattcata acggagtgga gcaagtgcgt 300
gttcgattga gtactccact gcagacgaac tgtactgctt ctgaaagtgt ggtgcagtct 360
ccatcagtag caaccaccgc ctctcctgct acaaaagagc agatcaaagc gggagaagaa 420
aagaaggatga aagagaagac tgaaaagaaa ggagagaaaa aggagaagca gcagtcggca 480
gcagcaagta ctgactccaa gcciatcgac gcatcgcgte tggatcttcg aattggttgt 540
attgttactg ccaagaagca cctgatgca gattcactgt atgtggagga agtagatgtg 600
ggagaagcag ccccgcgcac ggtcgtcagc gggctggatga atcatgttcc tctagaacag 660
atgcaaaatc gtatgggtggt ttactctgt aatctgaagc ctgcaaagat gcggggagtt 720

ctgtctcaag ccatgggtgat gtgtgccagt tcaccagaga aagtggagat tctggcccct 780
 cccaacgggt cgtttcctgg ggacagaatt acttttgatg cttttcctgg agagcctgac 840
 aaggagctaa accctaagaa gaagatctgg gagcagatcc agcctgacct gcacaccaat 900
 gctgagtgtg tggccacata caaaggagct ccctttgagg tgaaggggaa gggagtttgc 960
 agagcccaaa ccatggccaa tagtgggaatt aaataagtgc tctgttaactg aaagacattg 1020
 gcgaaaactt aataacaata aagagaagtg tgtttatcac ttacatat 1068

<210> 88

<211> 14848

<212> DNA

<213> *Mus musculus*

<400> 88

ggccggccct gtccgggtg ggccgggct tcgacgcggc gctgcaggtc tcggccgcca 60
 tcggcaccaa cctgcgccgg ttccgggcag tgtttgggga gagcggcggg ggaggcggca 120
 gcggagagga tgagcagttc ttaggttttg gctcagatga agaagtcaga gtgcgaagcc 180
 ccaccaggtc tccttcagtt aaagctagtc ctgaaaacc tcgcgggaga cctagaagtg 240
 gctctgaccg gaaccagcc atcctctcag acccatctgt gttttccct ctaaacaat 300
 cagagaccaa atctgcagat aaaatcaaga agaaagattc taagagcata gaaaagaaga 360
 gaggaagacc tcctaccitc cctggggtaa aaatcaaat cacacatgga aaggacattg 420
 cagagttaac acaaggaagc aaagaggata gcctgaaaa agttaaacgg accccttctg 480
 ccatgttcca gcaagccaca aagattaaaa agttaagagc aggtaaactg tctcctctca 540
 agtctaagtt taagacaggg aagctccaaa taggaaggaa ggggtgcag attgtaagac 600
 ggcgaggaag gcctccatct acagaacgga taaagacccc ttcaggtctt ctcattaat 660
 ctgaactgga aaagcctcag aaggctccgga aagacaagga aggaacaccc cctctcaca 720
 aagaagataa gacagttgtc agacaaagcc ctggaaggat taaaccggtc aggattatc 780
 cttcttgtaa aaggacagat gccacaattg ctaagcaact cctgcagagg gcaaagaagg 840
 gggcgcagaa gaaaattgag aaagaagcgg ctgagctgca gggaaggaag gtgaagacgc 900
 aggtcaagaa tatccggcag ttcattatgc ctgtggtcag cgccatctcc tcgaggatca 960

tcaagactcc cggcggttc atagaggatg aggattatga cccacccatg aagattgcac 1020
gccitggaatc tacccegaac agcagattca gcgccacgtc ctgtggatcc tcggagaagt 1080
ccagtgccgc ctcccagcac tcctctcaga tgccttcaga ctccctccga tccagcagcc 1140
ccagtatcga taccacctca gattctcagg cctctgaaga gatccaggca ctcccagagg 1200
agcgcagtaa taccctigaa gtctatctc cactgcctat tcccagtc ccagaaaatg 1260
agagtaatga taggagaagc agacggtatt cgatgtctga gagaagcttt ggatctagag 1320
caactaaaaa attaccaact ctacaaagt cccccagca gaagacctcc tcctcgccac 1380
ctccgctct gttaacccct cccctccac tgcagccagc ctccggcatc tctgaccaca 1440
caccttggct tatgcctccc accatccctt tagcatcacc atctctgcct gcttctgctg 1500
ctcccatgca aggaagcgg aaatctatct tgcgggagcc aacatttagg tggacttctt 1560
taaacattc gaggtcagag ccacagtact tttctcagc aaagtatgcc aaagaaggtc 1620
tgattcgcaa accaatatct gataacttcc gacccctcc gctgactccc gaggatgtcg 1680
gcttctgctc tggttttct gcatctggtc ctccgcttc ggcccggttg tttcaccac 1740
tccattctgg aacaaggctt gatattcata aaaggagccc cattctgaga gctcccagat 1800
ttactccaag tgaggcacac tctagaatat ttgagctctg gaccttgcct agtaatcgaa 1860
cttcttctgg agcgtctct tcgggagtat ctaatagaaa aaggaaaagg aaagtgttta 1920
gtccgattcg gtctgaacca agatcacctt ctactccat gaggacaaga agcgggaaggc 1980
ttagcacctc tgagctgtca cctctcactc cccgctctc tgtctcctcc tcattaagca 2040
tcccgttag tcctcttgcc gctagtgcct taaaccaac ttttactttt ccttctcatt 2100
ccctaactca gtctggggat tctacagaga aaaatcagag agcaaggaag cagactagt 2160
ctccggcaga gccattctcg tcaaatagcc ctgctctctt cccatggctc accccaggct 2220
ctcagaccga gaaggggaga aagaaagaca cagccccgga ggagctgtcc aaagatcgcg 2280
atgctgacaa gagcgtggag aaggacaaga gtagagagag agaccgggag cgagagaagg 2340
agaataagcg ggaatcaagg aaagagaaaa ggaanaaggc ctgagacatt cagagtagct 2400
ctgctttgta tcctgtgggt cgggtttcca aagagaaggt tgctggagaa gatgttggca 2460
cttcatcttc tgccaaaaaa gcaacagggc ggaagaagtc ttctcactt gattctgggg 2520
ctgatgttgc tcctgtgact ctgggggaca caacagctgt caaagccaaa attcttataa 2580
agaaaggag aggaatctg gaaaaaaca acttggatct cggcccagct gcccgtccc 2640
tggaagga gagaacccc tgcctttccg ctcttctc tagcactgtt aaacactcca 2700

cttctccat aggciccatg ttggctcagg cagacaagct tccaatgact gacaagaggg 2760
ttgccagcct cctaaaaaag gccaaagccc agctctgcaa gattgagaag agtaagagtc 2820
tcaaacagac tgaccagccc aaagcacagg gtcaagaaag tgattcatca gaaacctctg 2880
ttcgaggacc ccggattaaa catgtctaca gaagagctgc tgttgccctt ggccgcaaac 2940
gagctgtgtt tcctgatgac atgcccacct tgagtgccct accgtgggaa gaacgagaaa 3000
aaattttgtc ttccatgggg aatgatgaca agtcatcagt tgctggctca gaagatgccg 3060
agcctcttgc tctcccaatc aaaccaatta agcctgtcac cagaaacaag gcacctcagg 3120
agcctccggt gaagaaaggg cggcgatcaa ggcggtgcgg acaatgtcct ggctgccagg 3180
tgcttgagga ctgtggcatt tgcactaati gcctggacaa gccaagttt ggtggccgca 3240
atataaagaa gcaatgtctc aagatgagga aatgtcagaa tctgcagtgg atgccttcca 3300
aagcctccct tcagaagcag actaaagctg tgaaaaagaa agagaaaaag tctaagacca 3360
ctgaaaagaa agagagcaaa gagagcactt ctgtgaagag cccctiggag cctgtctaga 3420
aggctgcccc gccaccgcgg gaggagcctg ccccaaagaa gagcagcagt gagcctccac 3480
cccgcaaac tigtgaagaa aagagtgaag aagggggtgc ccttgcgcct gcccctgcgc 3540
ctgaacccaa acaggtcagc gcgccagcat cccggaagtc cagcaagcag gtctcccagc 3600
cagcagccgt cgtccccct cagcctccta gcacagcacc gcagaaaaaa gaagctccca 3660
aggccgttcc aagttagccc aagaaaaagc aacctccacc cccagaacca gggccagagc 3720
aaagcaagca gaaaaaagtg gccccctcc caagtatccc tgtaaaaca aaaccaaagg 3780
acaaggagaa gccacctcca gtaagtaaac aagagaatgc aggcactttg aacatcctca 3840
acctactctc gaatggcatc agttctaagc agaaaatccc agcagatgga gtccacagga 3900
tcagagtgga cttaaggaa gactgtgaag cagaaaatgt gtgggagatg ggaggcttag 3960
ggatcctgac ctctgtcccc ataacacca gagtagtgtg ctttctctgt tccagcagtg 4020
agcatgtaga gtttgtgtat tgccaagtgt gttgtgaacc ctccacaag ttttgcttag 4080
aggagaatga gcgccccctg gaggaccagc tggaaaactg gtgtgtctgc cgctgcaagt 4140
tttgccatgt gtgtggaaga cagcatcagg ctacaaagca gttgctggag tgtaacaagt 4200
gccgaaacag ctatcacccc gagtgccctg gaccaaacta cccacacaaa cccacgaaga 4260
aaaagaaagt gtggatctgc accaagtgtg tccgctgcaa gagctgtggc tccaccactc 4320
caggcaaagg gtgggacgca cagtggctc acgatttctc actgtgccaat gactgtgcca 4380
aactctttgc taaagggaac ttctgccctc tctgtgacaa gtgctacgat gacgatgact 4440

acgagagcaa gatgatgcag tgcgggaagt gtgaccgctg ggtccactcc aagtgcgaga 4500
gtctctcagg tacagaagat gagatgtatg agattctgtc caacttgcca gaaagtgtgg 4560
cctacacgtg tgtgaactgc actgagcggc acccccaga gtggagactg gccctggaga 4620
aggagctgca ggcgtccctc aagcaggctc tcacggccct gtigaattct cggactacca 4680
gtcacttgct ggcgtaccgt caggctgcca agcctccaga cttaaaccct gagactgagg 4740
aaagcatacc tccccgaagc tccccagagg ggccagaccc tcctgttctt actgaggctc 4800
gcaagcagga tgaacagcag ccgttagacc tcgaaggggt caagaagaga atggaccagg 4860
gcagctacgt atctgtgttg gagttcagcg atgatatgtt gaagatcatt caggcagcca 4920
ttaactcaga tggagggcag ccagagataa aaaaagccaa cagcatggct aagtccttct 4980
tcattcggca aatggagcga gtttttccgt ggttcagtgt caaaaagtct agattttggg 5040
agccaaataa agtatcaaac aacagtggga tgttaccaa cgcagtgcct ccgccttcac 5100
ttgaccataa ttatgctcag tggcaggagc gagaggagag cagccacact gagcagcctc 5160
ctctaataaa gaaaatcatt ccagctccca aacccaaagg acccgagag ccagactcgc 5220
ccacgccgt ccacccgcct acacccccga tcttgagtac tgatcggagt cgagaagaca 5280
gtccagagct gaatccaccc ccaggcatcg atgacaaccg acagtgtgca ctgtgtctga 5340
tgtacggcga tgacagtgtt aatgatgctg gccgtttgct gtacattggc caaatgagt 5400
ggacacatgt gaactgtgct ttgtggtcag cagaagtgtt tgaagatgat gacggatcac 5460
tgaagaatgt gcatatggct gtgattaggg gcaagcagct gagatgtgaa ttctgccaga 5520
agccaggagc caccgtgggt tgcctccca catcttcac cagcaactac catttcatgt 5580
gttccgggc caagaactgt gtcttcttg atgataaaaa agtgtatgt cagcggcatc 5640
gggatttgat caaaggcgag gtggttctg agaattgatt tgaagttttt agaagagtgt 5700
ttgtagattt tgaaggaatc agcttgcgca ggaagtccct taatggcttg gaaccagaaa 5760
atatccacat gatgataggc tcaatgacaa tcgactgttt gggaatcctg aatgacctct 5820
ctgactgtga agataaactc ttctctattg gataccagtg ttctcgggtg tactggagca 5880
ccacagatgc ccggaagcgc tgtgtgtaca catgcaagat catggagtgc cgcctcctg 5940
ttgtagagcc ggatatcaac agcacggttg agcacgatga caataggacc attgcccata 6000
gcccatcatc atttatagat gcatcgtgta aggacagtca aagcacagct gcaattctca 6060
gtcctccgtc gccagatcgg cctcattcac agacctcagg ctctgttat tatcatgtca 6120
tctcgaaggt ccctaggatt cgaacaccca gctactcgcc tacacagagg tcccctggct 6180

gccgcccatt gccttctgca ggaagtccta cccaaccac tcacgaaatc gtcacagtcg 6240
gtgacccggtt actgtcttct ggtcttcgga gcattggctc taggcgtcac agtacttctt 6300
ccttgtcacc cctgcggctc aagctccgca taatgtctcc agtgagaacg gggagcgctt 6360
actccaggag tagtgtttcc tcagtcceca gccttgggac tgccacagat cctgaggcca 6420
gtgccaaagc atcggatcga ggagggcigt tgagtccaag tgctaatttc gggcacagcg 6480
ctccccctc ttcaagctca cagaggacag ttggaggctc caaaaccagt catctggatg 6540
ggtcgtcacc ctcggaagtg aagcgggtga gtgctttaga ctgggtaccc aaaggctcct 6600
tagtaaaggg agagaaaaac agaacttcaa gtccaagag cacagatgga tctgcacata 6660
gcacagctta ccctggaatc cctaaactga caccacaggt tcataacgca actcctggag 6720
aactaaacat tagcaaaatt ggcagttttg ctgaaccctc tacagtgcc ttttcttcta 6780
aggatacagt gtctaccca cagctccact tgaggggcca aagaagtgc agagaccagc 6840
acaiggatcc ttcccagtc gtaaagccct ctccaaatga agatggtgaa atcaaacct 6900
tgaagctccc tggatgggc cacaggccat ccattctaca tgaacacata gggctagtt 6960
ctagagacag gagacagaaa gggaaaaagt ctcttaaaga gacttgcaa gaaaagcatt 7020
ccagtaaate ctacttgga cctggccagg tgacaaccgg tgaggaagga aacctaaagc 7080
cagagtttgc tgatgaggtg ttgactcctg ggtttcttgg gcaacgacca tgtaataatg 7140
tttcatctga gaagattgga gataaagtc ttctcttctc aggagtcctt aaaggctaat 7200
ccacacaagt ggaaggatct tccaaggagt tacaggcacc ccggaagtgc tcggtcaaag 7260
tgacacctct gaagatggaa ggtgagaatc aatccaaaa caccagaaa gagagtggcc 7320
ctggctcccc cgcacacata gactcagttg gccagcaga gccagtctca gcctccagaa 7380
gccaggagc tggcccagga gttcagccga gcccacaaa taccttatec caagatctc 7440
aaagtaacaa ctaccagaat ctccagAAC aggacagaaa cctgatgatt ccagatggcc 7500
ccaagcctca ggagatggc tcttttaaaa ggcggtaccc ccggcgcagt gccgcgcac 7560
ggtctaacat gtcttttggg ctacccccac tgtatggagt caggtcttac ggtgaagaag 7620
acattccgtt ctacagcaat tccactggga aaaagcgagg aaagagatca gcagaaggcc 7680
aggtagatgg ggccgacgac ctgagcactt ccgacgaaga tgacttatac tattacaact 7740
tcacgaggac tgtgatttcc tcgggtggag aggagcggct ggctcccat aatttatctc 7800
gggaggaaga acaatgtgat ctccaaaaa ttccacagct ggtggtgtg gatgatggga 7860
cagagagtga caccagtgtc actgccacaa gcaggaaaag cagccagatt ccaaagagaa 7920

atggcaaaga aaatggaaca gaaaacttaa agattgatcg acctgaagat gctggcgaga 7980
aagagcatgt cattaagagt gctgttggcc acaaaaacga gccaaagctg gataactgcc. 8040
actctgtaag cagagtgaag gcacagggcc aggattcctt ggaagctcag ctgagctccc 8100
tggaatcgag cgcagagtc cacacaagca cccctcaga caaaaactta ctggatactt 8160
acaacgctga gctgctgaag tcagactctg acaataacaa cagtgatgac tgtgggaaca 8220
tctgcccctc agatatcatg gactttgtac taaagaatac tccatctatg caggcccttg 8280
gtgagagccc cgagtcgtcc tctctgagc tcttgactct tggtaagga ctgggtcttg 8340
acagtaatag ggaaaaggat ataggctctt ttgaagtgtt ttctcagcaa ctgccagcga 8400
cagagcctgt ggacagtagt gtctccctct ccatctcagc agaggagcag ttgagctgc 8460
ctcttgagct gccatctgac ctctctgtcc tgaccaccgc cagccccact gtcccagcc 8520
agaatcccag cagactggcc gtaatctcag attcagggga gaagcgagtg accatcacag 8580
aaaaatcagt agcctcttcc gaggtgacc cagccctgct gaggccagga gtagaccctg 8640
ctcctgaagg ccacatgaca cccgatcatt tcatccaagg acacatggat gcagaccata 8700
tctccagccc tccctgtggc tccgtggaac aaggccatgg caacagtcag gatttaacta 8760
gaaacagtgg cactcctggc ctccaggtac ctgtttcccc cactgttccc gtccagaacc 8820
agaagtatgt gccagttcc actgacagcc ctggcccatc tcagatctct aacgcagctg 8880
tccagaccac tccacccac ctgaaaccag ccactgagaa actcatgtgt gttaatcaga 8940
acatgcagcc actttatgtt ctccagactc ttccaaatgg agtgaccaa aaaatccagt 9000
tgacctctcc tgttagttct acaccagtg tgatggagac aaatacctcg gtattggggc 9060
ccatgggaag tgggtcacc ctgaccacag gactaaaccc aagcttgcca cctctccgt 9120
ctctgttccc tctgtctagc aaaggattgc tctctgtgcc tcaccaccag cacctacatt 9180
ccttccccgc agctgtctaa agtagtttcc ctcccaacat cagcagtcct ccttcaggcc 9240
tgctcattgg ggtccagcct cctcccgatc cccaacttct gggttcagaa gccaaaccaga 9300
ggacagacct cactactaca gtggccactc catcctctgg actcaagaaa agaccataat 9360
ctcgtctgca cactcgaaag aataaaaaac ttgtccctc tagtgccct tcaaataattg 9420
ccccctctga tgtggtttct aacatgacgc tgattaactt cacaccctcc cagctttcaa 9480
accaccccag tctgttagac ttggggtcac ttaacccttc atctaccga actgtcccca 9540
acatcataaa aagatctaaa tctggcatca tgtattttga acaggcacc ctgttaccac 9600
cacagagtgt gggcggaacc gctgccacag cagcgggctc atcaacgata agccaggata 9660

ctagccacct gacatctggg cctgtgtctg ccttggcatt cggttcgtcc gtccatgaatg 9720
tggtatccat gcaaaactaca gcagccccta caagtagcac atcagttcca ggatcatgtca 9780
ccttagccaa ccagagggtg ctggggacce cagatatigg ctcaataagc catcttctaa 9840
tcaaagccag ccaccagagc ctgggcattc aggaccagcc tgtggcttta ccaccaagtt 9900
caggaatgtt cccccagctg gggacatcac agactccctc tgcgtctgca atgacagcag 9960
catctagtat ctgtgtgctc cctctttctc agactgcagg catgacagct gcatccctc 10020
ctggggaggc cgaagaacac tataagctac agcgaggaaa ccagctccta gctggcaaaa 10080
ccgttacct gacttcacag cgggaccggg atcccgattc tgctccgggg acccagccgt 10140
ccatcttcac ccagacagca gaagctccta acggtgtgag tctggagcaa aacaagactt 10200
tacctcagc taagccagcc agctccgct ctccaggag ctcccatcc tctggacagc 10260
agtcaggaag ttctcagtg ccaggtecca ctaaaccaaa accaaaagcc aaacggattc 10320
agctgcccct agacaagggg agcgtcaaga agcacaaagt ttccatttg cggaccagtt 10380
ctgaagcaca cattccacac cgagacaccg accccgcacc ccagccctca gtgacacgga 10440
ctcctagagc gaacaggag cagcaggatg cagctggagt ggagcagcca tgcagaagg 10500
agtgtgggca gccggcagga ccagtggctg ctcttcaga ggtccaggca acacagaatc 10560
cagccaatga gcaagaaaat gcagaacct aagcaatgga agaagaagag agtggttica 10620
gctctcctct gatgctctgg ctccagcaag aacaaaagag gaaagaaagc attactgaga 10680
ggaagcccaa gaaaggactc gttttgaaa ttcaagtga tgatggcttt cagatctgtg 10740
cggaaagtat tgaagatgcc tggaagtcac tgacagataa agtccaggag gcacgatcaa 10800
atgccgcct gaagcagctc tcatttgag gtgtgaacgg ttgcggatg ctggggattc 10860
tccatgatgc cgttgtgttt ctgattgagc agctggctgg ggccaagcac tgtcggaatt 10920
acaaattccg ttccacaaa ccagaagagg ccaacgaacc cccctigaac cctcacggt 10980
cagccagggc tgaggteccac ctaaggaagt cagcatttga catgtttaac ttctggctt 11040
ctaaacatcg acagccccct gagtacaacc ctaacgatga ggaagaggaa gaggtccagc 11100
tgaaatccgc acggagggca acaagcatgg atctccaat gcccatgaga ttccggcact 11160
tgaagaagac ttctaaggag gcggttggtg tctacaggc tccatccat ggtcggggtc 11220
ttttctgtaa gagaaacatc gatgcaggag agatggtgat tgaatacgcc ggcaacgtca 11280
tccgtccat ccagacagac aagcgtgaga agtactatga cagcaagggc attggttgct 11340
acatgttccg aattgatgac tcggaggtag tggatgccac catgcatgga aatgctgcac 11400

gcttcatcaa tcactcttgt gagcctaact gctactcccg ggcatcaat attgatgggc 11460
agaagcacat tgtcatcttc gccatgcgta agatctaccg gggggaggag ctcacclatg 11520
actataagtt ccccatlgag gacgccagca acaagctacc ctgcaactgt ggcgccaaaa 11580
aatgccgcaa gtccctgaac taaagctggt catcttcctg tgatggagaa ccaggaccca 11640
gggccaccca aagccatgct gaaggacttc ccagcaccca agagctccaa ggattgagca 11700
ggcagttgag ggtccctctg ctggtcctta gtgtcctaca tatacatcat gtgatcatag 11760
tcttgagag agagggtct caaagaaaag atccccagat ggctttcccc tgggccctct 11820
ttgatgttg aaaaacctga gaaactgggt cctgggagaa ttgcctgca aggagcatgt 11880
agagggttcc ttacagtggg tctgagcatg tccctagaga gcagtttgic atcctcatct 11940
tagccctctc cctaaaaacg atgggtcaga caagacccca gatacagggt tggtagata 12000
cctggtagtt tgccagttag gccagtcctg tggccatctg ttgaacaaac aaatgacct 12060
gtggttttcc ctactatctg cccacttaag agttcacttt ggttgggaga caggtttcct 12120
agcacctccg gtgtcaaaag gctgtcttgg ggttgtgcca attaatlacc aaacattgag 12180
cctgtggctg taagtgggag tgttaccctg tgagccttac cgtagccagt gacctttctt 12240
gacgatagga gcggctccct ctccatccct tctctttact cctcctccc ctctccatc 12300
cttcatctgc tgccttccca ttctttctgg gttagcgggag ctgacctccc tgctcaaggg 12360
cactccctac ttggtatagg aagtcctac agaaagtcct ccaagccagt aagcactcca 12420
ggtggggaat tggacagaag ccgttggccg taaccagacg gaatttggag atctcataaa 12480
gctccattga gagttttaaa gagatgtaig tagcgagggt tttttaaaca agagactaaa 12540
gattatttaa ataggatttg agtcatgcag cagcctgagt ccatagccag gatatgccc 12600
tccccctccc aggacgtgct tactctcttt cccctttctg aagacatagg aagatgagtt 12660
tctaaaaggt cagggtccag ctgaaagaac actaatcaga ttccaaggcc ccaaacttgg 12720
gggactagac cacatgtgct aaggacctc tgccaccctg gtgcagccctg tggctgagca 12780
agttcaatga cactactgcc ctggttactc cttaggggtg ggacagccag cagcaaatgt 12840
ttctttcttc cccaagaca gagtcttgaa cctgttagat taagtcattg gattttcttc 12900
tgttctgttt acagtttact atttaagggt ttataatgta aatatatttt gtatatattt 12960
ctatttgaag cacttcatag ggagaagcac ttatgacgag gctattttta aaccgcggta 13020
ttatcctaata ttaaaagaag atcggttttt aatgattttt tattttcata ggatgaagt 13080
agagaaaata ttacagctgc cacacaaagt ctggtttccc tgcccagctt ccccttgaa 13140

agtgtacttt ttgttgttcc atgtgtagct cgtttgtgcc cattgacata aatgttccctt 13200
 gggctcgtctc tttatagtaa ctgaaaaaga aggtcaccca ctccattagg ccactgccct 13260
 ccagggccaa ggactgaggg tacagaacct tagcacacca gtgtctcctc ctctttgctg 13320
 tattgcccc tccctctgga tcagccccag agtgggaagc agcaggctcc gtttcgctcc 13380
 cctttctctt tctgagtiag caaccaagaa gctgcaactt gacattcgcc atcacatctg 13440
 cctcatccat cactctcttt ccttctctgc ccaccaagtc ctgtaccg cagagaacct 13500
 actgaccgcc tctgcccctc tcggggcaga ttgttgaacc tgaagcacag tatgaccact 13560
 cagatcaag cagatctctg cgctgccac aaggtttcag gtagcgtag tccgagtga 13620
 gggcaggga ccttttctct tatggaagtc agcaaagcaa tatgatgcag ccagaaactc 13680
 tctgccagga ctggtggctc tgcgtgcct tccatcctgg gctccttcc ttctgtgacc 13740
 ttaagaactt tgtctggigg ctttgcctga acattgtcac tgtttccact gtgggaagcc 13800
 cagcactgtg gccaggatgg cagagatttc ctgtcatca tggagaagtg ccagcagggg 13860
 actggggaaa agcactctac ccagacctca cctcctacct tctttgccc atgaacaaga 13920
 cgcagtggcc caaggggttt cactagtgtc tggtttcctt cttattgcac tgtgtgaggt 13980
 ttttttgtaa atccttgtat tccaaatttt tttttatgaa aaaatgtaag ctgcatttgt 14040
 tactgaaaga ttaaatgcac tgatgggtca tgcgttcac ctgagagacc caaaggccag 14100
 tcagaggggtg gggggaactc agctaacaga cctagtcact gccctgctag gccatgctgt 14160
 actgtgagcc cctcctcat cctcttccca caaccccaat cctgaggac ggggggaacc 14220
 cacttttct cctcctccag ctggtttgcc ttgccctccc actcactgtc aaccacagaa 14280
 acgagaaatt cctctttcag ctacagcctg agtccattgc caaaattcag catacctgcc 14340
 agcaacttgg gggataagcc agagtatccc cacaagcggg agagaaggca acaaaacaga 14400
 aggcacagct gtctccaaaa cacatctgct ttgttttgaa agtgaccaag agaacctccg 14460
 cacaaaagt caggttgagg actttgcgt gggctattcc caagaatccc ccaaggggca 14520
 acccaccgcc tcaggagtga cagctgcgga cctcgagggt tccggctttg ctgctagaac 14580
 ctgttgtggc tgcgtttcct ggtggcagt acaactgtgt aaccagaata gctgcatggc 14640
 gctgacctt tggtcggaac ttggtccctg ggctccctca gtgtgccc tgtccagcac 14700
 aacctctccc tgtttttaaa ccaatcaca ttaaggagga agccctggca ctctttaggt 14760
 tttcaacca aactcctttt tcaggacca gctcacctct gtcaaaccgc ggccaatcca 14820
 ataagcacca tgcagcaacc ttgattta 14848

<210> 89

<211> 280

<212> DNA

<213> Mus musculus

<400> 89

caggccatca ccgttggacc acctgacagg atggttggc tcttccaccg tgggcgagtt 60
 tgtcaatgtg ttctgccatg gctccctagt tatgcagaat ctgggcgagg cttctacccc 120
 tacacagggc tcggtgctct ttggcacagt caacggcatg atagggctgg tgacctcgt 180
 gtcagagagc tggataacc tcctgttga catgcagaac cgatccataa aggtcatcaa 240
 aaccttggcc aggtttgggc actccttcgt gagatccttt 280

<210> 90

<211> 1841

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (131).. (1471)

<400> 90

gccagggcaa cagagtcgga gacccccctgc cccccccctc ccgatcgccg gtgcagtcac 60
 gagccccgcc tccccctggt gcacggagag gggcggggcc tggaacaagc aggtcgttc 120
 gtgacctact atg tct tcc ccc aca agt tct ctg gac act ccc gtg cct 169

Met Ser Ser Pro Thr Ser Ser Leu Asp Thr Pro Val Pro

1

5

10

ggg aat ggt tct cct cag ccc agt acc tcc gcc acg tca ccc act att 217

Gly	Asn	Gly	Ser	Pro	Gln	Pro	Ser	Thr	Ser	Ala	Thr	Ser	Pro	Thr	Ile		
15						20					25						
aag	gaa	gag	ggg	cag	gag	act	gat	cct	cct	cca	ggc	tct	gaa	ggg	tcc	265	
Lys	Glu	Glu	Gly	Gln	Glu	Thr	Asp	Pro	Pro	Pro	Gly	Ser	Glu	Gly	Ser		
30					35					40				45			
agc	tct	gcc	tac	atc	gtg	gtc	atc	tta	gag	cca	gag	gat	gag	cct	gag	313	
Ser	Ser	Ala	Tyr	Ile	Val	Val	Ile	Leu	Glu	Pro	Glu	Asp	Glu	Pro	Glu		
				50				55					60				
cgc	aag	cgg	aag	aag	ggg	ccg	gcc	ccg	aag	atg	ctg	ggc	cat	gag	ctg	361	
Arg	Lys	Arg	Lys	Lys	Gly	Pro	Ala	Pro	Lys	Met	Leu	Gly	His	Glu	Leu		
		65						70					75				
tgc	cgc	gtg	tgc	gga	gac	aag	gct	tgc	ggc	ttc	cac	tac	aac	gtg	ctc	409	
Cys	Arg	Val	Cys	Gly	Asp	Lys	Ala	Ser	Gly	Phe	His	Tyr	Asn	Val	Leu		
		80						85					90				
agc	tgt	gaa	ggc	tgc	aaa	ggc	ttc	ttc	cgg	cgc	agt	gtg	gtc	cac	ggt	457	
Ser	Cys	Glu	Gly	Cys	Lys	Gly	Phe	Phe	Arg	Arg	Ser	Val	Val	His	Gly		
		95				100					105						
ggg	gcc	ggg	cgc	tat	gcc	tgt	cgg	ggc	agc	gga	acc	tgc	cag	atg	gat	505	
Gly	Ala	Gly	Arg	Tyr	Ala	Cys	Arg	Gly	Ser	Gly	Thr	Cys	Gln	Met	Asp		
110					115					120				125			
gcc	ttc	atg	cgg	cgc	aag	tgc	cag	ctc	tgc	cgg	ctg	cgc	aag	tgc	aag	553	
Ala	Phe	Met	Arg	Arg	Lys	Cys	Gln	Leu	Cys	Arg	Leu	Arg	Lys	Cys	Lys		
				130				135					140				
gag	gct	ggc	atg	cgg	gag	cag	tgc	gtg	ctc	tct	gag	gag	cag	att	cgg	601	
Glu	Ala	Gly	Met	Arg	Glu	Gln	Cys	Val	Leu	Ser	Glu	Glu	Gln	Ile	Arg		
		145						150					155				
aag	aaa	agg	att	cag	aag	cag	caa	cag	cag	cag	cca	cca	ccc	cca	tct	649	
Lys	Lys	Arg	Ile	Gln	Lys	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Ser		
		160						165					170				

gag cca gca gcc agc agc tca ggc cgg cca gcg gcc tcc cct ggc act 697
 Glu Pro Ala Ala Ser Ser Ser Gly Arg Pro Ala Ala Ser Pro Gly Thr
 175 180 185
 tcg gaa gca agc agc cag ggc tcc ggg gaa gga gag ggc atc cag ctg 745
 Ser Glu Ala Ser Ser Gln Gly Ser Gly Glu Gly Glu Gly Ile Gln Leu
 190 195 200 205
 acc gcg gct cag gag ctg atg atc cag cag tta gtt gcc gcg cag ctg 793
 Thr Ala Ala Gln Glu Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu
 210 215 220
 cag tgc aac aaa cga tct ttc tcc gac cag ccc aaa gtc acg ccc tgg 841
 Gln Cys Asn Lys Arg Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp
 225 230 235
 ccc ctg ggt gca gac cct cag tcc cga gat gcc cgt cag caa cgc ttt 889
 Pro Leu Gly Ala Asp Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe
 240 245 250
 gcc cac ttc acc gag cta gcc atc atc tcg gtc cag gag att gtg gac 937
 Ala His Phe Thr Glu Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp
 255 260 265
 ttt gcc aag cag gtg cca ggg ttc ttg cag ttg ggc cgg gag gac cag 985
 Phe Ala Lys Gln Val Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln
 270 275 280 285
 atc gcc ctc ctg aag gcg tcc acc att gag atc atg ttg cta gaa aca 1033
 Ile Ala Leu Leu Lys Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr
 290 295 300
 gcc aga cgc tac aac cac gag aca gaa tgc atc acg ttc ctg aag gac 1081
 Ala Arg Arg Tyr Asn His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp
 305 310 315
 ttc acc tac agc aag gac gac ttc cac cgt gca ggc ttg cag gtg gaa 1129
 Phe Thr Tyr Ser Lys Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu

320	325	330	
ttc atc aat ccc atc ttc gag ttc tcg cgg gcc atg cgg cgg ctg ggc	1177		
Phe Ile Asn Pro Ile Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly			
335	340	345	
ctg gac gat gca gag tat gcc ttg ctt atc gcc atc aac atc ttc tca	1225		
Leu Asp Asp Ala Glu Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser			
350	355	360	365
gcc gat cgg cct aat gtg cag gag ccc agc cgt gtg gag gcc ctg cag	1273		
Ala Asp Arg Pro Asn Val Gln Glu Pro Ser Arg Val Glu Ala Leu Gln			
370	375	380	
cag ccc tac gtg gag gcg ctc ctc tcc tac acg agg atc aag cgc cca	1321		
Gln Pro Tyr Val Glu Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro			
385	390	395	
cag gac cag ctc cgc ttc cca cgc atg ctc atg aag ctg gtg agc ctg	1369		
Gln Asp Gln Leu Arg Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu			
400	405	410	
cgc acc ctc agc tcc gtg cac tcg gag cag gtc ttt gca ttg cga ctc	1417		
Arg Thr Leu Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu			
415	420	425	
cag gac aag aag ctg ccg ccc ttg ctg tcc gag atc tgg gat gtg cac	1465		
Gln Asp Lys Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His			
430	435	440	445
gag tag gggcagccac aagtgcacca gccttggtgg tgtcttcttg aagatggact	1521		
Glu			
cttcacctct cctcctgggg tgggaggaca ttgtcacggc ccagtcctc gggctcagcc	1581		
tcaaactcag cggcagttgg cactaagaag gccccacccc acccattgag tcttccaaga	1641		
gtggtgaggg tcacaggtcc tagcctctga ccgttcccag ctgccctccc acccagcctt	1701		
acacctcagc ctaccacacc atgcaccttg agtggagaga ggtagggca ggtggccccc	1761		
cacagttggg agaccacagg cctctcttc tgccccitit atttaataaa aaaacaaaaa	1821		

taaagtttga gtacaagcca

1841

<210> 91

<211> 446

<212> PRT

<213> Mus musculus

<400> 91

Met Ser Ser Pro Thr Ser Ser Leu Asp Thr Pro Val Pro Gly Asn Gly
 1 5 10 15
 Ser Pro Gln Pro Ser Thr Ser Ala Thr Ser Pro Thr Ile Lys Glu Glu
 20 25 30
 Gly Gln Glu Thr Asp Pro Pro Pro Gly Ser Glu Gly Ser Ser Ser Ala
 35 40 45
 Tyr Ile Val Val Ile Leu Glu Pro Glu Asp Glu Pro Glu Arg Lys Arg
 50 55 60
 Lys Lys Gly Pro Ala Pro Lys Met Leu Gly His Glu Leu Cys Arg Val
 65 70 75 80
 Cys Gly Asp Lys Ala Ser Gly Phe His Tyr Asn Val Leu Ser Cys Glu
 85 90 95
 Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Val His Gly Gly Ala Gly
 100 105 110
 Arg Tyr Ala Cys Arg Gly Ser Gly Thr Cys Gln Met Asp Ala Phe Met
 115 120 125
 Arg Arg Lys Cys Gln Leu Cys Arg Leu Arg Lys Cys Lys Glu Ala Gly
 130 135 140
 Met Arg Glu Gln Cys Val Leu Ser Glu Glu Gln Ile Arg Lys Lys Arg
 145 150 155 160
 Ile Gln Lys Gln Gln Gln Gln Pro Pro Pro Pro Ser Glu Pro Ala

	165	170	175
Ala Ser Ser Ser Gly Arg Pro Ala Ala Ser Pro Gly Thr Ser Glu Ala			
	180	185	190
Ser Ser Gln Gly Ser Gly Glu Gly Glu Gly Ile Gln Leu Thr Ala Ala			
	195	200	205
Gln Glu Leu Met Ile Gln Gln Leu Val Ala Ala Gln Leu Gln Cys Asn			
	210	215	220
Lys Arg Ser Phe Ser Asp Gln Pro Lys Val Thr Pro Trp Pro Leu Gly			
225	230	235	240
Ala Asp Pro Gln Ser Arg Asp Ala Arg Gln Gln Arg Phe Ala His Phe			
	245	250	255
Thr Glu Leu Ala Ile Ile Ser Val Gln Glu Ile Val Asp Phe Ala Lys			
	260	265	270
Gln Val Pro Gly Phe Leu Gln Leu Gly Arg Glu Asp Gln Ile Ala Leu			
	275	280	285
Leu Lys Ala Ser Thr Ile Glu Ile Met Leu Leu Glu Thr Ala Arg Arg			
	290	295	300
Tyr Asn His Glu Thr Glu Cys Ile Thr Phe Leu Lys Asp Phe Thr Tyr			
305	310	315	320
Ser Lys Asp Asp Phe His Arg Ala Gly Leu Gln Val Glu Phe Ile Asn			
	325	330	335
Pro Ile Phe Glu Phe Ser Arg Ala Met Arg Arg Leu Gly Leu Asp Asp			
	340	345	350
Ala Glu Tyr Ala Leu Leu Ile Ala Ile Asn Ile Phe Ser Ala Asp Arg			
	355	360	365
Pro Asn Val Gln Glu Pro Ser Arg Val Glu Ala Leu Gln Gln Pro Tyr			
	370	375	380
Val Glu Ala Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln			
385	390	395	400

Leu Arg Phe Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu

405

410

415

Ser Ser Val His Ser Glu Gln Val Phe Ala Leu Arg Leu Gln Asp Lys

420

425

430

Lys Leu Pro Pro Leu Leu Ser Glu Ile Trp Asp Val His Glu

435

440

445

<210> 92

<211> 480

<212> DNA

<213> Mus musculus

<400> 92

atcttgctct tgcgcgtgc tgggtgtgga ggacctccc cgctgcagat ttgcaacagc 60
 atgaatcaag aaaagttagc caaacttcaa gctcagggtcc ggataggggg caagggtaca 120
 gctcgcagga agaagaaggt ggtacatagg acagctactg ctgatgacaa aaagcttcag 180
 agttcactaa agaaactggc tgtgaacaat atagctggta ttgaagaggt gaatatgatt 240
 aaagacgatg gcacggttat tcatttcaac aatcccaaag tccaagcttc cctctccgct 300
 aacacctttg caattactgg tcatgcagaa gccaaaccaa tcacagaaat gcttcctggg 360
 atattaagtc agcttgggtgc tgacagctta acgagccita gaaagttagc tgaacagttc 420
 ccacggcaag tattggatag taaagcgccc aaaccagaag acatcgatga agaggatgat 480

<210> 93

<211> 439

<212> DNA

<213> Mus musculus

<400> 93

gattcggcac ggggggagga ggccctggag ctcatcaatg gctatatcca gaagattaag 60

tcaggagagg aagactttga atctctggcc tcacagttca gtgattgcag ctctgccaaa 120
gccaggggag acctgggtcc cticagcaga ggtcagatgc agaaaccatt tgaggatgcg 180
tcgtttgctc tacggacagg ggagatgagt tggcccggtg tcacggactc gggcatccat 240
atcatcctgc gcacagaatg agggcaggca cctggccagc ctgctctggc tgccacacag 300
cccacggatg cccttccctgc tactgtcaca cagtatttat tggttcctaa aatgactggg 360
gaggggctct gagcatcccg ctccctgttt gccctattc ggggctgtcc tagccaggct 420
ccttctggag gaattgact 439

<210> 94

<211> 352

<212> DNA

<213> Mus musculus

<400> 94

cgcgacgagt cggigtctgg ttggcgctggc tcgcgagag tgcggctggc tgaagacacc 60
ccagcttgct ctacctgccg ttttaaggct tcctcttctt ggctctgct tgagtcaccag 120
acctactcct gaggtccacc ctgcacccta gctcacatg gggaaccact tgactgaaat 180
ggccctaca gcctcgctct tctgcccga ctccaggcc ctgcatgtc tcgtcattgg 240
gttgattcc gcggggaaga ctcccttct ttaccgtctc aagtcaagg agtttgtcca 300
gagcgtcccc accaagggt ttaatactga gaagatccgc gtgccctgg gg 352

<210> 95

<211> 483

<212> DNA

<213> Mus musculus

<400> 95

tttggaaaag cggtttcttg acaaggcggg agaactcaac atgatctcct tgaaggggca 60
caggtcagtg ggaggcattc gtgcctctct gtataacgct gtcacaaccg aagacgttga 120

gaagctggcg gccttcatga agaatttctt ggagatgcat cagctgtgaa catgaccagc 180
 cagcctctgc ctgtgagcag caccgagcgt cgtttagagt aacttgggat tgactacaga 240
 aacttaacag acatggattt ttttttccca aatacatgct tattacagat tcctttctca 300
 aagaataacg actaaacatc agggcactgc agagctgagg aaactcccag ctaacagcca 360
 ccttcattct catgtgacct ggaagcattt tgaagcttt ctttctgtt gctcttctaa 420
 atgaattcag cctgtcagcc atctttgctg ccccttctc taggtggact gccttgggct 480
 ttg 483

<210> 96

<211> 971

<212> DNA

<213> *Mus musculus*

<400> 96

ggatccctgcc tgcctctttc acatctttat tgagtgttgt ccggtctgca agagagatta 60
 atctctttct tccccctct tgtcttcaca ggacgcattg aaattttcat cgaagatctt 120
 ccaaggacac gttacaggat ttgtaatag taaacatatg gaaagtatta gacatattha 180
 ttgcctgtac atactgtaaa tgcattggga tcaaactgtc tccccaggaa actgcacatg 240
 ggatcatgtga atatttttcc cttttgcaa ggctaatacca attattcctg tcatgtttac 300
 cataatttat ttgtcaact gatgtattta ttgttaaag tatcttgggt ctgtgactc 360
 tgtttttttg taacataatg cactttaggt atacatatcg agtatgtgga tgaatttaac 420
 acataaaaagg atctctatth tgtggttcat tttaatgagt tctgaaatat aattatctag 480
 actgatttcc tctgtgcat gtaaaaatgg cagtatttha aatttgthaa ataatgtcta 540
 ataaaatata atctaattat accatgactc acaatgtgaa ttttattctt taaagtttct 600
 aatcagagaa acacaacaca atttttttta attctacttg aatataatcc taaacttaat 660
 atgtttatat gggccatcta ttccaatgtg tccacattag cttttagtta aaaaccactt 720
 aaaatgtatt ctgtccaata tttcagttca agtcaataaa atggctgaac agcctgaact 780
 tcaagttgaa ataattggcaa caaagggcaa aaataaataa gtagagaagt cagaagaaaa 840
 ggtcaaagag gttatccaga gttaaaacca gagggagagg tggaccaag actttgactc 900

tgaataaaatt ttgccaatat aaagtttagt ttgcaagggc ttgtctcatt cataacaata 960
atgaaagatc t 971

<210> 97

<211> 7331

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (642).. (2345)

<400> 97

gaattccggc acagatgttt tggggaaact tgaaattttc taaaaggcct caataagttg 60
tttattattt ttattattat tattattatt attattatac acagagtga aaaatggaag 120
tttaatcaga acaattgtta aacagacaac atacaaactg gacttcattc atttgaagtc 180
agagcagtgt tatgaattgt tgtcctccaa gtaacattag cattacaiga ttttagccat 240
cttgaaatca gagtagcctt gattaccatc aaggacacct tataagacca gggctaattc 300
acattgtcat tgtcattgga aggcaagggg cacttatagg gctcacgagg cccatgtagc 360
tcaaataact caatgtgtac ctagatccct tgtcctccat cctcaggac aagacacact 420
tttcttcagt tattcaattg acagtaagtt tctcatgcta ttacagttaa ctctggagct 480
ttgggagtaa cccatactg atgtcccagc ggggtacagg gtccccatta cttgaaggat 540
aaggctggca cggctccgac gtcgtgtggt aagcttctcc ctcccttctg agcttctcta 600
gactccttac agcgcacggc acagaatttc agtttcctaa g atg gag tca agc aaa 656

Met Glu Ser Ser Lys

1

5

aag atg gat gct gct ggc aca ctg cag cct aac cca ccc cta aag ctg 704

Lys Met Asp Ala Ala Gly Thr Leu Gln Pro Asn Pro Pro Leu Lys Leu

10

15

20

cag cct gat cgc ggc gca ggg tcc gtg ctc gtg ccg gag caa gga ggc	752
Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val Pro Glu Gln Gly Gly	
25 30 35	
tac aag gag aag ttt gtg aag acg gtg gaa gac aag tac aag tgc gag	800
Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp Lys Tyr Lys Cys Glu	
40 45 50	
aag tgc cgc ctg gtg ctg tgc aac ccg aag cag acg gag tgt ggc cac	848
Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln Thr Glu Cys Gly His	
55 60 65	
cgg ttc tgg cag agc tgc atg gcc gcc ctg ctg agc tcc tcc agt cca	896
Arg Phe Trp Gln Ser Cys Met Ala Ala Leu Leu Ser Ser Ser Ser Pro	
70 75 80 85	
aaa tgc aca gcg tgc caa gaa agc atc atc aaa gac aag gta ttt aag	944
Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys Asp Lys Val Phe Lys	
90 95 100	
gat aat tgc tgc aag aga gag att ctg gcc ctt cag gtc tac tgt cgg	992
Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu Gln Val Tyr Cys Arg	
105 110 115	
aat gaa ggc aga ggt tgt gcg gag cag ctg act ctg gga cat ctg ctg	1040
Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr Leu Gly His Leu Leu	
120 125 130	
gtg cac cta aaa aat gaa tgt cag ttt gag gaa ctt ccc tgt ctg cgt	1088
Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu Leu Pro Cys Leu Arg	
135 140 145	
gcc gac tgc aaa gaa aaa gta ctg aga aaa gac ttg cgg gat cac gtg	1136
Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp Leu Arg Asp His Val	
150 155 160 165	
gaa aag gcc tgt aaa tac cgc gag gcc acg tgc agt cac tgc aag agc	1184
Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys Ser His Cys Lys Ser	

170	175	180	
caa gtg ccc atg atc aaa ctg cag aaa cat gaa gac aca gat tgt ccc			1232
Gln Val Pro Met Ile Lys Leu Gln Lys His Glu Asp Thr Asp Cys Pro			
185	190	195	
tgt gtg gtg gta tcc tgc cct cac aag tgc agc gtt cag act ctt cta			1280
Cys Val Val Val Ser Cys Pro His Lys Cys Ser Val Gln Thr Leu Leu			
200	205	210	
agg agt gag ttg agt gca cac ttg tcc gag tgt gtc aat gcc ccc agc			1328
Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys Val Asn Ala Pro Ser			
215	220	225	
acc tgt agt ttt aag cgc tat ggc tgc gtt ttt cag ggt aca aac cag			1376
Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe Gln Gly Thr Asn Gln			
230	235	240	245
cag atc aag gcc cat gag gcc agc tcc gcg gta cag cac gtg aac ctg			1424
Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val Gln His Val Asn Leu			
250	255	260	
ctg aag gag tgg agc aac tcc ctg gag aag aag gtt tcc ctg ctg cag			1472
Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys Val Ser Leu Leu Gln			
265	270	275	
aat gaa agt gtt gag aaa aac aag agc atc caa agc ctg cac aac cag			1520
Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln Ser Leu His Asn Gln			
280	285	290	
atc tgc agc ttt gag atc gag att gag agg cag aag gag atg ctc cga			1568
Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln Lys Glu Met Leu Arg			
295	300	305	
aac aac gag tcc aag atc ctt cac ctg cag cgg gta atc gac agc caa			1616
Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg Val Ile Asp Ser Gln			
310	315	320	325
gca gag aaa ctg aaa gaa ctg gac aag gag atc cgt ccc ttc cgg cag			1664

Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile Arg Pro Phe Arg Gln	
330	335 340
aac tgg gag gaa gcg gac agc atg aag agc agt gtg gag tcc ctc cag	1712
Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser Val Glu Ser Leu Gln	
345	350 355
aac cga gtg act gag ctg gag agc gta gac aaa agt gcg ggg cag gcg	1760
Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys Ser Ala Gly Gln Ala	
360	365 370
gct cgc aac aca ggc ttg ctg gag tcc cag ctg agc cgg cat gac cag	1808
Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu Ser Arg His Asp Gln	
375	380 385
atg ttg agt gtt cat gac atc cgc ttg gcc gac atg gac ctg cgg ttc	1856
Met Leu Ser Val His Asp Ile Arg Leu Ala Asp Met Asp Leu Arg Phe	
390	395 400 405
cag gtc ctc gag acc gcc agc tac aac ggg gtg ctg atc tgg aag atc	1904
Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val Leu Ile Trp Lys Ile	
410	415 420
cgt gac tac aag cgc cgg aag cag gag gcc gtc atg ggg aag acc ctg	1952
Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val Met Gly Lys Thr Leu	
425	430 435
tct ctc tac agc cag cct ttc tac aca ggt tat ttt ggc tat aag atg	2000
Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr Phe Gly Tyr Lys Met	
440	445 450
tgt gcc agg gtc tac ctg aat ggg gac gga atg ggg aaa ggg aca cac	2048
Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met Gly Lys Gly Thr His	
455	460 465
ttg tcg ctg ttt ttt gtc att atg cgt gga gaa tat gat gct ctg ttg	2096
Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu	
470	475 480 485

cca tgg ccg ttc aag cag aaa gtg aca ctt atg ctg atg gat cag ggg 2144
 Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met Leu Met Asp Gln Gly
 490 495 500

tcc tct cgc cgt cat ctg gga gat gcg ttc aag cct gac ccc aac agc 2192
 Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys Pro Asp Pro Asn Ser
 505 510 515

agc agc ttc aag aaa ccc acc gga gag atg aat atc gcc tct ggc tgc 2240
 Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn Ile Ala Ser Gly Cys
 520 525 530

cca gtc ttt gtc gcc caa act gtt cta gag aac ggg acg tat att aaa 2288
 Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn Gly Thr Tyr Ile Lys
 535 540 545

gat gat aca atc ttt att aag gtc ata gtg gat acc tcg gat ctg cct 2336
 Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp Thr Ser Asp Leu Pro
 550 555 560 565

gac ccc tga caagaaagca gggcgggtgga ttcagcagaa ggtaactcct 2385
 Asp Pro

ctgggggggt gagctagtgt cttcacggag gtccctgccc tcagaaagga ccttgtggga 2445
 cagaggaagc agccggagga ggagaaggag gtcgagtggc tggcaggaga gccacatgtg 2505
 aaaacagacc ccaacggatt ttctaataga ctagccacac ccactctgaa ggattattta 2565
 tccatcaaca agataaatac tgcgtcaga gaaggttttc attttcattt taaaagatct 2625
 agttaattaa ggtgggaaca tataatgctaa aaagaaacat gatttttctt ccttaactta 2685
 aacaccaaaa agagaacaca tgtgggggta gctggatgtg tcagcatgtt aacctacgag 2745
 gagaacttat gaaatcataa cacaatcccc atatactcat cctaaaattc aagagtgcaa 2805
 tcttgtttca aatatagtat attgtctatt ttttaaggcct catctggctt ctgttttaat 2865
 aatttgtttg tcagaagacc ctgagtaggc agaaggcttc taaattcaga agtcattttt 2925
 aatttaaaagt tctacaaata attgttactg caaacatttt gttttaaaac gttgatagac 2985
 tgatatttct tggaagaaaa tgtaaaatat caaacacttg ttatcacttg tgataggaaa 3045
 gagaataattg aacctgctgt tatttctcgt tagaaatgta acccttcgat atctgtcgta 3105

gtagtgaca ctacttcaca atgactatga gagggacaat gctcatggat gctgtgcatc 3165
atttcagact taacaattgt ttccacccta aaatagggca ttagttgaac ttiggagttc 3225
taaacaaaat cctatagggt tttaacaattc tgccccaatgt ttagacaagc tctgtttgctg 3285
acagcaccag ccttgggtctc cagtgtcggg gtccggggat aggcagggtga cccgtgccgc 3345
aggcaggagg cccagcagag catcccatcc tgcatactg ctgcatccgg ctagcgcgct 3405
ccgaaagcaa catccgtgct cagagatggg ggcatacggg acttgtgcct tagatgtgac 3465
atgctgttcc ttgtccctgg gtttgcgttc accatggttc tagaaagtgt cagttaacc 3525
agatctctct ccaccaccag aactttgtct ctgccagggc cctcaggcaa ctctgaacct 3585
gcctggggat gccaggcctc cattggcagc tcttgaagcc tctgtctgta aatattcaca 3645
gattccaacc gtagggccct aagagcagct cagtccact ccaagggagg gaggtgtgag 3705
cagaagccac acccttccag gtctctgcaa gggccctgaa atccccacag catgaaggag 3765
aagtgcccta gtcccaagcg ttcccgagac cactgggtctg gggcctgccc gggctggcag 3825
cagcaaccct ggccctccctg tgaggagggc agccagctga tgcccagccc tgtgagtga 3885
gagggccgcc ctctcagctc actgttccca ctgtgatgag aagcctggag cctgccccg 3945
gtgccccctt tgctatgcac cacacttcac ggtgtctctac actgatgggt gctacacgcg 4005
acagggtgctt cttaggcaaa accaatgtgt gcaaaccacc acatctgtgc cacttgccca 4065
aaaggcgcgc ccacaattgg ccagctgggc ctgcgcttca gactgccctg ctctgggctc 4125
tcccatggg cgacgggga cagctgggtt ggtgcccggg agcccacctt gtctctggtg 4185
ctgccatctg tccgtgggtgt gccttcgccc cagtgcctgc tggaagtgcc ctctctcgc 4245
acacctgtcc ccgtgcttcc atgagcgacc tcttgggttc gagcactcac cctgcccctc 4305
catggctgaa gcgtttgggt tgtcctctgc tcccgcctc tctccattat gctgggattg 4365
cttgggggta agtcagcaac cttgggtctg cccacaagga aagaccgcag agctcaagtt 4425
ctttcaaagg tgccctcctc ttcccttagg cctgtcacca gggttccctc cccaaagacc 4485
tgaggttggg gggaacaccc agcagtcctt ggctggcttc aggaagcctt tctgtggcca 4545
gatgtcagca acggggccat cctgtagct cccccctca gagaaatcag tgcagtatca 4605
acagggttag gccagcagca tctgtctga caaaaagcat gtctgtcctt agtttcagac 4665
ccttgtatga gggtagacct gacatgtcct cgggccctga acaatgtcac agcttccctg 4725
agtgtgttgt gtctattgca ttctcggta actgtagaat agtgggcaag cttgcccctc 4785
tgtgccctgt ctcagtgtgt gaagggcac tccgtggagg tgtggagcag gctgcgtcct 4845

gccctgggtg tgccttgctc tgcctccatct cagcattcct tgggtgtcac caccggggg 4905
tgtggggcat tgttgggctg tgggtctcagc atagctgtgg ctaccagtcc tagcagctag 4965
ccctcacat atcacagggt cctggccaatg agaagtatgg ggtgtcatgc ggcgtgtgta 5025
cctggctgtg caaaagtgtc aagtgtcat cttttaagag gccggtagt tgcattggctc 5085
tgtggggaaa ttggatacaa ctctgtcttg ccgggggtgtt gttgtacct gctcacagct 5145
gacctggga agatggcagc cactaacatg cagtgtgtcc tgaggcccag cctgcagttt 5205
tttgtgaata gctgaaagct tgtgtcagta acaaccagg gccttcacc ttcgttggtc 5265
agggagaaga aggtagcctg ggggtccctg gccgagcctc cttcacctct tggggataga 5325
cagagccagc ggaggccaca catgtaggcc gcgtgtgaga gggatgggtg agactgtgaa 5385
tgagtgtaac acactgagtg tgagctgggc tcacacagga gagcagagcc catgccagc 5445
attccaggaa gcaaagggt gtgagagggt ccgcattctc ttcctttcta aagtagcctg 5505
tgcacagatg gcgccatgtc cctaagacag cacaacagtc agacagcaca gccatgagct 5565
gaggagggtg tctgcttaca gccaccgtcc gcctccttc tttctctgtc cttttccgt 5625
ttattccaag gactgggcag cctccagcag ggcttcaga cccaccccca ccagatccct 5685
ttgaaatatg tggtcagcct catgagaacc tagctgtcag cccctgttg atagctagcc 5745
accttccat ccttcttag tcagccctg tcccaccagg agttgggacc tcatgccgtc 5805
tatcttgggc ctgacattaa ctgaacagta tacatagcag tcaccacgg cagacctggc 5865
aaccagtga cagcatccag caaagatgag gatgtctggg caccgcaagt aacggggctc 5925
taggtggacc actcctgccg gcccaagagg agaccagggg gagtgccagg gtcagcagca 5985
tgcccttgc tgccttccc cctgtgact gccatgcatt gcagggactt ttgtacctgg 6045
ccaaggcatt tccccgaca ggtgacaggg ttgtcagtc ctactctcc catacatccc 6105
tctgttggg agcatcagtg aatagagaag ggcttgaatg tgcttagggg actatTTTT 6165
tactttcaat ccagaagagc tagtgtgggc tcatgccat catgtctga gtgtgtgtga 6225
caaatgaggg tctgactctc gaatctctc agaccaagac tctatcttct atttgcacac 6285
ccatagcagc tgttttctc aagctcaaat gtgccacgg ggtctgatc aggtgagggt 6345
atcattggca agtgaccag ccgttgccag ctctcccacc ccggtgtgt ctgctagcca 6405
cgaggactgt ggcgtccagg agccatccc ccaacctgga cctatcctag cctgttgtct 6465
gcttgggcac cattactagg taggcaggca aggcagtac ccacacaaa gccagcccta 6525
cagctgagca tgcctcagca cccaagcagc gggatgatc caattcccta accgcaccac 6585

gtctggagtc tgtccigtga gctcacigtg gaaaggaggt tacaagccca ggctactgtg 6645
 ccactccata gtcagtggcg accagcgtgc acccctaatic cccttagtca ctttaagaaaa 6705
 ccttcaaagg caaataaatg acctaatigg aaaacacaaa agccggcctt cctcccaagg 6765
 attccctaag aatctgtggg cgctctgact gagtaggttg gggtcagtgc agacagctgc 6825
 agactgttct aagticcgtt cttatctctg atggcacacc tctcgtgttc agtictatta 6885
 cccaaaaaac aaagaccaa gaaggccaat ctctcatttg accgtatitt taatctgcct 6945
 gttttgacac atgccgtctg tagtaaccgc tcgctgtgag gcccacatct gacagtccaa 7005
 gtgatcgtga ccagtgatta gcgtcccggt ttctaattgct cttctaagaa actgagacag 7065
 tgtgaattat tgcicagcaa taatcatgtc accaggagtt agcagcacgc ctcatctcct 7125
 gatagcatta tgatgtttcg tgttttgitt accgtgtgtt acatgtaagg tttcatttgg 7185
 tatttatttg tgttttgagg tcttgcatg tttctgttct gctgctaata ataaagtitt 7245
 taagactgta gaatgcagaa ttttgtaatg ctcaagtgtc tattagagga aaataaagct 7305
 gattcaagaa aaaaaaaaaa aaaaaa 7331

<210> 98

<211> 567

<212> PRT

<213> Mus musculus

<400> 98

Met Glu Ser Ser Lys Lys Met Asp Ala Ala Gly Thr Leu Gln Pro Asn

1

5

10

15

Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val

20

25

30

Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp

35

40

45

Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln

50

55

60

Thr Glu Cys Gly His Arg Phe Trp Gln Ser Cys Met Ala Ala Leu Leu

65	70	75	80
Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys			
	85	90	95
Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu			
	100	105	110
Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr			
	115	120	125
Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu			
	130	135	140
Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp			
145	150	155	160
Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys			
	165	170	175
Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu			
	180	185	190
Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser			
	195	200	205
Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys			
	210	215	220
Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe			
225	230	235	240
Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val			
	245	250	255
Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys			
	260	265	270
Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln			
	275	280	285
Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln			
	290	295	300

Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
 305 310 315 320
 Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
 325 330 335
 Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
 340 345 350
 Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
 355 360 365
 Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
 370 375 380
 Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala Asp
 385 390 395 400
 Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
 405 410 415
 Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
 420 425 430
 Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
 435 440 445
 Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
 450 455 460
 Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
 465 470 475 480
 Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
 485 490 495
 Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
 500 505 510
 Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
 515 520 525
 Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn

530 535 540
 Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp .
 545 550 555 560
 Thr Ser Asp Leu Pro Asp Pro
 565

<210> 99

<211> 369

<212> DNA

<213> Mus musculus

<400> 99

cctaagtact gtttcccaaa ctatgtcgga cggccaaagc acatgcgngg ttatggctgg 60
 agccctggag ggggacctgt tcattggacc gaaagcagag gagcaccggg ggctgctgac 120
 catccgatac cccaatggaac acggtgtggt acgggattgg aatgacatgg aacgcatctg 180
 gcagtacgtc tactctaaagg accagctgca gaccttctct gaggagcatc ctgttcttct 240
 aacggaggcc ccactgaacc ccagtaagaa cggggacact ctcttccaat atcgtgctgt 300
 cagggggctc aacactcttc aaaggctttg gagacagggt actaagtga gtaaagaagc 360
 ttgccccga 369

<210> 100

<211> 456

<212> DNA

<213> Mus musculus

<400> 100

ccaatgtgct ggagatctgg aacctcgtgt tcatccagta taacaggag tcggatggig 60
 ttctgaaacc tcttccaag aaaagcatcg acacagggat gggcctagag aggctgggtg 120
 ctgtgctgca gaacaagatg tccaactacg acaccgacct tttcatgcct tacttcgaag 180

ccattcagaa gggcaccggc gcccnnggccc tatactggga aggttggigc tgaggatgca 240
gacggaatcg acatggccta cgggttctg gctgaccacg cccggaccat cactgtggcg 300
ctggctgatg gcggccggcc tgacaacaca ggacgggggt acgtgctgag acggatcctt 360
cgccgagctg ttcggtattc ccatgagaaa ctgaatgcca gcaggggttt cticgtaca 420
ttggttgatg ttgtcgttca atccctggga aacgct 456

<210> 101

<211> 478

<212> DNA

<213> *Mus musculus*

<400> 101

aattcggaac gaggaagcga tcctcgggct ggcgacgtag aagaagacgc ttcccagctt 60
atctttccca aagagtttga gacagcggag actctgctga actcggaagt ccacatgctt 120
ctggagcatc gaaagcagca gaacgagagc gcggaggacg agcaggagct gtcggaggtc 180
ttcatgaaaa ccctcaacta cacggcccgc ttcagccggt tcaaaaacag agagaccatt 240
gccagtgtgc gcacgttgc tctccagaaa aagttacata agtttgagtt ggccigtitta 300
gccaatcttt gcccgagac tgctgaagag tccaaagctc tgattccaag cctggaaggg 360
cgttttgaag atgaggagct gcagcagatt ctgatgaca tccagacgaa gcgcacgttc 420
cagtactgat ccgcagacgt cactctgctc cttaggttac agcaccacgg tctgaagc. 478

<210> 102

<211> 676

<212> DNA

<213> *Mus musculus*

<400> 102

cgttttctc tgaaatcatc tcttcaattt cggatgtgaa attcagccac agtgggaggt 60
atatcatgac cagagactat ctgaccgtga aagtctggga cctcaacatg gaaaatcgcc 120

ccattgagac ataccagggt catgactacc tccgcagcaa gttgtgctcc ctctatgaaa 180
 acgactgcat ttttgataaa tttagagtgtg tatggaatgg gtcagacagc gtcacatga 240
 caggctccta caataacttc ttcaggatgt tgcaccgaaa caccaagcgt gatgtgaccc 300
 ttgaggcctc aagggaatac agcaaaccac gggctatcct caaaccaccga aaagtgtgcg 360
 tcgggggcaa gcgaagaaaa gatgagatca gtgttgacag tctggacttt agcaaaaaga 420
 tcttgcatat agcttggcat ccttcagaaa acattatagc agttgaggct acgaataact 480
 tatatatatt ccaagacaag gttaactaga aggacgagct actacttagt ctcacatact 540
 gaatactagt cagaacaagt ttttagatgt tcgtttgggt cctcattttg atgcattgac 600
 ttccagttcc ctattcataa aacaatttga atagaccitt taaaggagtc aatgttccga 660
 ctccccaatc taagaa 676

<210> 103

<211> 2836

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (233).. (781)

<400> 103

ggccggcaac ggctgaggcg ggccggcgta gcgtgggttg ggctccaagc acacggccgc 60
 acctcagcct ccctggagcg ggaggccacg cggcggggct cctgaaaca agagaagcgg 120
 ggtccgggt gcccggggtg ggccgtcaag gcggtcagca ccggagcccg ccagcgggtg 180
 cccgcgcgag cctggggagc gcggccggcc ggccggccct gagggcggga ag atg ccg 238

Met Pro

1

cgc gtc gtc ccg gac cag agg agc aag ttc gag aac gag gag ttc ttc 286
 Arg Val Val Pro Asp Gln Arg Ser Lys Phe Glu Asn Glu Glu Phe Phe

5	10	15	
agg aag ctg agc cgc gag tgc gag att aag tac acg ggc ttc agg gac	334		
Arg Lys Leu Ser Arg Glu Cys Glu Ile Lys Tyr Thr Gly Phe Arg Asp			
20	25	30	
cgg ccc cac gag gag cgc cag aca cgc ttc cag aac gcc tgc cgc gac	382		
Arg Pro His Glu Glu Arg Gln Thr Arg Phe Gln Asn Ala Cys Arg Asp			
35	40	45	50
ggt cgc tcg gag atc gct ttt gtg gct aca gga acc aat ctg tct ctc	430		
Gly Arg Ser Glu Ile Ala Phe Val Ala Thr Gly Thr Asn Leu Ser Leu			
55	60	65	
cag ttt ttt ccg gcc agc tgg cag gga gaa cag cga caa aca cct agc	478		
Gln Phe Phe Pro Ala Ser Trp Gln Gly Glu Gln Arg Gln Thr Pro Ser			
70	75	80	
cgg gaa tat gtc gac tta gag aga gaa gca ggc aag gta tac ttg aag	526		
Arg Glu Tyr Val Asp Leu Glu Arg Glu Ala Gly Lys Val Tyr Leu Lys			
85	90	95	
gct ccc atg att ctg aat gga gtg tgt gtt ata tgg aag ggc tgg att	574		
Ala Pro Met Ile Leu Asn Gly Val Cys Val Ile Trp Lys Gly Trp Ile			
100	105	110	
gat ctc cac aga ttg gat ggt atg ggt tgc ctg gag ttt gat gag gag	622		
Asp Leu His Arg Leu Asp Gly Met Gly Cys Leu Glu Phe Asp Glu Glu			
115	120	125	130
cga gcc cag cag gaa gat gca tta gca caa cag gcc ttt gaa gag gct	670		
Arg Ala Gln Gln Glu Asp Ala Leu Ala Gln Gln Ala Phe Glu Glu Ala			
135	140	145	
cga aga aga act cga gaa ttt gag gat aga gac agg tct cac cgg gag	718		
Arg Arg Arg Thr Arg Glu Phe Glu Asp Arg Asp Arg Ser His Arg Glu			
150	155	160	
gaa atg gag gtg aga gtt tca cag ctg ctg gca gta act ggc aag aag	766		

Glu Met Glu Val Arg Val Ser Gln Leu Leu Ala Val Thr Gly Lys Lys

165

170

175

aca gca aga ccc tag tcctggttct aacttaggtg gcggtagatga tctcaaactt 821

Thr Ala Arg Pro

180

cgtaaagtgg agcacagctt atgtgcccc a tctctacaca cactgcttct agttgggtata 881
 aataactcat tgggcgacca gaaactgtga caactggagg gactgcagtt ggtttcatgg 941
 cctgaggcag tgaagacgtc acccactgcc atggttttgc actataatgc ctgcatttct 1001
 aattttttaa atatgtagcc agtaataatt tgaattttt ttctatgcaa gcttatcttg 1061
 ttggcattat tttagttgta tcgaaagtat atactttctt cattttaact taaaagctca 1121
 tgtcatttag aaacaagata agaaattaaa atttgtatca gggttgctta acattctttt 1181
 atactttcag acgagttggg tatacagctt tcctccttag ataagggttc ttggtttttg 1241
 ttgttttct ctacatcatt tcgtgttttt gtattctgca ccattttaca aatgaagatg 1301
 tgtttgcagt tattttttcc agctataaac ctagaataga gctgtctgcc acagcctcct 1361
 aaaacaaacg ttacagttg ttaaagccac agtatccttt caaatgciga tagtcaccct 1421
 atccccitta gacaaaaatt cacattagta ttaaattttg tctcagaccc tgtttcaagg 1481
 tatactttgt aatcatgagt ttgggtagag atgctcttca caggtgagaa tgctctacag 1541
 aaatgcccaa agaagccaca gactggcttc tgttttattc agggattttt tttttaatca 1601
 gtcagaaaaa ggatactgga acttgttgta tgtaacagca tattaaactg gaggcagtga 1661
 taaatcagct acacaggtaa atttgtgtta aataatgttt aagatagctg ctttcatgtg 1721
 tattttgtat ttgtattgc atgcitttgt agaaacaaaa ttgggtgatg aagatgagtc 1781
 ttagaaaatg ttcatctggg cagaagatgc atttctccca ttgattccgg gcaaacatt 1841
 cacagatata gatgatgga ttttacaaaa ggactattaa tagtgccitt tgagatgaat 1901
 caatgtaacg atatttttaa aacaggctta gtgtcaaatt gcaattttt aaatataaaa 1961
 ctggaaaaag tgctaagtca ttggcacatg cttacaatac ttccgtggg cgtattcatt 2021
 aaatgttact acatttctga atttttgcaa aaatgtatit tatcataaaa tggcattatt 2081
 ttagaaaatt ttaaaaactg acatgggtcaa ttcagaaaag tctgaataag gtcattgcat 2141
 ttaaaaagca tataaagata cttgattgtg gaagtgtgtc ttccattgta tataggcttt 2201
 ataattcata aacaagtacc ctgtatctca aaataaaaa atttgttata tatttgaagt 2261

cgtgcatgat aaggattgtg ttigaattat tataaacaat aatgtgttac agaagctgat 2321
 gctgaccttg tgttactgag cactatgaat gaatttgctt ggtatttggt gttgtacagc 2381
 tcacaigttt acactctcag tgccttgatg cctctcgga gttacctttt taaagtgatc 2441
 ctttcttttt taaaataaca tctcggtagt acattttctc tgttgcttct cgccaagagc 2501
 ttccagtcgc gcagtcagta agatcacatg gtgttaatgt ggccgtccct ctgtaaatag 2561
 caaatgttcc ttactgggtc tgcactgctt ctgtctgtct taatgctggc gttaagatca 2621
 taaactcctt ttcttcggta gtgcaggctt tgaaaattaa gttattgatg caatttcata 2681
 tttttcataa tctgtattta aaatgacatc attgcatcat tttttaaga ttcatctcca 2741
 ttaaaacttg ccttaagctt ccagattgct ttgccgtag cttactgta tatttgatg 2801
 ttttatttac ttccacatta aaattctgtg tactg 2836

<210> 104

<211> 182

<212> PRT

<213> Mus musculus

<400> 104

Met	Pro	Arg	Val	Val	Pro	Asp	Gln	Arg	Ser	Lys	Phe	Glu	Asn	Glu	Glu
1				5						10				15	
Phe	Phe	Arg	Lys	Leu	Ser	Arg	Glu	Cys	Glu	Ile	Lys	Tyr	Thr	Gly	Phe
				20						25				30	
Arg	Asp	Arg	Pro	His	Glu	Glu	Arg	Gln	Thr	Arg	Phe	Gln	Asn	Ala	Cys
				35						40				45	
Arg	Asp	Gly	Arg	Ser	Glu	Ile	Ala	Phe	Val	Ala	Thr	Gly	Thr	Asn	Leu
				50						55				60	
Ser	Leu	Gln	Phe	Phe	Pro	Ala	Ser	Trp	Gln	Gly	Glu	Gln	Arg	Gln	Thr
				65						70				75	
Pro	Ser	Arg	Glu	Tyr	Val	Asp	Leu	Glu	Arg	Glu	Ala	Gly	Lys	Val	Tyr
				85						90				95	

Leu Lys Ala Pro Met Ile Leu Asn Gly Val Cys Val Ile Trp Lys Gly

100

105

110

Trp Ile Asp Leu His Arg Leu Asp Gly Met Gly Cys Leu Glu Phe Asp

115

120

125

Glu Glu Arg Ala Gln Gln Glu Asp Ala Leu Ala Gln Gln Ala Phe Glu

130

135

140

Glu Ala Arg Arg Arg Thr Arg Glu Phe Glu Asp Arg Asp Arg Ser His

145

150

155

160

Arg Glu Glu Met Glu Val Arg Val Ser Gln Leu Leu Ala Val Thr Gly

165

170

175

Lys Lys Thr Ala Arg Pro

180

<210> 105

<211> 2768

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (94).. (1734)

<400> 105

gctgggtttcc tgtaattaag caggcctaag tgatttgtcc tgtgtgctgc tgggtactgt 60
gaaggaagct caggcaagtt ctgaaagtgc gac atg atg agg ata ttg tca ctt 114

Met Met Arg Ile Leu Ser Leu

1

5

ccc aca gag aac gca gtg acg tac tat gat gtc ctg gtg agc ttt act 162
Pro Thr Glu Asn Ala Val Thr Tyr Tyr Asp Val Leu Val Ser Phe Thr

10	15	20	
cag gaa gaa tgg gct ttg ctg gat cct tcc cag aag agt ctc tac aaa	210		
Gln Glu Glu Trp Ala Leu Leu Asp Pro Ser Gln Lys Ser Leu Tyr Lys			
25	30	35	
gat gtg atg ctc gaa acc tat agg aac ctc act gcc ata ggc tat aac	258		
Asp Val Met Leu Glu Thr Tyr Arg Asn Leu Thr Ala Ile Gly Tyr Asn			
40	45	50	55
tgg gaa gaa gat aat att gaa gaa gat tgt gaa aat tct gga aga ccc	306		
Trp Glu Glu Asp Asn Ile Glu Glu Asp Cys Glu Asn Ser Gly Arg Pro			
	60	65	70
act agg cat ctt caa agg gat gga cca agt aat act gga gag aaa ccc	354		
Thr Arg His Leu Gln Arg Asp Gly Pro Ser Asn Thr Gly Glu Lys Pro			
	75	80	85
ttt gaa tgt att caa tat gat gga gcc ttt gca aga aac cat cat cag	402		
Phe Glu Cys Ile Gln Tyr Asp Gly Ala Phe Ala Arg Asn His His Gln			
	90	95	100
tta cat aag gac act gga tct ttc atg tct tat act gat cgt caa ata	450		
Leu His Lys Asp Thr Gly Ser Phe Met Ser Tyr Thr Asp Arg Gln Ile			
	105	110	115
cat aga aga cca cac act gaa gaa aaa gtc tat gat ggt aac caa tgt	498		
His Arg Arg Pro His Thr Glu Glu Lys Val Tyr Asp Gly Asn Gln Cys			
	120	125	130
ggg aaa acc ttt tca tgt cac aac cat ttt gaa atc cgt aaa gga aca	546		
Gly Lys Thr Phe Ser Cys His Asn His Phe Glu Ile Arg Lys Gly Thr			
	140	145	150
tat act gga gaa aaa ccc tat gaa tgt aat caa tgt ggg aaa gcc ttt	594		
Tyr Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe			
	155	160	165
gca cgc aac agc aat ctt cta gac cat aaa aga ata cat act gga gag	642		

Ala Arg Asn Ser Asn Leu Leu Asp His Lys Arg Ile His Thr Gly Glu
 170 175 180
 aaa ccc tat aaa tgt aag caa tgt ggc aaa gac ttt acc cat cac agt 690
 Lys Pro Tyr Lys Cys Lys Gln Cys Gly Lys Asp Phe Thr His His Ser
 185 190 195
 act ctt cat atc cat aaa aga ata cat act aga gag aaa acc tat aaa 738
 Thr Leu His Ile His Lys Arg Ile His Thr Arg Glu Lys Thr Tyr Lys
 200 205 210 215
 tgt aac cag tgt atg acc att gct cat ctt caa tgt cat aaa ata aca 786
 Cys Asn Gln Cys Met Thr Ile Ala His Leu Gln Cys His Lys Ile Thr
 220 225 230
 cat act gga gag aaa ctc tgt gaa tat aac caa tgt tgg aaa gcc ttt 834
 His Thr Gly Glu Lys Leu Cys Glu Tyr Asn Gln Cys Trp Lys Ala Phe
 235 240 245
 gca tat cac aaa act ctt caa atc cat gaa aga aca cat act gga gaa 882
 Ala Tyr His Lys Thr Leu Gln Ile His Glu Arg Thr His Thr Gly Glu
 250 255 260
 aaa ctc tat caa tgt aac caa tgt gcc aaa gcc ttt cca tat cac aga 930
 Lys Leu Tyr Gln Cys Asn Gln Cys Ala Lys Ala Phe Pro Tyr His Arg
 265 270 275
 act ctt caa atc cat gaa aga aca cat act gga gag aaa cca tat gaa 978
 Thr Leu Gln Ile His Glu Arg Thr His Thr Gly Glu Lys Pro Tyr Glu
 280 285 290 295
 tgt aat caa tgt ggc aaa gcc ttt gca tgt ctt aga aat ctt caa aat 1026
 Cys Asn Gln Cys Gly Lys Ala Phe Ala Cys Leu Arg Asn Leu Gln Asn
 300 305 310
 cat aaa aca aca cat act gga gag aaa ccc tat gaa tgt aac cag tgt 1074
 His Lys Thr Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys
 315 320 325

ggc aga gcc ttt aga caa tat gtt tat ctt cag tgt cat gaa aga ata 1122
 Gly Arg Ala Phe Arg Gln Tyr Val Tyr Leu Gln Cys His Glu Arg Ile
 330 335 340
 cat act gga gag aaa ccc ttt gaa tgt aat caa tgt ggc aaa gcc ttt 1170
 His Thr Gly Glu Lys Pro Phe Glu Cys Asn Gln Cys Gly Lys Ala Phe
 345 350 355
 gca cat cac agc act ctt caa aga cat aaa aga aca cat act gga gag 1218
 Ala His His Ser Thr Leu Gln Arg His Lys Arg Thr His Thr Gly Glu
 360 365 370 375
 aaa ccc tat gaa tgt aat caa tgt ggc aaa gcc ttt gca tgt ccc aga 1266
 Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ala Cys Pro Arg
 380 385 390
 tac ctt caa atc cat aaa aga aca cat act gga gag aaa ccc tat gaa 1314
 Tyr Leu Gln Ile His Lys Arg Thr His Thr Gly Glu Lys Pro Tyr Glu
 395 400 405
 tgt aat caa tgt ggc aaa gcc ttt gct tgt tac caa tct ttt caa atc 1362
 Cys Asn Gln Cys Gly Lys Ala Phe Ala Cys Tyr Gln Ser Phe Gln Ile
 410 415 420
 cat aaa aga aca cat act gga gag aaa ccc tat gaa tgt aat caa tgt 1410
 His Lys Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys
 425 430 435
 gga aaa gcc ttt gca tgt aac aga tac ctt caa atc cat aaa aga aca 1458
 Gly Lys Ala Phe Ala Cys Asn Arg Tyr Leu Gln Ile His Lys Arg Thr
 440 445 450 455
 cat act gga gag aga cct tat gaa tgt aat cag tgt ggc aag gcc ttt 1506
 His Thr Gly Glu Arg Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe
 460 465 470
 aca tgt cgc agt aat ctt caa atc cat aaa aga aca cat act gga gag 1554
 Thr Cys Arg Ser Asn Leu Gln Ile His Lys Arg Thr His Thr Gly Glu

475 480 485
 aaa ccc tat gaa tgt aac cag tgt ggc aaa gcc ttt aca caa ttt ttt 1602
 Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Thr Gln Phe Phe
 490 495 500
 cct ctt aaa cgt cat gaa ata aca cat acc aaa gag aaa ccc tat gaa 1650
 Pro Leu Lys Arg His Glu Ile Thr His Thr Lys Glu Lys Pro Tyr Glu
 505 510 515
 tgt aac cag tgt ggc aaa gcc ttt aca cgc cac agt act ctt caa atc 1698
 Cys Asn Gln Cys Gly Lys Ala Phe Thr Arg His Ser Thr Leu Gln Ile
 520 525 530 535
 cat aaa aga aca cat act gga gaa aaa ccc gta tga atgtaatcaa 1744
 His Lys Arg Thr His Thr Gly Glu Lys Pro Val
 540 545
 tgtgcaaagc ctttgcaggt cacagtactc ttcaaaatca taaaagaata catactggag 1804
 agaagcccta tgaatttaac cagtgtagca aagcttttac acaatttgtt catcttcagt 1864
 gtcatcaaag gttacatact ggagagaaac cctatgaatg taaataatgt gtcaaagcct 1924
 ttacatgtca cagtactctt caaatccgta aaagaacacg tactggagaa aaaccctgtg 1984
 tatgtaaaca atgtggcaaa gccittgcat gtcacagtac tccatgaatt cataaaagaa 2044
 cacatactgg agagataccc tatgaatgta accagtgtgg caaagccttt acacaatttt 2104
 ttctctttaa acgtcatgaa ataacacata ccaaagagaa accctatgaa tgtaaacaat 2164
 gtggcaaagc ctttacacgc cacagtactc ttcaaatcca taaaagaaca catactggag 2224
 aaaaaccgt atgaatgtaa tcaatgtggc aaagcctttg caggtcacag tactcttcaa 2284
 aatcataaaa gaatacatac tggagagaaa ccctatgaat ttaaccagtg tagcaaagct 2344
 ttacacaat ttgttcatct tcagtgtcat caaagggtac atactggaga gaaaccctat 2404
 gaatgtaaat aatgtgtcaa agcctttaca tgtcacagta ctcttcaa at ccgtaaaaga 2464
 acacgtactg gagaaaaacc ctgtgtatgt aaacaatgtg gcaaagcctt tgcattgtac 2524
 agtactccat gaaticataa aagaacacat actggagaga taccctatga atgtaaccag 2584
 tgtggtaaaa cctttgcacg acacagtcag ctccaacac ataaaagaat acatattgaa 2644
 gaaaaaccg gataatgcag tgaatgtgat aaaggctttg ttattgtagt ctgaaaagga 2704

attttaaaaa caaatctctg tgaaaaccct ataaatgtaa tcaatctaataaagccattt 2764
gtta 2768

<210> 106

<211> 546

<212> PRT

<213> Mus musculus

<400> 106

Met	Met	Arg	Ile	Leu	Ser	Leu	Pro	Thr	Glu	Asn	Ala	Val	Thr	Tyr	Tyr
1				5					10					15	
Asp	Val	Leu	Val	Ser	Phe	Thr	Gln	Glu	Glu	Trp	Ala	Leu	Leu	Asp	Pro
			20					25						30	
Ser	Gln	Lys	Ser	Leu	Tyr	Lys	Asp	Val	Met	Leu	Glu	Thr	Tyr	Arg	Asn
		35					40						45		
Leu	Thr	Ala	Ile	Gly	Tyr	Asn	Trp	Glu	Glu	Asp	Asn	Ile	Glu	Glu	Asp
	50					55					60				
Cys	Glu	Asn	Ser	Gly	Arg	Pro	Thr	Arg	His	Leu	Gln	Arg	Asp	Gly	Pro
65					70					75				80	
Ser	Asn	Thr	Gly	Glu	Lys	Pro	Phe	Glu	Cys	Ile	Gln	Tyr	Asp	Gly	Ala
				85					90					95	
Phe	Ala	Arg	Asn	His	His	Gln	Leu	His	Lys	Asp	Thr	Gly	Ser	Phe	Met
			100						105					110	
Ser	Tyr	Thr	Asp	Arg	Gln	Ile	His	Arg	Arg	Pro	His	Thr	Glu	Glu	Lys
			115						120					125	
Val	Tyr	Asp	Gly	Asn	Gln	Cys	Gly	Lys	Thr	Phe	Ser	Cys	His	Asn	His
		130					135							140	
Phe	Glu	Ile	Arg	Lys	Gly	Thr	Tyr	Thr	Gly	Glu	Lys	Pro	Tyr	Glu	Cys
145					150					155				160	

Asn Gln Cys Gly Lys Ala Phe Ala Arg Asn Ser Asn Leu Leu Asp His
 165 170 175
 Lys Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Gln Cys Gly
 180 185 190
 Lys Asp Phe Thr His His Ser Thr Leu His Ile His Lys Arg Ile His
 195 200 205
 Thr Arg Glu Lys Thr Tyr Lys Cys Asn Gln Cys Met Thr Ile Ala His
 210 215 220
 Leu Gln Cys His Lys Ile Thr His Thr Gly Glu Lys Leu Cys Glu Tyr
 225 230 235 240
 Asn Gln Cys Trp Lys Ala Phe Ala Tyr His Lys Thr Leu Gln Ile His
 245 250 255
 Glu Arg Thr His Thr Gly Glu Lys Leu Tyr Gln Cys Asn Gln Cys Ala
 260 265 270
 Lys Ala Phe Pro Tyr His Arg Thr Leu Gln Ile His Glu Arg Thr His
 275 280 285
 Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ala
 290 295 300
 Cys Leu Arg Asn Leu Gln Asn His Lys Thr Thr His Thr Gly Glu Lys
 305 310 315 320
 Pro Tyr Glu Cys Asn Gln Cys Gly Arg Ala Phe Arg Gln Tyr Val Tyr
 325 330 335
 Leu Gln Cys His Glu Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys
 340 345 350
 Asn Gln Cys Gly Lys Ala Phe Ala His His Ser Thr Leu Gln Arg His
 355 360 365
 Lys Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly
 370 375 380
 Lys Ala Phe Ala Cys Pro Arg Tyr Leu Gln Ile His Lys Arg Thr His

385 390 395 400
 Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ala
 405 410 415
 Cys Tyr Gln Ser Phe Gln Ile His Lys Arg Thr His Thr Gly Glu Lys
 420 425 430
 Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Ala Cys Asn Arg Tyr
 435 440 445
 Leu Gln Ile His Lys Arg Thr His Thr Gly Glu Arg Pro Tyr Glu Cys
 450 455 460
 Asn Gln Cys Gly Lys Ala Phe Thr Cys Arg Ser Asn Leu Gln Ile His
 465 470 475 480
 Lys Arg Thr His Thr Gly Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly
 485 490 495
 Lys Ala Phe Thr Gln Phe Phe Pro Leu Lys Arg His Glu Ile Thr His
 500 505 510
 Thr Lys Glu Lys Pro Tyr Glu Cys Asn Gln Cys Gly Lys Ala Phe Thr
 515 520 525
 Arg His Ser Thr Leu Gln Ile His Lys Arg Thr His Thr Gly Glu Lys
 530 535 540
 Pro Val
 545

<210> 107

<211> 384

<212> DNA

<213> Mus musculus

<400> 107

ttcggcacag gctgttcccc gaagttcagc ctcaagacgg tgctgttgct ggccgaccag 60

atgatcagcc gcacgagta catacactcc aagaacttca tccaccggga tgtgaagccc 120
 gacaacttcc tcatgggcct gggaagaaa ggcaacctgg tgiacatcat tgacttcggc 180
 ctggccaaga agtaccgga tgcccgaca caccagcata ttccctaccg ggaaaacaag 240
 aacctgaccg gcactgccc ctatgcctct atcaacaccc acctgggcat tgagcaaagc 300
 cgtcgagatg acctagagag ctggggctat gtgctcatgt acttcaacct gggctccctg 360
 cccitggcagg cctcgaag cagc 384

<210> 108

<211> 2543

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (248).. (1255)

<400> 108

ccagcacatc ccggtgcttc ttctcaggcg cagcagcttt cctctgcggc agccgcacct 60
 cgccaaacgg cgtagtgtg caggctcgcc cgagttgtg ctgtctgcct ctgtgcccgc 120
 tgccgcgggc cgccctgcgc ggaccgtagg ctgcgcagac gccacctcg atcctgtatc 180
 gctgcgggcg cctcggcgcg cctgtgatc cgcaatcctg cggcgggchg catgggataa 240
 tgcggcc atg gtg cgc cga gat cgc ttg cgc agg atg aga gag tgg tgg 289
 Met Val Arg Arg Asp Arg Leu Arg Arg Met Arg Glu Trp Trp
 1 5 10
 gtc caa gla ggg ctc ctg gct gtg ccc ttg ctg gct gcg tac ctg cac 337
 Val Gln Val Gly Leu Leu Ala Val Pro Leu Leu Ala Ala Tyr Leu His
 15 20 25 30
 atc ccg ccc cct cag ctc tcc cct gct ctg cac tca tgg aag act tct 385
 Ile Pro Pro Pro Gln Leu Ser Pro Ala Leu His Ser Trp Lys Thr Ser

35	40	45	
ggc aag ttt ttc acc tac aaa ggc cta cgc atc ttc tac caa gat tct			433
Gly Lys Phe Phe Thr Tyr Lys Gly Leu Arg Ile Phe Tyr Gln Asp Ser			
50	55	60	
gtc ggt gtg gtc gga agc cct gag ata gtt gtg ctt tta cat ggc ttt			481
Val Gly Val Val Gly Ser Pro Glu Ile Val Val Leu Leu His Gly Phe			
65	70	75	
cca aca tcc agc tat gac tgg tac aag atc tgg gaa ggg ctg acc ctg			529
Pro Thr Ser Ser Tyr Asp Trp Tyr Lys Ile Trp Glu Gly Leu Thr Leu			
80	85	90	
agg ttc cat cga gtg atc gcc ctt gat ttc tta ggc ttt ggc ttc agt			577
Arg Phe His Arg Val Ile Ala Leu Asp Phe Leu Gly Phe Gly Phe Ser			
95	100	105	110
gac aag ccg aga cca cat cag tac tcc ata ttt gag cag gcc agc atc			625
Asp Lys Pro Arg Pro His Gln Tyr Ser Ile Phe Glu Gln Ala Ser Ile			
115	120	125	
gta gag tcc ctt ctg cgg cac ctg ggg ctc cag aac cgc aga atc aac			673
Val Glu Ser Leu Leu Arg His Leu Gly Leu Gln Asn Arg Arg Ile Asn			
130	135	140	
ctg ctg tct cac gat tat gga gat atc gtt gct cag gaa ctg ctg tac			721
Leu Leu Ser His Asp Tyr Gly Asp Ile Val Ala Gln Glu Leu Leu Tyr			
145	150	155	
agg tac aag cag aat cga tct ggc cgg ctc acc ata aag agt ctc tgt			769
Arg Tyr Lys Gln Asn Arg Ser Gly Arg Leu Thr Ile Lys Ser Leu Cys			
160	165	170	
ctg tcg aat gga ggt atc ttt cct gag acg cat cgt cct ctc ctt ctc			817
Leu Ser Asn Gly Gly Ile Phe Pro Glu Thr His Arg Pro Leu Leu Leu			
175	180	185	190
caa aag ctc ctc aaa gac gga ggt gtg ctt tcc ccc atc ctc acc agg			865

Gln Lys Leu Leu Lys Asp Gly Gly Val Leu Ser Pro Ile Leu Thr Arg
 195 200 205
 ctc atg aat ttc ttc gtg ttc tct cga ggt ctc act cca gtc ttt gga 913
 Leu Met Asn Phe Phe Val Phe Ser Arg Gly Leu Thr Pro Val Phe Gly
 210 215 220
 ccg tat act cga ccc act gag agt gag ctg tgg gac atg tgg gct gtg 961
 Pro Tyr Thr Arg Pro Thr Glu Ser Glu Leu Trp Asp Met Trp Ala Val
 225 230 235
 att cgc aac aat gac ggc aac ctg gtc atc gac agt ctt tta cag tac 1009
 Ile Arg Asn Asn Asp Gly Asn Leu Val Ile Asp Ser Leu Leu Gln Tyr
 240 245 250
 att aat caa agg aag aaa ttc aga aga cgc tgg gtg gga gcg ctt gct 1057
 Ile Asn Gln Arg Lys Lys Phe Arg Arg Arg Trp Val Gly Ala Leu Ala
 255 260 265 270
 tct gtg tcc atc ccc att cat ttt atc tat ggg cca ttg gat cct ata 1105
 Ser Val Ser Ile Pro Ile His Phe Ile Tyr Gly Pro Leu Asp Pro Ile
 275 280 285
 aat ccg tat cca gag ttt ttg gag ctg tac agg aaa acg ctg ccg cgg 1153
 Asn Pro Tyr Pro Glu Phe Leu Glu Leu Tyr Arg Lys Thr Leu Pro Arg
 290 295 300
 tcc aca gtg tcg att ctg gat gac cac att agc cac tac cca cag cta 1201
 Ser Thr Val Ser Ile Leu Asp Asp His Ile Ser His Tyr Pro Gln Leu
 305 310 315
 gag gat ccc atg ggc ttc ttg aat gca tat atg ggc ttc atc aac tcc 1249
 Glu Asp Pro Met Gly Phe Leu Asn Ala Tyr Met Gly Phe Ile Asn Ser
 320 325 330
 ttc tga gctggaaaga gtagcctccc tgtattacct ccccatctct cgtatctgtg 1305
 Phe
 335

tgtattccac ttagaaatgc ccaaaagagg tcctggccat caaatactat cctttcatca 1365
 aagtcatttt ccttcacatt ggigaacaaa ctacaggaat caggcagctg gaactctata 1425
 gggtgacaca atagtcacc tcattctctaa gggtgacatg ataatcctct catttctgtg 1485
 acatctgacc aaataaatag agctgctgtt gttttgtgtt attaggacat tctgactaat 1545
 aacacttttc atttatgtag aaaaacagca ttagatattc ttttttggtg ttaaataacct 1605
 caaaaaaccc ccaaaacata ataacaacaa aaaccagtt tctgtggact ttattaaaat 1665
 atttagaagt gctcccttcc ggcccaatcc taactggaat acagagtgag ggaggagctt 1725
 gctatctccc tttcaggatc tgttacagtt tatgagaggg atcatcttgt cactccttta 1785
 catttagttt catcggtgc ttctaacaga catttttgtt aaaacagaca ttggcttagg 1845
 gggctgggga agtagctcag tggtagtgtg cctgcctagc atgttaaagc ccttgggttc 1905
 agttcccagc actctcccca ccccagccca tgaacctaa atagacattg gcgtaaatac 1965
 agtgttctga gtatgagtct aagactgatt tgcatactca tgtatatatt tacaacagt 2025
 tggcccttgc taagaagaaa acctcattat atatagaatt tgtgaataaa caggttgaaa 2085
 ttatttgcag aatttcctaa aactgccagg cattagaac tgcattctgt ccagagattt 2145
 actgttactg ttagaaaagt ccaagctgaa tagtaaataa cagcctaggg gcagctcctc 2205
 cagggctgac gtggagggga agggacatgt aagtgcggaa tgaatgtcca ttggctcctc 2265
 tatgatggcc gctcagcatc ccgctggctg ttcagaaagg ctttctcata taactcctgt 2325
 acttaaacag gcaagtttcc agagacatta agaacaaatt ctgaaagacc taagagcaaa 2385
 tggctgtgaa tactttttta agccacagtt ttaacttagt taaagcagca ttattgatta 2445
 ttttaaatte gtttttttaa ttagaaattt caaglatagc aactttgaaa ctggaatgaa 2505
 tgagtgttta ttttctatta ataaaaacaa actgtgac 2543

<210> 109

<211> 335

<212> PRT

<213> Mus musculus

<400> 109

Met Val Arg Arg Asp Arg Leu Arg Arg Met Arg Glu Trp Trp Val Gln

1	5	10	15
Val Gly Leu Leu Ala Val Pro Leu Leu Ala Ala Tyr Leu His Ile Pro			
20	25	30	
Pro Pro Gln Leu Ser Pro Ala Leu His Ser Trp Lys Thr Ser Gly Lys			
35	40	45	
Phe Phe Thr Tyr Lys Gly Leu Arg Ile Phe Tyr Gln Asp Ser Val Gly			
50	55	60	
Val Val Gly Ser Pro Glu Ile Val Val Leu Leu His Gly Phe Pro Thr			
65	70	75	80
Ser Ser Tyr Asp Trp Tyr Lys Ile Trp Glu Gly Leu Thr Leu Arg Phe			
85	90	95	
His Arg Val Ile Ala Leu Asp Phe Leu Gly Phe Gly Phe Ser Asp Lys			
100	105	110	
Pro Arg Pro His Gln Tyr Ser Ile Phe Glu Gln Ala Ser Ile Val Glu			
115	120	125	
Ser Leu Leu Arg His Leu Gly Leu Gln Asn Arg Arg Ile Asn Leu Leu			
130	135	140	
Ser His Asp Tyr Gly Asp Ile Val Ala Gln Glu Leu Leu Tyr Arg Tyr			
145	150	155	160
Lys Gln Asn Arg Ser Gly Arg Leu Thr Ile Lys Ser Leu Cys Leu Ser			
165	170	175	
Asn Gly Gly Ile Phe Pro Glu Thr His Arg Pro Leu Leu Leu Gln Lys			
180	185	190	
Leu Leu Lys Asp Gly Gly Val Leu Ser Pro Ile Leu Thr Arg Leu Met			
195	200	205	
Asn Phe Phe Val Phe Ser Arg Gly Leu Thr Pro Val Phe Gly Pro Tyr			
210	215	220	
Thr Arg Pro Thr Glu Ser Glu Leu Trp Asp Met Trp Ala Val Ile Arg			
225	230	235	240

Asn Asn Asp Gly Asn Leu Val Ile Asp Ser Leu Leu Gln Tyr Ile Asn

245

250

255

Gln Arg Lys Lys Phe Arg Arg Arg Trp Val Gly Ala Leu Ala Ser Val

260

265

270

Ser Ile Pro Ile His Phe Ile Tyr Gly Pro Leu Asp Pro Ile Asn Pro

275

280

285

Tyr Pro Glu Phe Leu Glu Leu Tyr Arg Lys Thr Leu Pro Arg Ser Thr

290

295

300

Val Ser Ile Leu Asp Asp His Ile Ser His Tyr Pro Gln Leu Glu Asp

305

310

315

320

Pro Met Gly Phe Leu Asn Ala Tyr Met Gly Phe Ile Asn Ser Phe

325

330

335

<210> 110

<211> 608

<212> DNA

<213> Mus musculus

<400> 110

attcgatcc tgcgggcctt gagggaggag aggaaattga atcctatctc atcctctagt 60
 ttattttacat cattggatta tattcctgtt tggaaactta actggctctc atggcgtttt 120
 cgggcacagg gacactgggtg gcttccattg tctccaagat gacatcttca gcagccatgg 180
 tcaaagctgg aggggcagtc tctggcacca ttctagctgg ttcgaagggg ctcatcctgt 240
 taacacagag tgccctgggc tctgcaacat ctgcacttgg agcactgaag gttggcacca 300
 ttttatctgg gtctcttgcc tccaccttgg ctgcttcccc cattggagcc aaggctgttg 360
 tggctgtgct tgggggagcc atgacagtag ctgctgtacc acctgcgctg agtgcctgtg 420
 gcttcaccgc ctgaggaatt gcagcctcct ctctagcagc taagatgatg tccttgtcag 480
 ctattgctaa tgggggtgga gtcccagctg gtggcctggg ggcatttctg aagctctgtg 540
 gagctgctgg actctccgtg caatctactg tcatccgtgg ctctcagggg tctgccgttg 600

tgccagtg

608

<210> 111

<211> 1361

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (27).. (476)

<400> 111

tccgttcttc cttcttcgct cgcacc atg gct gat cag ctg act gaa gag cag 53

Met Ala Asp Gln Leu Thr Glu Glu Gln

1

5

att gct gaa ttc aag gaa gct ttc tcc cta ttc gat aag gat ggt gac 101

Ile Ala Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp

10

15

20

25

ggc acc atc aca acc aag gaa ctg ggg acc gtc atg cgg tca ctg ggt 149

Gly Thr Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly

30

35

40

cag aac cca aca gaa gcc gag ctg cag gat atg atc aac gaa gtg gat 197

Gln Asn Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp

45

50

55

gct gat ggc aat ggc acc att gac ttc cca gag ttc ttg act atg atg 245

Ala Asp Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe Leu Thr Met Met

60

65

70

gct aga aaa atg aaa gac aca gat agc gaa gaa gag atc cgc gag gcc 293

Ala Arg Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala

75	80	85	
ttc cga gtg ttt gac aag gat ggg aat ggt tac atc agt gcg gca gaa	341		
Phe Arg Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu			
90	95	100	105
ctg cgc cac gtc atg aca aac tta gga gaa aag cta aca gat gaa gaa	389		
Leu Arg His Val Met Thr Asn Leu Gly Glu Lys Leu Thr Asp Glu Glu			
110	115	120	
gta gat gaa atg atc aga gaa gca gat att gat ggc gac gga caa gtc	437		
Val Asp Glu Met Ile Arg Glu Ala Asp Ile Asp Gly Asp Gly Gln Val			
125	130	135	
aac tat gaa gaa ttc gta cag atg atg act gca aaa tga agacctactt	486		
Asn Tyr Glu Glu Phe Val Gln Met Met Thr Ala Lys			
140	145	150	
tcaactactt tttccctctt agaagaatca aattgaaatc ttttacttac ctcttagaaa	546		
aaaaagaaaa aaaaagaaaa gttcatttct tcatctgtt tgtatctagc gaagctgatg	606		
tcagaagccc ctctgtccac acacaaagtc tgcatgtatt ggtcgggtgtt cctgccccta	666		
aagtcaagcc cctacatcag ttttacagta taaatactcg tactaccita taaggaagca	726		
cttagtggac tccttaaagt tccatttgc t aatgattaat acactgtttg ggctggccag	786		
tttctcatgc atgcagcttg atgattgagc acagtcaggc attgtattaa aactgaaaaa	846		
tggaaaaaac aaattcaaaa tctcagatgg ctcttagttc aatctgttca gataaattgt	906		
cagcagccag tttactgcaa gcaaacattt aaaattgggt tacctcagga tgattgatgt	966		
gcagagatgg gaaggcaaac tctgagacac agccccagaa gtaggacagt cctcatcaag	1026		
tgccccagtc ccatgggtgac agtgactccc tgggtggcgag cccgagtgtg atggttcatt	1086		
gctgtgcgca ttgcattgga gtgactgaac aacaaggctg tcaccaaate ccacacattt	1146		
tattaagaaa tgtttcctaa gggagcattt ttggactgtg ttttaaaacc tagtgaacca	1206		
tgactcggag ccagagagta ggctgtgtct gtggacttga gcacaccate aacattgctg	1266		
ttcaggaaat gatattttacg tccattccaa gttgtaaatg ctagtctttt attttttttt	1326		
tttccaataa aaagaccatt aacttaaaaa aaaaa	1361		

<210> 112

<211> 149

<212> PRT

<213> Mus musculus

<400> 112

Met Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala

1

5

10

15

Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu

20

25

30

Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu

35

40

45

Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile

50

55

60

Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr

65

70

75

80

Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp

85

90

95

Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn

100

105

110

Leu Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu

115

120

125

Ala Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln

130

135

140

Met Met Thr Ala Lys

145

<210> 113

<211> 3733

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (310).. (3249)

<400> 113

ccccttctct cctccatttt ctcccttccc ctctctcccc tcttgcccg ccccttgctt 60
 ttccacctgt ccttctcccc cgctgctggg gagacaccgt ttggattag ttgggggcca 120
 ccgccggcgg cgggggaggg ggcccagtgg actgccctct ccccgggccc cagcctcacc 180
 agcaccacgc atcgagcac ctcttggttg tcttctctcg ggctcagagg gagcccagcc 240
 ctccgtccca ccaggatccg tggcgagtgg gggccgcggc agctgcgtcc ccatgaggag 300
 gggaggaag atg ccg gct gag ctg ctg ctg ctg ata gtc gcc ttc gcc 351

Met Pro Ala Glu Leu Leu Leu Leu Leu Ile Val Ala Phe Ala

1

5

10

aat ccc agc tgc cag gtg ctg tca tca ctg cgc atg gct gca atc ctg 399

Asn Pro Ser Cys Gln Val Leu Ser Ser Leu Arg Met Ala Ala Ile Leu

15

20

25

30

gac gac cag acc gtg tgt ggc cgt ggt gag cgt ctg gcc ctg gcc ctg 447

Asp Asp Gln Thr Val Cys Gly Arg Gly Glu Arg Leu Ala Leu Ala Leu

35

40

45

gcc cga gag cag atc aat ggg atc atc gag gtc cca gcc aag gcc aga 495

Ala Arg Glu Gln Ile Asn Gly Ile Ile Glu Val Pro Ala Lys Ala Arg

50

55

60

gtg gaa gta gac atc ttt gag ctg cag cgg gac agc cag tac gag acc 543

Val Glu Val Asp Ile Phe Glu Leu Gln Arg Asp Ser Gln Tyr Glu Thr

65

70

75

acg gac acc atg tgt cag atc ctg ccc aag ggg gtt gta tct gtc ttg 591

Thr Asp Thr Met Cys Gln Ile Leu Pro Lys Gly Val Val Ser Val Leu
 80 85 90
 gga ccc tcc tcc agc cca gct tct gcc tcc acc gtg agc cat atc tgt 639
 Gly Pro Ser Ser Ser Pro Ala Ser Ala Ser Thr Val Ser His Ile Cys
 95 100 105 110
 ggg gag aag gag att ccc cac atc aag gtg ggt cct gag gag acg ccc 687
 Gly Glu Lys Glu Ile Pro His Ile Lys Val Gly Pro Glu Glu Thr Pro
 115 120 125
 cgc ctt cag tac ctt cgc ttc gca tct gtc agc ctg tac ccc agt aat 735
 Arg Leu Gln Tyr Leu Arg Phe Ala Ser Val Ser Leu Tyr Pro Ser Asn
 130 135 140
 gaa gat gtc agc ctg gca gtc tcc cga atc ctc aag tcc ttt aac tac 783
 Glu Asp Val Ser Leu Ala Val Ser Arg Ile Leu Lys Ser Phe Asn Tyr
 145 150 155
 ccc tca gct agc ctc atc tgc gcc aag gct gag tgc ctg ctg cgg cta 831
 Pro Ser Ala Ser Leu Ile Cys Ala Lys Ala Glu Cys Leu Leu Arg Leu
 160 165 170
 gaa gaa ctg gtg cga ggc ttc ctc atc tcc aag gag aca ctg tcc gtg 879
 Glu Glu Leu Val Arg Gly Phe Leu Ile Ser Lys Glu Thr Leu Ser Val
 175 180 185 190
 agg atg ctt gat gac agc cgg gac ccc acg ccg cta ctc aag gag atc 927
 Arg Met Leu Asp Asp Ser Arg Asp Pro Thr Pro Leu Leu Lys Glu Ile
 195 200 205
 cga gat gac aaa gtg tcc acc atc atc att gat gcc aat gcg tcc atc 975
 Arg Asp Asp Lys Val Ser Thr Ile Ile Ile Asp Ala Asn Ala Ser Ile
 210 215 220
 tcc cac ctt gtc ctc cgt aag gct tgc gag ctg gga atg acc tca gcg 1023
 Ser His Leu Val Leu Arg Lys Ala Ser Glu Leu Gly Met Thr Ser Ala
 225 230 235

ttt tac aag tac atc ctc acc acc atg gac ttt ccc atc ctg cat ctg 1071
 Phe Tyr Lys Tyr Ile Leu Thr Thr Met Asp Phe Pro Ile Leu His Leu
 240 245 250
 gat ggt atc gtg gag gac tcc tcc aac atc ctg ggc ttt tcc atg ttc 1119
 Asp Gly Ile Val Glu Asp Ser Ser Asn Ile Leu Gly Phe Ser Met Phe
 255 260 265 270
 aac acc tcc cac ccc ttc tac cca gag ttt gtg cgc agc ctc aac atg 1167
 Asn Thr Ser His Pro Phe Tyr Pro Glu Phe Val Arg Ser Leu Asn Met
 275 280 285
 tcc tgg agg gag aac tgt gaa gcc agc acc tat cct ggc cct gcg ctg 1215
 Ser Trp Arg Glu Asn Cys Glu Ala Ser Thr Tyr Pro Gly Pro Ala Leu
 290 295 300
 tcc gca gcc ctg atg ttt gac gct gtg cac gtg gtg gta agc gct gtc 1263
 Ser Ala Ala Leu Met Phe Asp Ala Val His Val Val Val Ser Ala Val
 305 310 315
 cga gaa ctg aac cga agc cag gag att ggc gtc aag cca ctg gcc tgc 1311
 Arg Glu Leu Asn Arg Ser Gln Glu Ile Gly Val Lys Pro Leu Ala Cys
 320 325 330
 act tcg gcc aac att tgg ccc cat ggg acc agc ctt atg aac tac ctt 1359
 Thr Ser Ala Asn Ile Trp Pro His Gly Thr Ser Leu Met Asn Tyr Leu
 335 340 345 350
 cga atg gta gag tat gac ggg ctg acc ggg cgg gtt gag ttc aac agc 1407
 Arg Met Val Glu Tyr Asp Gly Leu Thr Gly Arg Val Glu Phe Asn Ser
 355 360 365
 aaa ggg cag agg acc aac tac aca cta cgc atc ctg gag aag tcc cgc 1455
 Lys Gly Gln Arg Thr Asn Tyr Thr Leu Arg Ile Leu Glu Lys Ser Arg
 370 375 380
 cag ggc cac cgt gag ata ggg gtg tgg tac tct aac cgg acc ctg gcc 1503
 Gln Gly His Arg Glu Ile Gly Val Trp Tyr Ser Asn Arg Thr Leu Ala

385	390	395	
atg aat gcc acc acc ctg gac atc aac ctg tca cag act cta gcc aac	1551		
Met Asn Ala Thr Thr Leu Asp Ile Asn Leu Ser Gln Thr Leu Ala Asn			
400	405	410	
aag act ctg gtg gtc aca act atc ctg gag aac ccg tat gtt atg cgc	1599		
Lys Thr Leu Val Val Thr Thr Ile Leu Glu Asn Pro Tyr Val Met Arg			
415	420	425	430
cgg ccc aac ttc cag gcc ttg tca ggg aat gag cgc ttc gag ggc ttc	1647		
Arg Pro Asn Phe Gln Ala Leu Ser Gly Asn Glu Arg Phe Glu Gly Phe			
435	440	445	
tgc gtg gac atg ctc agg gag ctg gcc gag ctg ctg cgc ttc cga tac	1695		
Cys Val Asp Met Leu Arg Glu Leu Ala Glu Leu Leu Arg Phe Arg Tyr			
450	455	460	
cgc ctg cgg ttg gta gag gac gga ctc tac ggg gca cct gag ccc aac	1743		
Arg Leu Arg Leu Val Glu Asp Gly Leu Tyr Gly Ala Pro Glu Pro Asn			
465	470	475	
ggt tcc tgg aca ggc atg gtt gga gaa ctc atc aac cgg aag gca gac	1791		
Gly Ser Trp Thr Gly Met Val Gly Glu Leu Ile Asn Arg Lys Ala Asp			
480	485	490	
ctg gct gtg gca gcc ttc acc atc acc gcc gag agg gag aag gtc atc	1839		
Leu Ala Val Ala Ala Phe Thr Ile Thr Ala Glu Arg Glu Lys Val Ile			
495	500	505	510
gac ttc tcc aag ccc ttc atg acc ctg ggg atc agc atc ctc tac agg	1887		
Asp Phe Ser Lys Pro Phe Met Thr Leu Gly Ile Ser Ile Leu Tyr Arg			
515	520	525	
gtg cac atg ggc cgc aag cct ggc tac ttc tcc ttc ctg gac ccc ttc	1935		
Val His Met Gly Arg Lys Pro Gly Tyr Phe Ser Phe Leu Asp Pro Phe			
530	535	540	
tcc cct gcc gtg tgg ctc ttc atg ctt ctt gcc tac ctg gct gtc agc	1983		

Ser Pro Ala Val Trp Leu Phe Met Leu Leu Ala Tyr Leu Ala Val Ser
 545 550 555
 tgt gtc ttg ttc ctg gct gcc agg ctg agc cct tat gag tgg tac aac 2031
 Cys Val Leu Phe Leu Ala Ala Arg Leu Ser Pro Tyr Glu Trp Tyr Asn
 560 565 570
 cca cac ccg tgt ctc cgg gcg cgt ccc cat atc ctg gag aac cag tac 2079
 Pro His Pro Cys Leu Arg Ala Arg Pro His Ile Leu Glu Asn Gln Tyr
 575 580 585 590
 acg ctg ggc aac agc ctc tgg ttc ccc gtg ggt ggc ttc atg cag cag 2127
 Thr Leu Gly Asn Ser Leu Trp Phe Pro Val Gly Gly Phe Met Gln Gln
 595 600 605
 ggc tcg gag gtc atg ccg cgg gca ctg tcc aca cgc tgt gtc agc gga 2175
 Gly Ser Glu Val Met Pro Arg Ala Leu Ser Thr Arg Cys Val Ser Gly
 610 615 620
 gtc tgg tgg gcc ttc acc ttg atc atc atc tcc tcc tac acg gcc aac 2223
 Val Trp Trp Ala Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala Asn
 625 630 635
 ctg gct gcc ttc ctc acg gtg cag cgc atg gag gtg ccg gtg gag tcg 2271
 Leu Ala Ala Phe Leu Thr Val Gln Arg Met Glu Val Pro Val Glu Ser
 640 645 650
 gct gac gac ctg gcg gat cag acc aac att gag tac ggc act atc cac 2319
 Ala Asp Asp Leu Ala Asp Gln Thr Asn Ile Glu Tyr Gly Thr Ile His
 655 660 665 670
 gct ggc tcc acc atg acc ttc ttc cag aac tcg cgg tac cag acg tac. 2367
 Ala Gly Ser Thr Met Thr Phe Phe Gln Asn Ser Arg Tyr Gln Thr Tyr
 675 680 685
 cag cgg atg tgg aac tac atg caa tcg aag cag ccc agc gtg ttt gtc 2415
 Gln Arg Met Trp Asn Tyr Met Gln Ser Lys Gln Pro Ser Val Phe Val
 690 695 700

aag agc aca gag gag gga atc gcc cgc gtc ctc aac tcc cgc tat gcc 2463
Lys Ser Thr Glu Glu Gly Ile Ala Arg Val Leu Asn Ser Arg Tyr Ala
705 710 715
ttc ctg ctg gag tcc acc atg aac gag tac cac agg cgc ctc aat tgc 2511
Phe Leu Leu Glu Ser Thr Met Asn Glu Tyr His Arg Arg Leu Asn Cys
720 725 730
aac ctc acc cag atc ggg ggc ctc ctc gac acc aag ggc tac ggc atc 2559
Asn Leu Thr Gln Ile Gly Gly Leu Leu Asp Thr Lys Gly Tyr Gly Ile
735 740 745 750
ggc atg ccg ctg ggc tcc cct ttc cgg gat gag atc aca ctg gcc atc 2607
Gly Met Pro Leu Gly Ser Pro Phe Arg Asp Glu Ile Thr Leu Ala Ile
755 760 765
ctg cag ctc cag gag aac aac agg ctg gag atc ctg aag cgc aag tgg 2655
Leu Gln Leu Gln Glu Asn Asn Arg Leu Glu Ile Leu Lys Arg Lys Trp
770 775 780
tgg gag ggc ggc cgg tgc ccc aag gag gag gac cac agg gcc aaa ggt 2703
Trp Glu Gly Gly Arg Cys Pro Lys Glu Glu Asp His Arg Ala Lys Gly
785 790 795
ttg ggc atg gag aac att ggc ggc att ttt gtc gtg ctg atc tgt ggc 2751
Leu Gly Met Glu Asn Ile Gly Gly Ile Phe Val Val Leu Ile Cys Gly
800 805 810
ctc atc att gct gtc ttc gtg gcg gtc atg gag ttc atc tgg tcc acg 2799
Leu Ile Ile Ala Val Phe Val Ala Val Met Glu Phe Ile Trp Ser Thr
815 820 825 830
cgg agg tca gcg gag tcc gag gag gtg tcg gtg tgc cag gag atg ctg 2847
Arg Arg Ser Ala Glu Ser Glu Glu Val Ser Val Cys Gln Glu Met Leu
835 840 845
cag gag cta cgc cac gcc gtg tct tgc cga aag acc tcg cgt tcc cgc 2895
Gln Glu Leu Arg His Ala Val Ser Cys Arg Lys Thr Ser Arg Ser Arg

850	855	860	
cgg cgc cgg cgc cct ggt ggc ccg agc cgg gcc ctg ctg tgc ctg cgc			2943
Arg Arg Arg Arg Pro Gly Gly Pro Ser Arg Ala Leu Leu Ser Leu Arg			
865	870	875	
gca gtc cgc gag atg cga ctc agc aac ggc aag ctc tac tgc gcc ggc			2991
Ala Val Arg Glu Met Arg Leu Ser Asn Gly Lys Leu Tyr Ser Ala Gly			
880	885	890	
gcg ggc ggg gac gcg ggc gcg cac ggg ggt ccg cag cgc ctc ctg gac			3039
Ala Gly Gly Asp Ala Gly Ala His Gly Gly Pro Gln Arg Leu Leu Asp			
895	900	905	910
gac ccc gga cct cct ggg gga ccc cgg ccc cag gct ccc acg ccc tgc			3087
Asp Pro Gly Pro Pro Gly Gly Pro Arg Pro Gln Ala Pro Thr Pro Cys			
915	920	925	
acg cac gtg cgc gtc tgc cag gag tgc agg cgc atc cag gcg ctg cga			3135
Thr His Val Arg Val Cys Gln Glu Cys Arg Arg Ile Gln Ala Leu Arg			
930	935	940	
gct tgc ggg gcc ggg gcg ccc cca cgt ggc ctg ggc acc cca gcc gaa			3183
Ala Ser Gly Ala Gly Ala Pro Pro Arg Gly Leu Gly Thr Pro Ala Glu			
945	950	955	
gcc acc agc ccg cct cgg ccg cgg cca ggc ccc acc gga ccc cgc gag			3231
Ala Thr Ser Pro Pro Arg Pro Arg Pro Gly Pro Thr Gly Pro Arg Glu			
960	965	970	
ctg acc gag cac gaa tga ccgtggacgg ggccgggcgt gcgccgactg			3279
Leu Thr Glu His Glu			
975	980		
actgcaggga cgcgatgcgc ccagacgga caggacgccg cgattttgcc ttcaattcct			3339
ggatgaagtcc gagcccggct ccggagcagg cctgcgcctc ctagtggact tgagcaaggg			3399
tgtcgcggac gccgcattct atccgcaccg tggcggagga gcgcagagac cgaggactct			3459
aagggccgcg gactgtgggg gctgctcccg gagttggaaa gcggtccgcg ggaggacccc			3519

aacctgggac tgcccagatg ccccaagact tgacacggct ctccacactt ctggagggtg 3579
 ggagggctct ggacatgtgg gtgtaccctg tgccctctc tctctttct ctcttttttg 3639
 gggggagaaa cctcagaaat ttctatgaga cgccccagg gagagggtct ctggggcccc 3699
 tataaccicc cctgccacat cccagtcctg ttgg 3733

<210> 114

<211> 979

<212> PRT

<213> Mus musculus

<400> 114

Met Pro Ala Glu Leu Leu Leu Leu Ile Val Ala Phe Ala Asn Pro
 1 5 10 15
 Ser Cys Gln Val Leu Ser Ser Leu Arg Met Ala Ala Ile Leu Asp Asp
 20 25 30
 Gln Thr Val Cys Gly Arg Gly Glu Arg Leu Ala Leu Ala Leu Ala Arg
 35 40 45
 Glu Gln Ile Asn Gly Ile Ile Glu Val Pro Ala Lys Ala Arg Val Glu
 50 55 60
 Val Asp Ile Phe Glu Leu Gln Arg Asp Ser Gln Tyr Glu Thr Thr Asp
 65 70 75 80
 Thr Met Cys Gln Ile Leu Pro Lys Gly Val Val Ser Val Leu Gly Pro
 85 90 95
 Ser Ser Ser Pro Ala Ser Ala Ser Thr Val Ser His Ile Cys Gly Glu
 100 105 110
 Lys Glu Ile Pro His Ile Lys Val Gly Pro Glu Glu Thr Pro Arg Leu
 115 120 125
 Gln Tyr Leu Arg Phe Ala Ser Val Ser Leu Tyr Pro Ser Asn Glu Asp
 130 135 140

Val Ser Leu Ala Val Ser Arg Ile Leu Lys Ser Phe Asn Tyr Pro Ser
 145 150 155 160
 Ala Ser Leu Ile Cys Ala Lys Ala Glu Cys Leu Leu Arg Leu Glu Glu
 165 170 175
 Leu Val Arg Gly Phe Leu Ile Ser Lys Glu Thr Leu Ser Val Arg Met
 180 185 190
 Leu Asp Asp Ser Arg Asp Pro Thr Pro Leu Leu Lys Glu Ile Arg Asp
 195 200 205
 Asp Lys Val Ser Thr Ile Ile Ile Asp Ala Asn Ala Ser Ile Ser His
 210 215 220
 Leu Val Leu Arg Lys Ala Ser Glu Leu Gly Met Thr Ser Ala Phe Tyr
 225 230 235 240
 Lys Tyr Ile Leu Thr Thr Met Asp Phe Pro Ile Leu His Leu Asp Gly
 245 250 255
 Ile Val Glu Asp Ser Ser Asn Ile Leu Gly Phe Ser Met Phe Asn Thr
 260 265 270
 Ser His Pro Phe Tyr Pro Glu Phe Val Arg Ser Leu Asn Met Ser Trp
 275 280 285
 Arg Glu Asn Cys Glu Ala Ser Thr Tyr Pro Gly Pro Ala Leu Ser Ala
 290 295 300
 Ala Leu Met Phe Asp Ala Val His Val Val Val Ser Ala Val Arg Glu
 305 310 315 320
 Leu Asn Arg Ser Gln Glu Ile Gly Val Lys Pro Leu Ala Cys Thr Ser
 325 330 335
 Ala Asn Ile Trp Pro His Gly Thr Ser Leu Met Asn Tyr Leu Arg Met
 340 345 350
 Val Glu Tyr Asp Gly Leu Thr Gly Arg Val Glu Phe Asn Ser Lys Gly
 355 360 365
 Gln Arg Thr Asn Tyr Thr Leu Arg Ile Leu Glu Lys Ser Arg Gln Gly

370	375	380	
His Arg Glu Ile Gly Val Trp Tyr Ser Asn Arg Thr Leu Ala Met Asn			
385	390	395	400
Ala Thr Thr Leu Asp Ile Asn Leu Ser Gln Thr Leu Ala Asn Lys Thr			
405	410	415	
Leu Val Val Thr Thr Ile Leu Glu Asn Pro Tyr Val Met Arg Arg Pro			
420	425	430	
Asn Phe Gln Ala Leu Ser Gly Asn Glu Arg Phe Glu Gly Phe Cys Val			
435	440	445	
Asp Met Leu Arg Glu Leu Ala Glu Leu Leu Arg Phe Arg Tyr Arg Leu			
450	455	460	
Arg Leu Val Glu Asp Gly Leu Tyr Gly Ala Pro Glu Pro Asn Gly Ser			
465	470	475	480
Trp Thr Gly Met Val Gly Glu Leu Ile Asn Arg Lys Ala Asp Leu Ala			
485	490	495	
Val Ala Ala Phe Thr Ile Thr Ala Glu Arg Glu Lys Val Ile Asp Phe			
500	505	510	
Ser Lys Pro Phe Met Thr Leu Gly Ile Ser Ile Leu Tyr Arg Val His			
515	520	525	
Met Gly Arg Lys Pro Gly Tyr Phe Ser Phe Leu Asp Pro Phe Ser Pro			
530	535	540	
Ala Val Trp Leu Phe Met Leu Leu Ala Tyr Leu Ala Val Ser Cys Val			
545	550	555	560
Leu Phe Leu Ala Ala Arg Leu Ser Pro Tyr Glu Trp Tyr Asn Pro His			
565	570	575	
Pro Cys Leu Arg Ala Arg Pro His Ile Leu Glu Asn Gln Tyr Thr Leu			
580	585	590	
Gly Asn Ser Leu Trp Phe Pro Val Gly Gly Phe Met Gln Gln Gly Ser			
595	600	605	

Glu Val Met Pro Arg Ala Leu Ser Thr Arg Cys Val Ser Gly Val Trp
 610 615 620
 Trp Ala Phe Thr Leu Ile Ile Ile Ser Ser Tyr Thr Ala Asn Leu Ala
 625 630 635 640
 Ala Phe Leu Thr Val Gln Arg Met Glu Val Pro Val Glu Ser Ala Asp
 645 650 655
 Asp Leu Ala Asp Gln Thr Asn Ile Glu Tyr Gly Thr Ile His Ala Gly
 660 665 670
 Ser Thr Met Thr Phe Phe Gln Asn Ser Arg Tyr Gln Thr Tyr Gln Arg
 675 680 685
 Met Trp Asn Tyr Met Gln Ser Lys Gln Pro Ser Val Phe Val Lys Ser
 690 695 700
 Thr Glu Glu Gly Ile Ala Arg Val Leu Asn Ser Arg Tyr Ala Phe Leu
 705 710 715 720
 Leu Glu Ser Thr Met Asn Glu Tyr His Arg Arg Leu Asn Cys Asn Leu
 725 730 735
 Thr Gln Ile Gly Gly Leu Leu Asp Thr Lys Gly Tyr Gly Ile Gly Met
 740 745 750
 Pro Leu Gly Ser Pro Phe Arg Asp Glu Ile Thr Leu Ala Ile Leu Gln
 755 760 765
 Leu Gln Glu Asn Asn Arg Leu Glu Ile Leu Lys Arg Lys Trp Trp Glu
 770 775 780
 Gly Gly Arg Cys Pro Lys Glu Glu Asp His Arg Ala Lys Gly Leu Gly
 785 790 795 800
 Met Glu Asn Ile Gly Gly Ile Phe Val Val Leu Ile Cys Gly Leu Ile
 805 810 815
 Ile Ala Val Phe Val Ala Val Met Glu Phe Ile Trp Ser Thr Arg Arg
 820 825 830
 Ser Ala Glu Ser Glu Glu Val Ser Val Cys Gln Glu Met Leu Gln Glu

835	840	845
Leu Arg His Ala Val Ser Cys Arg Lys Thr Ser Arg Ser Arg Arg Arg		
850	855	860
Arg Arg Pro Gly Gly Pro Ser Arg Ala Leu Leu Ser Leu Arg Ala Val		
865	870	875
Arg Glu Met Arg Leu Ser Asn Gly Lys Leu Tyr Ser Ala Gly Ala Gly		
885	890	895
Gly Asp Ala Gly Ala His Gly Gly Pro Gln Arg Leu Leu Asp Asp Pro		
900	905	910
Gly Pro Pro Gly Gly Pro Arg Pro Gln Ala Pro Thr Pro Cys Thr His		
915	920	925
Val Arg Val Cys Gln Glu Cys Arg Arg Ile Gln Ala Leu Arg Ala Ser		
930	935	940
Gly Ala Gly Ala Pro Pro Arg Gly Leu Gly Thr Pro Ala Glu Ala Thr		
945	950	955
Ser Pro Pro Arg Pro Arg Pro Gly Pro Thr Gly Pro Arg Glu Leu Thr		
965	970	975
Glu His Glu		

<210> 115

<211> 1792

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (8).. (1666)

<400> 115

cagcgcg atg tgg gtt ccc ggc ttc gga tcc gcg cga ctt ccc cag cgc	49
Met Trp Val Pro Gly Phe Gly Ser Ala Arg Leu Pro Gln Arg	
1 5 10	
cgg cgc tcc ggg ttg gag tca tcc tcg gtg cgg ccg ctg tgg ctg ctg	97
Arg Arg Ser Gly Leu Glu Ser Ser Ser Val Arg Pro Leu Trp Leu Leu	
15 20 25 30	
ctg ctg ttc ctg ctg gca gcc gtg cgg cca gtg cgc gcc tgg gag agc	145
Leu Leu Phe Leu Leu Ala Ala Val Arg Pro Val Arg Ala Trp Glu Ser	
35 40 45	
gga gac ctg gag ttg ttc gac ttg gtg gaa gag gtg cag ttg aac ttc	193
Gly Asp Leu Glu Leu Phe Asp Leu Val Glu Glu Val Gln Leu Asn Phe	
50 55 60	
tac gag ttc ctc ggg gtg cag cag gat gct tca tct gca gac atc aga	241
Tyr Glu Phe Leu Gly Val Gln Gln Asp Ala Ser Ser Ala Asp Ile Arg	
65 70 75	
aaa gca tat cgt aag ctt tca cta acc tta cat cca gac aag aat aaa	289
Lys Ala Tyr Arg Lys Leu Ser Leu Thr Leu His Pro Asp Lys Asn Lys	
80 85 90	
gat gaa aat gca gaa act caa ttt aga caa ttg gtg gcc att tat gaa	337
Asp Glu Asn Ala Glu Thr Gln Phe Arg Gln Leu Val Ala Ile Tyr Glu	
95 100 105 110	
gtt tta aag gat gat gaa aga agg cag agg tat gat gat gtt ctg atc	385
Val Leu Lys Asp Asp Glu Arg Arg Gln Arg Tyr Asp Asp Val Leu Ile	
115 120 125	
aat gga ctt cca gat tgg cga cag cct gta ttc tac tac agg cga gtg	433
Asn Gly Leu Pro Asp Trp Arg Gln Pro Val Phe Tyr Tyr Arg Arg Val	
130 135 140	
aga aaa atg agc aat gct gag ctg gct ttg ctc ttg ttc att att ctc	481
Arg Lys Met Ser Asn Ala Glu Leu Ala Leu Leu Leu Phe Ile Ile Leu	

145	150	155	
aca gtg ggt cac tat gct gtg gtt tgg tcc atc tac ctg gaa aag caa			529
Thr Val Gly His Tyr Ala Val Val Trp Ser Ile Tyr Leu Glu Lys Gln			
160	165	170	
ctg gat gaa ctg ctt ggt aga aaa aag aga gaa agg aag aag aag aca			577
Leu Asp Glu Leu Leu Gly Arg Lys Lys Arg Glu Arg Lys Lys Lys Thr			
175	180	185	190
gga agc aag agt gtg gac gca gca aaa ctt ggt gct tct gaa aag aac			625
Gly Ser Lys Ser Val Asp Ala Ala Lys Leu Gly Ala Ser Glu Lys Asn			
195	200	205	
gaa aga ttg ctt ata aaa cca caa tgg cat gat ttg ctt cca tgc aaa			673
Glu Arg Leu Leu Ile Lys Pro Gln Trp His Asp Leu Leu Pro Cys Lys			
210	215	220	
ctg ggg att tgg ttt tgc ctt aca cta aaa gca ttg cct cat cta atc			721
Leu Gly Ile Trp Phe Cys Leu Thr Leu Lys Ala Leu Pro His Leu Ile			
225	230	235	
cag gat gct ggg cag ttt tat gca aaa tat aag gag aca aaa ttg aag			769
Gln Asp Ala Gly Gln Phe Tyr Ala Lys Tyr Lys Glu Thr Lys Leu Lys			
240	245	250	
gaa aaa gaa gac gca ctg gct aga att gaa att gaa acc ctt caa aaa			817
Glu Lys Glu Asp Ala Leu Ala Arg Ile Glu Ile Glu Thr Leu Gln Lys			
255	260	265	270
cag aag aaa gtt aaa gtt aaa aaa cca aaa cca gaa ttt cct gtg tat			865
Gln Lys Lys Val Lys Val Lys Lys Pro Lys Pro Glu Phe Pro Val Tyr			
275	280	285	
atg cct tta gaa aat acg tat att cag tct tat gat cat gga act tct			913
Met Pro Leu Glu Asn Thr Tyr Ile Gln Ser Tyr Asp His Gly Thr Ser			
290	295	300	
att gaa gaa att gag gag caa atg gat gac tgg ctg gaa aac agg aaa			961

Ile Glu Glu Ile Glu Glu Gln Met Asp Asp Trp Leu Glu Asn Arg Lys
 305 310 315
 aga aca cag aaa aga cag gca cct gaa tgg aca gaa gag gac ctc agt 1009
 Arg Thr Gln Lys Arg Gln Ala Pro Glu Trp Thr Glu Glu Asp Leu Ser
 320 325 330
 caa ctg aca aga agt atg gtt aag ttc cca gga ggg act cca ggt cga 1057
 Gln Leu Thr Arg Ser Met Val Lys Phe Pro Gly Gly Thr Pro Gly Arg
 335 340 345 350
 tgg gac aag att gcc cat gaa ttg ggt cga tct gtg aca gat gtg aca 1105
 Trp Asp Lys Ile Ala His Glu Leu Gly Arg Ser Val Thr Asp Val Thr
 355 360 365
 acc aaa gcc aag gaa ctg aag gac tca gtc acc agc tcc ccc gga atg 1153
 Thr Lys Ala Lys Glu Leu Lys Asp Ser Val Thr Ser Ser Pro Gly Met
 370 375 380
 acc agg ctc tct gaa ctt aag tca aat ggt cag aat tcc agg cca atc 1201
 Thr Arg Leu Ser Glu Leu Lys Ser Asn Gly Gln Asn Ser Arg Pro Ile
 385 390 395
 aag ata gcc aca gcc ttg cca gat gac atc atc acg cag cgg gag gac 1249
 Lys Ile Ala Thr Ala Leu Pro Asp Asp Ile Ile Thr Gln Arg Glu Asp
 400 405 410
 tca gca ggg gcc atg gag gat gag gag cac gag gct gct gag ggt gag 1297
 Ser Ala Gly Ala Met Glu Asp Glu Glu His Glu Ala Ala Glu Gly Glu
 415 420 425 430
 cag gag tca gcg acc aca gaa gcc cga cct cgg agg cgg aag tca gcc 1345
 Gln Glu Ser Ala Thr Thr Glu Ala Arg Pro Arg Arg Arg Lys Ser Ala
 435 440 445
 agg gcg gcc gag gct gta acc aga gtg gag cca gag gag aag ctg aga 1393
 Arg Ala Ala Glu Ala Val Thr Arg Val Glu Pro Glu Glu Lys Leu Arg
 450 455 460

gga aag agg caa aaa gac ttt gat ata tca gaa caa aac gat tcc agt 1441
 Gly Lys Arg Gln Lys Asp Phe Asp Ile Ser Glu Gln Asn Asp Ser Ser
 465 470 475
 gac gaa gag aaa caa cga aaa gaa aga act cgt gct gca gag gag gcg 1489
 Asp Glu Glu Lys Gln Arg Lys Glu Arg Thr Arg Ala Ala Glu Glu Ala
 480 485 490
 tgg act cag agt cag cag aaa ctt ctg gaa ttg gca tta cag caa tac 1537
 Trp Thr Gln Ser Gln Gln Lys Leu Leu Glu Leu Ala Leu Gln Gln Tyr
 495 500 505 510
 cct aaa gga gct tct gac cgc tgg gac aaa ata gcc aaa tgt gtc ccg 1585
 Pro Lys Gly Ala Ser Asp Arg Trp Asp Lys Ile Ala Lys Cys Val Pro
 515 520 525
 tct aag agt aag gaa gac tgc att gct aga tac aag ctg ctg gtt gaa 1633
 Ser Lys Ser Lys Glu Asp Cys Ile Ala Arg Tyr Lys Leu Leu Val Glu
 530 535 540
 ctg gtc caa aag aaa aag cag gct aaa agc tga atcttctgga aggtgacgat 1686
 Leu Val Gln Lys Lys Lys Gln Ala Lys Ser
 545 550
 caatgaccat catittccaa acaagtactic gagaaatctc atgcagaaac ttatatatttg 1746
 tacctcagta tttctaaaca tcatgtgcct tagtaaaaaa aaaaaa 1792

<210> 116

<211> 552

<212> PRT

<213> Mus musculus

<400> 116

Met Trp Val Pro Gly Phe Gly Ser Ala Arg Leu Pro Gln Arg Arg Arg

1	5	10	15
Ser Gly Leu Glu Ser Ser Ser Val Arg Pro Leu Trp Leu Leu Leu Leu			
20	25	30	
Phe Leu Leu Ala Ala Val Arg Pro Val Arg Ala Trp Glu Ser Gly Asp			
35	40	45	
Leu Glu Leu Phe Asp Leu Val Glu Glu Val Gln Leu Asn Phe Tyr Glu			
50	55	60	
Phe Leu Gly Val Gln Gln Asp Ala Ser Ser Ala Asp Ile Arg Lys Ala			
65	70	75	80
Tyr Arg Lys Leu Ser Leu Thr Leu His Pro Asp Lys Asn Lys Asp Glu			
85	90	95	
Asn Ala Glu Thr Gln Phe Arg Gln Leu Val Ala Ile Tyr Glu Val Leu			
100	105	110	
Lys Asp Asp Glu Arg Arg Gln Arg Tyr Asp Asp Val Leu Ile Asn Gly			
115	120	125	
Leu Pro Asp Trp Arg Gln Pro Val Phe Tyr Tyr Arg Arg Val Arg Lys			
130	135	140	
Met Ser Asn Ala Glu Leu Ala Leu Leu Leu Phe Ile Ile Leu Thr Val			
145	150	155	160
Gly His Tyr Ala Val Val Trp Ser Ile Tyr Leu Glu Lys Gln Leu Asp			
165	170	175	
Glu Leu Leu Gly Arg Lys Lys Arg Glu Arg Lys Lys Lys Thr Gly Ser			
180	185	190	
Lys Ser Val Asp Ala Ala Lys Leu Gly Ala Ser Glu Lys Asn Glu Arg			
195	200	205	
Leu Leu Ile Lys Pro Gln Trp His Asp Leu Leu Pro Cys Lys Leu Gly			
210	215	220	
Ile Trp Phe Cys Leu Thr Leu Lys Ala Leu Pro His Leu Ile Gln Asp			
225	230	235	240

Ala Gly Gln Phe Tyr Ala Lys Tyr Lys Glu Thr Lys Leu Lys Glu Lys
 245 250 255
 Glu Asp Ala Leu Ala Arg Ile Glu Ile Glu Thr Leu Gln Lys Gln Lys
 260 265 270
 Lys Val Lys Val Lys Lys Pro Lys Pro Glu Phe Pro Val Tyr Met Pro
 275 280 285
 Leu Glu Asn Thr Tyr Ile Gln Ser Tyr Asp His Gly Thr Ser Ile Glu
 290 295 300
 Glu Ile Glu Glu Gln Met Asp Asp Trp Leu Glu Asn Arg Lys Arg Thr
 305 310 315 320
 Gln Lys Arg Gln Ala Pro Glu Trp Thr Glu Glu Asp Leu Ser Gln Leu
 325 330 335
 Thr Arg Ser Met Val Lys Phe Pro Gly Gly Thr Pro Gly Arg Trp Asp
 340 345 350
 Lys Ile Ala His Glu Leu Gly Arg Ser Val Thr Asp Val Thr Thr Lys
 355 360 365
 Ala Lys Glu Leu Lys Asp Ser Val Thr Ser Ser Pro Gly Met Thr Arg
 370 375 380
 Leu Ser Glu Leu Lys Ser Asn Gly Gln Asn Ser Arg Pro Ile Lys Ile
 385 390 395 400
 Ala Thr Ala Leu Pro Asp Asp Ile Ile Thr Gln Arg Glu Asp Ser Ala
 405 410 415
 Gly Ala Met Glu Asp Glu Glu His Glu Ala Ala Glu Gly Glu Gln Glu
 420 425 430
 Ser Ala Thr Thr Glu Ala Arg Pro Arg Arg Arg Lys Ser Ala Arg Ala
 435 440 445
 Ala Glu Ala Val Thr Arg Val Glu Pro Glu Glu Lys Leu Arg Gly Lys
 450 455 460
 Arg Gln Lys Asp Phe Asp Ile Ser Glu Gln Asn Asp Ser Ser Asp Glu

465 470 475 480
 Glu Lys Gln Arg Lys Glu Arg Thr Arg Ala Ala Glu Glu Ala Trp Thr
 485 490 495
 Gln Ser Gln Gln Lys Leu Leu Glu Leu Ala Leu Gln Gln Tyr Pro Lys
 500 505 510
 Gly Ala Ser Asp Arg Trp Asp Lys Ile Ala Lys Cys Val Pro Ser Lys
 515 520 525
 Ser Lys Glu Asp Cys Ile Ala Arg Tyr Lys Leu Leu Val Glu Leu Val
 530 535 540
 Gln Lys Lys Lys Gln Ala Lys Ser
 545 550

<210> 117

<211> 1634

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (21).. (1271)

<400> 117

cgctcccagc agtcgcaagg atg gag ttc gtc aag tgt cta ggc cac ccg gag 53

Met Glu Phe Val Lys Cys Leu Gly His Pro Glu

1

5

10

gag ttc tat aac ctg ctg cga ttc cgc atg gga ggc cgg cgg aat ttt 101

Glu Phe Tyr Asn Leu Leu Arg Phe Arg Met Gly Gly Arg Arg Asn Phe

15

20

25

ata ccc aag atg gac cag gac tca ctc agc agc agc ttg aag acc tgc 149

Ile Pro Lys Met Asp Gln Asp Ser Leu Ser Ser Ser Leu Lys Thr Cys
 30 35 40
 tac aag tat ctc aat cag acc agt cgc agc ttt gcc gcg gtt atc cag 197
 Tyr Lys Tyr Leu Asn Gln Thr Ser Arg Ser Phe Ala Ala Val Ile Gln
 45 50 55
 gcg ctg gat ggg gac ata cgg cac gcc ata tgt gtg ttc tac ctg gtt 245
 Ala Leu Asp Gly Asp Ile Arg His Ala Ile Cys Val Phe Tyr Leu Val
 60 65 70 75
 ctc cga gcc ctg gat aca gtg gag gat gac atg agc atc agt gtg gag 293
 Leu Arg Ala Leu Asp Thr Val Glu Asp Asp Met Ser Ile Ser Val Glu
 80 85 90
 aag aag atc cca ctg ctg tgt aac ttc cac act ttc ctc tat gac cca 341
 Lys Lys Ile Pro Leu Leu Cys Asn Phe His Thr Phe Leu Tyr Asp Pro
 95 100 105
 gag tgg cgg ttc act gag agc aag gag aag gac cga caa gtg ctg gag 389
 Glu Trp Arg Phe Thr Glu Ser Lys Glu Lys Asp Arg Gln Val Leu Glu
 110 115 120
 gac ttc ccc acg atc tcc ctg gag ttt aga aat ttg gct gag aaa tat 437
 Asp Phe Pro Thr Ile Ser Leu Glu Phe Arg Asn Leu Ala Glu Lys Tyr
 125 130 135
 caa aca gtg atc gat gac atc tgc cac cag atg ggg tgt ggg atg gca 485
 Gln Thr Val Ile Asp Asp Ile Cys His Gln Met Gly Cys Gly Met Ala
 140 145 150 155
 gaa ttt gta gac aag gat gtg acc tcc aaa cag gac tgg gac aag tac 533
 Glu Phe Val Asp Lys Asp Val Thr Ser Lys Gln Asp Trp Asp Lys Tyr
 160 165 170
 tgc cac tac gtt gct ggg ctg gtg gga att ggc ctt tct cgt cta ttc 581
 Cys His Tyr Val Ala Gly Leu Val Gly Ile Gly Leu Ser Arg Leu Phe
 175 180 185

tct gcc tca gag ttt gaa gac ccc ata gtt ggt gaa gac ata gag tgt	629
Ser Ala Ser Glu Phe Glu Asp Pro Ile Val Gly Glu Asp Ile Glu Cys	
190 195 200	
gcc aac tca atg ggt ctg ttc ctg cag aaa aca aat atc att cgt gat	677
Ala Asn Ser Met Gly Leu Phe Leu Gln Lys Thr Asn Ile Ile Arg Asp	
205 210 215	
tat ctg gaa gac caa cag gaa gga agg aag ttt tgg cct cag gag gtg	725
Tyr Leu Glu Asp Gln Gln Glu Gly Arg Lys Phe Trp Pro Gln Glu Val	
220 225 230 235	
tgg ggc aga tac att aag aag ttg gaa gac ttt gct aag cca gag aac	773
Trp Gly Arg Tyr Ile Lys Lys Leu Glu Asp Phe Ala Lys Pro Glu Asn	
240 245 250	
gta gat gtg gcc gtg cag tgc ttg aat gaa ctc ata acc aac acc cta	821
Val Asp Val Ala Val Gln Cys Leu Asn Glu Leu Ile Thr Asn Thr Leu	
255 260 265	
cag cac atc cct gac gtc ctc acc tac ctg tca agg ctc cgg aac cag	869
Gln His Ile Pro Asp Val Leu Thr Tyr Leu Ser Arg Leu Arg Asn Gln	
270 275 280	
agt gtg ttt aac ttc tgt gct att cca cag gta atg gcc att gcc aca	917
Ser Val Phe Asn Phe Cys Ala Ile Pro Gln Val Met Ala Ile Ala Thr	
285 290 295	
ctg gct gcc tgt tac aat aac cag cag gta ttc aaa gga gta gtg aag	965
Leu Ala Ala Cys Tyr Asn Asn Gln Gln Val Phe Lys Gly Val Val Lys	
300 305 310 315	
att cgg aag ggg caa gca gtc acc ctc atg atg gat gcc acc aac atg	1013
Ile Arg Lys Gly Gln Ala Val Thr Leu Met Met Asp Ala Thr Asn Met	
320 325 330	
cct gcc gtc aaa gct atc ata tac cag tac ata gaa gag att tat cac	1061
Pro Ala Val Lys Ala Ile Ile Tyr Gln Tyr Ile Glu Glu Ile Tyr His	

```

          335          340          345
cgg atc ccc aac tca gac cca tca tca agc aaa acc aag cag gtc atc 1109
Arg Ile Pro Asn Ser Asp Pro Ser Ser Ser Lys Thr Lys Gln Val Ile

          350          355          360
tcc aag atc agg aca cag aac ctt ccc aac tgc cag ctc atc tcc cga 1157
Ser Lys Ile Arg Thr Gln Asn Leu Pro Asn Cys Gln Leu Ile Ser Arg

          365          370          375
agc cac tac tcg ccc att tac ctg tca ttt atc atg ctc ttg gct gcc 1205
Ser His Tyr Ser Pro Ile Tyr Leu Ser Phe Ile Met Leu Leu Ala Ala

380          385          390          395
ctg agc tgg cag tac ctg agc acc ctg tcc cag gtc aca gaa gac tat 1253
Leu Ser Trp Gln Tyr Leu Ser Thr Leu Ser Gln Val Thr Glu Asp Tyr

          400          405          410
gtc cag aga gaa cac tga tttgttttag ccggaagtgg aagttcccg 1301
Val Gln Arg Glu His

          415
ggagigggtt tttccttttc ctccagctgg attttgactt cccttgtttt tcctcctact 1361
ctaaaatctt tgggagaact gagtgtggga ccttaggaa ctgggagagg aaaggatgcc 1421
ttgccctcag cagcctgggtg ctggctggga cttggttcct ctgcctcttg tagccactgg 1481
cagcgtgccg actgctgcac ttgtgaggcc acgtgtgatg gtcacaagag cctagtgaac 1541
ctggctagaa tgcigattgg atttatitaa ttigaaacag cctttgaata cctatgacaa 1601
tagaaaatga aagcaaaaaa aaaaaaaaaa aaa 1634

```

<210> 118

<211> 416

<212> PRT

<213> Mus musculus

<400> 118

Met Glu Phe Val Lys Cys Leu Gly His Pro Glu Glu Phe Tyr Asn Leu
 1. 5 10 15
 Leu Arg Phe Arg Met Gly Gly Arg Arg Asn Phe Ile Pro Lys Met Asp
 20 25 30
 Gln Asp Ser Leu Ser Ser Ser Leu Lys Thr Cys Tyr Lys Tyr Leu Asn
 35 40 45
 Gln Thr Ser Arg Ser Phe Ala Ala Val Ile Gln Ala Leu Asp Gly Asp
 50 55 60
 Ile Arg His Ala Ile Cys Val Phe Tyr Leu Val Leu Arg Ala Leu Asp
 65 70 75 80
 Thr Val Glu Asp Asp Met Ser Ile Ser Val Glu Lys Lys Ile Pro Leu
 85 90 95
 Leu Cys Asn Phe His Thr Phe Leu Tyr Asp Pro Glu Trp Arg Phe Thr
 100 105 110
 Glu Ser Lys Glu Lys Asp Arg Gln Val Leu Glu Asp Phe Pro Thr Ile
 115 120 125
 Ser Leu Glu Phe Arg Asn Leu Ala Glu Lys Tyr Gln Thr Val Ile Asp
 130 135 140
 Asp Ile Cys His Gln Met Gly Cys Gly Met Ala Glu Phe Val Asp Lys
 145 150 155 160
 Asp Val Thr Ser Lys Gln Asp Trp Asp Lys Tyr Cys His Tyr Val Ala
 165 170 175
 Gly Leu Val Gly Ile Gly Leu Ser Arg Leu Phe Ser Ala Ser Glu Phe
 180 185 190
 Glu Asp Pro Ile Val Gly Glu Asp Ile Glu Cys Ala Asn Ser Met Gly
 195 200 205
 Leu Phe Leu Gln Lys Thr Asn Ile Ile Arg Asp Tyr Leu Glu Asp Gln
 210 215 220
 Gln Glu Gly Arg Lys Phe Trp Pro Gln Glu Val Trp Gly Arg Tyr Ile

225	230	235	240
Lys Lys Leu Glu Asp Phe Ala Lys Pro Glu Asn Val Asp Val Ala Val			
245	250	255	
Gln Cys Leu Asn Glu Leu Ile Thr Asn Thr Leu Gln His Ile Pro Asp			
260	265	270	
Val Leu Thr Tyr Leu Ser Arg Leu Arg Asn Gln Ser Val Phe Asn Phe			
275	280	285	
Cys Ala Ile Pro Gln Val Met Ala Ile Ala Thr Leu Ala Ala Cys Tyr			
290	295	300	
Asn Asn Gln Gln Val Phe Lys Gly Val Val Lys Ile Arg Lys Gly Gln			
305	310	315	320
Ala Val Thr Leu Met Met Asp Ala Thr Asn Met Pro Ala Val Lys Ala			
325	330	335	
Ile Ile Tyr Gln Tyr Ile Glu Glu Ile Tyr His Arg Ile Pro Asn Ser			
340	345	350	
Asp Pro Ser Ser Ser Lys Thr Lys Gln Val Ile Ser Lys Ile Arg Thr			
355	360	365	
Gln Asn Leu Pro Asn Cys Gln Leu Ile Ser Arg Ser His Tyr Ser Pro			
370	375	380	
Ile Tyr Leu Ser Phe Ile Met Leu Leu Ala Ala Leu Ser Trp Gln Tyr			
385	390	395	400
Leu Ser Thr Leu Ser Gln Val Thr Glu Asp Tyr Val Gln Arg Glu His			
405	410	415	

<210> 119

<211> 183

<212> DNA

<213> Mus musculus

<400> 119

gatcggctcg gtgacggaat cccctgcaggc gtgtaagctg gccctctcca atggctgggg 60
 cgtcatggcg tcccaccgtt ctgagcaaac tgaggacact gtcacgcag accctgggg 120
 tgtggctctg cactgggcag atcaatgact ggatgccct tgaggattcg agcgtgtgag 180
 caa 183

<210> 120

<211> 920

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (132).. (701)

<400> 120

ctgggtggaa acitcagtc tctgactga gagtagaaa ctgacagtga gcaccaactg 60
 aaggctttta caggctccat ctcatcttc tcagacttct aaggcctctc ctgcagccac 120
 cccaccccaa g atg gtg acc atg ctg atg ttc ctg gcc acg ctg gcg ggt 170
 Met Val Thr Met Leu Met Phe Leu Ala Thr Leu Ala Gly
 1 5 10
 ctc ttc acc aca gcc aaa gga caa aat ttc cat ctt ggg aaa tgc ccg 218
 Leu Phe Thr Thr Ala Lys Gly Gln Asn Phe His Leu Gly Lys Cys Pro
 15 20 25
 tct cct cct gtg caa gag aat ttt gac gtg aaa aag tat ctt gga aga 266
 Ser Pro Pro Val Gln Glu Asn Phe Asp Val Lys Lys Tyr Leu Gly Arg
 30 35 40 45
 tgg tac gaa att gag aag atc cca gcg agc ttt gag aaa gga aac tgc 314
 Trp Tyr Glu Ile Glu Lys Ile Pro Ala Ser Phe Glu Lys Gly Asn Cys

	50	55	60	
att caa gcc aac tac tcg ctg atg gag aac gga aac atc gaa gtg cta				362
Ile Gln Ala Asn Tyr Ser Leu Met Glu Asn Gly Asn Ile Glu Val Leu				
	65	70	75	
aac aag gag ctg agt cct gat gga acc atg aac caa gta aag ggt gaa				410
Asn Lys Glu Leu Ser Pro Asp Gly Thr Met Asn Gln Val Lys Gly Glu				
	80	85	90	
gcc aaa cag agc aac gtc tca gag cca gcc aag ctg gaa gtc cag ttc				458
Ala Lys Gln Ser Asn Val Ser Glu Pro Ala Lys Leu Glu Val Gln Phe				
	95	100	105	
ttc ccg ttg atg cca ccg gca ccc tac tgg atc ctg gcc act gat tat				506
Phe Pro Leu Met Pro Pro Ala Pro Tyr Trp Ile Leu Ala Thr Asp Tyr				
110	115	120	125	
gaa aac tat gcc ctc gtc tac tcc tgc acc acc ttc ttc tgg ctc ttc				554
Glu Asn Tyr Ala Leu Val Tyr Ser Cys Thr Thr Phe Phe Trp Leu Phe				
	130	135	140	
cat gtg gat ttt gtt tgg att ctt gga aga aat cct tat ctc cct cca				602
His Val Asp Phe Val Trp Ile Leu Gly Arg Asn Pro Tyr Leu Pro Pro				
	145	150	155	
gaa aca ata acc tac cta aaa gat atc ctt act tct aat ggc atc gac				650
Glu Thr Ile Thr Tyr Leu Lys Asp Ile Leu Thr Ser Asn Gly Ile Asp				
	160	165	170	
atc gaa aaa atg aca aca aca gat caa gcg aac tgc ccg gac ttc ctg				698
Ile Glu Lys Met Thr Thr Thr Asp Gln Ala Asn Cys Pro Asp Phe Leu				
	175	180	185	
taa agggggcggg ggcgaaaacc acaccagggtt atttctttgc ttgctgtcc				751
190				
ctggctccac cccacgcct cgtaaggacc aagcaaccat ggcaggcact agaggagag				811
taaggctata gaagccaatg gagggagggg actcatggaa agttggccca aaccaacct				871

gacccacac tgtcaccttg ctagcccaat aataaacatt ttgctgatc

920

<210> 121

<211> 189

<212> PRT

<213> Mus musculus

<400> 121

Met	Val	Thr	Met	Leu	Met	Phe	Leu	Ala	Thr	Leu	Ala	Gly	Leu	Phe	Thr
1				5					10					15	
Thr	Ala	Lys	Gly	Gln	Asn	Phe	His	Leu	Gly	Lys	Cys	Pro	Ser	Pro	Pro
			20					25						30	
Val	Gln	Glu	Asn	Phe	Asp	Val	Lys	Lys	Tyr	Leu	Gly	Arg	Trp	Tyr	Glu
		35					40					45			
Ile	Glu	Lys	Ile	Pro	Ala	Ser	Phe	Glu	Lys	Gly	Asn	Cys	Ile	Gln	Ala
	50					55					60				
Asn	Tyr	Ser	Leu	Met	Glu	Asn	Gly	Asn	Ile	Glu	Val	Leu	Asn	Lys	Glu
	65					70				75				80	
Leu	Ser	Pro	Asp	Gly	Thr	Met	Asn	Gln	Val	Lys	Gly	Glu	Ala	Lys	Gln
			85					90						95	
Ser	Asn	Val	Ser	Glu	Pro	Ala	Lys	Leu	Glu	Val	Gln	Phe	Phe	Pro	Leu
		100						105						110	
Met	Pro	Pro	Ala	Pro	Tyr	Trp	Ile	Leu	Ala	Thr	Asp	Tyr	Glu	Asn	Tyr
		115						120						125	
Ala	Leu	Val	Tyr	Ser	Cys	Thr	Thr	Phe	Phe	Trp	Leu	Phe	His	Val	Asp
	130							135						140	
Phe	Val	Trp	Ile	Leu	Gly	Arg	Asn	Pro	Tyr	Leu	Pro	Pro	Glu	Thr	Ile
	145						150						155		160
Thr	Tyr	Leu	Lys	Asp	Ile	Leu	Thr	Ser	Asn	Gly	Ile	Asp	Ile	Glu	Lys

	165	170	175
Met Thr Thr Thr Asp Gln Ala Asn Cys Pro Asp Phe Leu			
	180	185	

<210> 122

<211> 2129

<212> DNA

<213> Mus musculus

<400> 122

```

gggcgattct acttcctcag tctttagccc atccagggtt ttttacgtca attggtcaga 60
tgactgactt gatccataat gagaaagacc tggtagacatc actaaaagat tatattaaag 120
cagaagagga caagttagag caaatcaaaa aatgggcaga gaagttagac cggctaacga 180
gtagagcaac aaaagaccca gaggggtttg ttgggcatcc tgtaaacgca ttcaagttaa 240
tgaaacgtct gaacactgag tggagtgagt tggagaatct gatcctcaag gacatgtcgg 300
atggcttcat ctctaaccia accattcaga ggcagtactt ccctaattgat gaagatcagg 360
ttggagctgc taaagctctg tttcggctgc aagacacctt caatctggac acaaataaca 420
tctcaaaggg gaatcttcca ggagtgcac ataagtcitt cctgacagct gaggactgct 480
ttgagctggg caaagtggcc tatacagagg cagattatta ccacacggaa ctgtggatgg 540
agcaggctct gacgcagctg gaggaggag agctgtctac ttagataaaa gtctctgttc 600
tggattacct gagctatgcg gtgtaccagc agggagacct ggataaggcg cttctcctca 660
ccaagaagct tcttgagcta gatcctgaac atcagagagc taatggtaac ttagtatatt 720
ttgaatatat aatgagttaa gaaaaagatg ccaataagtc agcgtcgggc gaccaatctg 780
atcagaaaac tgcaccaaag aaaaaaggga tagctgtgga ttacctgcca gagagacaga 840
agtacgaaat gctgtgccgt ggggagggtt tcaaaatgac tccccggaga cagaaaagac 900
tgttctgccg ctacatgat gggaaccgga atcctaagtt catcctggcc ccagccaagc 960
aggaggacga gtgggacaag ccccggatta tccgtttcca tgacatcatc tctgacgcgg 1020
agattgagat tgtcaaatac ttagcaaaac caaggctgag ccgagctaca gtacatgacc 1080
ctgagacggg gaaattgacc acagcacagt acagagtatc taagagtgtt tggctgtctg 1140

```

gctacgaaga ccctgtggta tcccgaatta atatgagaat acaagatctc acaggactgg 1200
 atgtttctac ggccgaggag ttacaggtag caaattatgg agttggagga cagtatgagc 1260
 cccattttga ctttgcacgg aaagaatgagc cggatgcctt tagagagctt gggacaggaa 1320
 ataggattgc cacgtggctg ttctatatga gcgaatgtgc tgcaggagga gctactgitt 1380
 ttctgaagt gggagccagt gtttggccca aaaaaggcac tgctgtcttc tggataatc 1440
 tgtttgccag tggggaagga gattacagta cacggcatgc agcctgtccc gtgctagttg 1500
 gaaacaaatg ggtatccaac aaatggctcc atgaacgtgg acaagaattt cgaaggccgt 1560
 gcacctgtc agaattggaa tgacaaccag gcttcccttg gctcctgttg tctctaacg 1620
 caccaggcac gatggctgat tataactccg acgtttacag ctgactaaca ctccatgatt 1680
 aattgggcca tgagctcagc cccaatgtc accgttggac aatcacttat tttgtggatt 1740
 tctttaatta atactcaatc accacatgat gtaaaactta tggttcagtt ttcacaggat 1800
 acaaggcatt gaaaatgagg aacctaatit tgttgtttta aagagctttt tggttaaitt 1860
 ttttaaaaaa agcatccaga agtagatttc accacaagtc aggagctggt ggagcaggcg 1920
 aggcgtgtgt gcaggcgtgc aggtggcagg cgacagacct gtgggcttac agacggcagg 1980
 catgcagacg ccagtgtgct gctcttcga tgtgtggact gctgagcact ggtaactaac 2040
 tagggcccag tcaggctctg tattccacgt gcagagtcc tattatttaa agaaactctt 2100
 tttatcaaat cccctctc accacgggt 2129

<210> 123

<211> 397

<212> DNA

<213> Mus musculus

<400> 123

attcggcaca ggacagaaac aggggaaggg tcccgccagc tccitggaatc taaagtcaag 60
 ctaatcgcta accctttgtg caactccga caactctatg accacaccat cgatgacagt 120
 atgattttgt cggggaacct tcagaagccc ggatcagaca cctgccaggg tgactcgggg 180
 ggccctctaa cctgtgagaa ggatggaact tactacgtct acgggattgt aagctggggc 240
 caggaatgtg ggaagaagcc aggagtctac actcaagtca ccaagttcct gaattggata 300

aagaccacca tgcacaggga ggctggcctc tgagggtgctg tctgcagagc cttgaagccc 360
ctcgcttitta gcaccaaaca agaggggctt cctgcgt 397

<210> 124

<211> 1519

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (120).. (656)

<400> 124

gtggcgcagg caaggaccct gaaaataaac agccgctgct ttgcgagtcg ctttcttggt 60
tcttcgtccg agtctcctcc gctgtgggca gctcagacgc cgaagctcta actgcagct 119
atg agc agc aac gaa tgc ttc aag tgt gga cga tct ggc cac tgg gcc 167
Met Ser Ser Asn Glu Cys Phe Lys Cys Gly Arg Ser Gly His Trp Ala
1 5 10 15
agg gag tgc cct act ggt gga ggt cgg ggt cgt gga atg aga agc cgc 215
Arg Glu Cys Pro Thr Gly Gly Gly Arg Gly Arg Gly Met Arg Ser Arg
20 25 30
ggc aga ggt ggt ttt acc tcg gat aga ggg ttc cag ttt gtt tcc tcg 263
Gly Arg Gly Gly Phe Thr Ser Asp Arg Gly Phe Gln Phe Val Ser Ser
35 40 45
tct ctc cct gac atc tgc tac cgc tgt ggt gag tct ggt cat ctt gcc 311
Ser Leu Pro Asp Ile Cys Tyr Arg Cys Gly Glu Ser Gly His Leu Ala
50 55 60
aag gat tgt gat ctg cag gag gat gaa gcc tgc tat aac tgc ggt aga 359
Lys Asp Cys Asp Leu Gln Glu Asp Glu Ala Cys Tyr Asn Cys Gly Arg

65	70	75	80	
ggc ggc cac att gcc aag gac tgc aag gag ccc aag aga gag cga gag				407
Gly Gly His Ile Ala Lys Asp Cys Lys Glu Pro Lys Arg Glu Arg Glu				
	85	90	95	
caa tgc tgc tac aat tgt ggc aag cca ggc cat ctg gct cgt gac tgt				455
Gln Cys Cys Tyr Asn Cys Gly Lys Pro Gly His Leu Ala Arg Asp Cys				
	100	105	110	
gac cac gcg gat gag cag aag tgc tat tct tgt ggt gaa ttt gga cat				503
Asp His Ala Asp Glu Gln Lys Cys Tyr Ser Cys Gly Glu Phe Gly His				
	115	120	125	
att caa aaa gac tgc acc aag gtg aag tgc tat agg tgt ggt gaa act				551
Ile Gln Lys Asp Cys Thr Lys Val Lys Cys Tyr Arg Cys Gly Glu Thr				
	130	135	140	
ggt cat gta gcc atc aat tgc agc aag aca agt gaa gtc aac tgt tac				599
Gly His Val Ala Ile Asn Cys Ser Lys Thr Ser Glu Val Asn Cys Tyr				
	145	150	155	160
cgc tgt ggc gag tca ggg cat ctt gca cgg gaa tgc aca att gag gct				647
Arg Cys Gly Glu Ser Gly His Leu Ala Arg Glu Cys Thr Ile Glu Ala				
	165	170	175	
aca gcc taa ttattttcct ttgtcgcccc tccittttct gattgatggt				696
Thr Ala				
tgtattatit tctctgaatc ctcttcactg gccaaagggt ggcagataga ggctgttccc				756
aggccagtga gctttacttg cagtgtaaaa ggaggaaagg ggtggaaaaa accgaatttc				816
tgcatttaac tacaaaaaaa gtttatgttt agtttggttag aggtgttatg tataatgctt				876
tgttaaagaa ccccttttcc gtgccactgg tgaataggga ttaatgaatg ggaagagttc				936
agtcagacca gtaagccctt ctgggtttga gtgtgttccc atgtaggagg taaaaccaat				996
tctggaagca tctaagcttc cataaataac ttttaattctt agcataatga cggccttgga				1056
ttgtctgacc tcagtagcta ttaaataaca tcgagtaaca tctgcatcag gccctcagaa				1116
tatacagttg agttgggagt aaactgaaaa gacaaatgtg ttgaagctat gccagggaat				1176

ctgctcaaag cctaacacag aagcagcttc atcccagtgga cgatgctgga cgtacagatg 1236
 gtgatggcaa aggtgtagaa cacatTTTTT caaagactaa atctaaaacc cagagtaaac 1296
 atccgatgct cagagttagc ataatttTga gctattcagg aattgcagag aaatgcattt 1356
 tcacagaaat caagatgtta tttttgtata ctatactact tagacaactg tgtttcattt 1416
 gctgtaatca gtttttaaaa gtcagatgga aaaagcaact gaagtcctag aaaatagaaa 1476
 atgtaatttt aaactattcc aataaagctg gaggaggaag ggg 1519

<210> 125

<211> 178

<212> PRT

<213> Mus musculus

<400> 125

Met	Ser	Ser	Asn	Glu	Cys	Phe	Lys	Cys	Gly	Arg	Ser	Gly	His	Trp	Ala
1				5					10					15	
Arg	Glu	Cys	Pro	Thr	Gly	Gly	Gly	Arg	Gly	Arg	Gly	Met	Arg	Ser	Arg
			20					25						30	
Gly	Arg	Gly	Gly	Phe	Thr	Ser	Asp	Arg	Gly	Phe	Gln	Phe	Val	Ser	Ser
		35					40					45			
Ser	Leu	Pro	Asp	Ile	Cys	Tyr	Arg	Cys	Gly	Glu	Ser	Gly	His	Leu	Ala
		50					55					60			
Lys	Asp	Cys	Asp	Leu	Gln	Glu	Asp	Glu	Ala	Cys	Tyr	Asn	Cys	Gly	Arg
	65				70					75				80	
Gly	Gly	His	Ile	Ala	Lys	Asp	Cys	Lys	Glu	Pro	Lys	Arg	Glu	Arg	Glu
			85						90					95	
Gln	Cys	Cys	Tyr	Asn	Cys	Gly	Lys	Pro	Gly	His	Leu	Ala	Arg	Asp	Cys
			100						105					110	
Asp	His	Ala	Asp	Glu	Gln	Lys	Cys	Tyr	Ser	Cys	Gly	Glu	Phe	Gly	His
			115						120					125	

Ile Gln Lys Asp Cys Thr Lys Val Lys Cys Tyr Arg Cys Gly Glu Thr
 130 135 140
 Gly His Val Ala Ile Asn Cys Ser Lys Thr Ser Glu Val Asn Cys Tyr
 145 150 155 160
 Arg Cys Gly Glu Ser Gly His Leu Ala Arg Glu Cys Thr Ile Glu Ala
 165 170 175
 Thr Ala

<210> 126

<211> 2080

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (56).. (1687)

<400> 126

gcggttggga acgcggagcg gacgaattcg attcaacggg gticcgggcc aggct atg 58

Met

1

gag cag gtg aat gag cta aag gag aag ggc aat aag gcc ctg agt gct 106

Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser Ala

5

10

15

ggg aac att gat gat gcc tta cag tgc tac tct gag gca att aaa cta 154

Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys Leu

20

25

30

gat ccc cag aac cat gtg ctc tac agc aat cgc tct gca gcc tac gcc 202

Asp Pro Gln Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr Ala

35	40	45	
aag aaa gga gac tac cag aag gcc tat gag gac ggc tgc aag act gtt			250
Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr Val			
50	55	60	65
gac ctg aag cct gac tgg ggc aag ggt tat tca aga aaa gca gca gcc			298
Asp Leu Lys Pro Asp Trp Gly Lys Gly Tyr Ser Arg Lys Ala Ala Ala			
70	75	80	
ctt gaa ttc cta aac cgg ttt gag gaa gcc aaa cga acc tat gaa gaa			346
Leu Glu Phe Leu Asn Arg Phe Glu Glu Ala Lys Arg Thr Tyr Glu Glu			
85	90	95	
ggt tta aaa cat gaa gcc aat aat ctc cag ctt aag gag ggc ttg cag			394
Gly Leu Lys His Glu Ala Asn Asn Leu Gln Leu Lys Glu Gly Leu Gln			
100	105	110	
aac atg gag gcc agg ttg gca gag agg aaa ttc atg aat cca ttc aac			442
Asn Met Glu Ala Arg Leu Ala Glu Arg Lys Phe Met Asn Pro Phe Asn			
115	120	125	
ttg cct aat cta tac caa aag ttg gaa aac gac ccc agg aca agg tcg			490
Leu Pro Asn Leu Tyr Gln Lys Leu Glu Asn Asp Pro Arg Thr Arg Ser			
130	135	140	145
ctg ctc agt gac ccc acc tac agg gag ctc ata gaa cag ctg cag aac			538
Leu Leu Ser Asp Pro Thr Tyr Arg Glu Leu Ile Glu Gln Leu Gln Asn			
150	155	160	
aag ccg tca gac ctg ggc acg aaa cta cag gat ccc cgg gtg atg act			586
Lys Pro Ser Asp Leu Gly Thr Lys Leu Gln Asp Pro Arg Val Met Thr			
165	170	175	
act ctg agt gtc ctc ctt ggg gtt gat ctg ggc agc atg gat gaa gag			634
Thr Leu Ser Val Leu Leu Gly Val Asp Leu Gly Ser Met Asp Glu Glu			
180	185	190	
gaa gag gca gca aca ccc cca ccc cca cct cct ccc aaa aag gag ccc			682

Glu Glu Ala Ala Thr Pro Pro Pro Pro Pro Pro Pro Lys Lys Glu Pro
 195 200 205
 aag cca gaa cca atg gaa gaa gat ctt cca gag aat aag aaa cag gca 730
 Lys Pro Glu Pro Met Glu Glu Asp Leu Pro Glu Asn Lys Lys Gln Ala
 210 215 220 225
 ctg aaa gag aag gag ctg gga aat gat gcc tac aag aag aaa gat ttt 778
 Leu Lys Glu Lys Glu Leu Gly Asn Asp Ala Tyr Lys Lys Lys Asp Phe
 230 235 240
 gac aag gcc ctg aag cat tat gac aga gcc aag gaa ctg gac cct acc 826
 Asp Lys Ala Leu Lys His Tyr Asp Arg Ala Lys Glu Leu Asp Pro Thr
 245 250 255
 aac atg acc tac ata act aat caa gca gct gtg cac ttt gag aag ggc 874
 Asn Met Thr Tyr Ile Thr Asn Gln Ala Ala Val His Phe Glu Lys Gly
 260 265 270
 gac tat aac aaa tgc cgg gag ctc tgt gag aag gcc att gaa gtg ggc 922
 Asp Tyr Asn Lys Cys Arg Glu Leu Cys Glu Lys Ala Ile Glu Val Gly
 275 280 285
 aga gag aac cga gag gac tac cgg cag atc gcc aaa gct tat gcc cga 970
 Arg Glu Asn Arg Glu Asp Tyr Arg Gln Ile Ala Lys Ala Tyr Ala Arg
 290 295 300 305
 att ggc aat tcc tat ttc aaa gaa gaa aag tac aag gat gct ata cat 1018
 Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile His
 310 315 320
 ttc tac aac aag tct cta gca gag cac cga acc cca gat gtg ctc aag 1066
 Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu Lys
 325 330 335
 aag tgc cag cag gca gag aaa att ctg aag gaa cag gag cgc ttg gct 1114
 Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu Ala
 340 345 350

tat atc aac cct gac ttg gct ttg gag gag aag aac aag ggc aac gaa	1162
Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn Glu	
355 360 365	
tgc ttc cag aaa ggg gac tac ccc caa gcc atg aag cac tat aca gaa	1210
Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr Glu	
370 375 380 385	
gcc att aaa agg aac ccg aga gat gcc aaa ctg tac agc aac cga gct	1258
Ala Ile Lys Arg Asn Pro Arg Asp Ala Lys Leu Tyr Ser Asn Arg Ala	
390 395 400	
gcc tgc tac acc aag ctc ctg gag ttt cag ctg gca ctc aag gac tgt	1306
Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp Cys	
405 410 415	
gag gag tgc atc cag cta gag cca acc ttc atc aag ggt tat aca cgg	1354
Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr Arg	
420 425 430	
aaa gca gct gct ctg gaa gcc atg aag gac tat aca aaa gcc atg gat	1402
Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met Asp	
435 440 445	
gtg tac caa aaa gcg tta gac ctg gac tcc agc tgt aag gaa gca gca	1450
Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala Ala	
450 455 460 465	
gat ggt tac caa cgc tgt atg atg gca cag tac aac aga cat gat agc	1498
Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp Ser	
470 475 480	
cct gag gat gtg aag cgg cgg gcc atg gct gac cct gag gtg cag cag	1546
Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln Gln	
485 490 495	
ata atg agt gac cca gcc atg aga ctc atc ctg gag cag atg caa aag	1594
Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln Lys	

500 505 510
 gac ccc cag gct ctg agc gaa cac tta aag aat cct gta ata gcg cag 1642
 Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala Gln
 515 520 525
 aag atc cag aag ctg atg gat gtg ggt ctc atc gca att cgg tga 1687
 Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg
 530 535 540
 taacttgctt tccccctct tcccttcgcc aatgaggaag gcgagctggg aagggtggcga 1747
 gcagcactgg gcagaggggg ggagaagaaa ggcttatctt tatatttata catgcctaca 1807
 aggaagacag atcatccag cgccacctcg ggccctccca gcacacgcat ggtctcttca 1867
 ctgctgccct caatccgagt gtccttccct gccagtcct agcctccccg tcactgtctc 1927
 ggctgtctcc ccaatagtig gttatTTTT atttggggca gtgggtgcat acgggggagg 1987
 gaggtgttc tcccaacct aggttcccag ctgtcttcac ctgttcttac ccacgtccct 2047
 cctcaataaa gaagccagtc aggcgtgggtt ata 2080

<210> 127

<211> 543

<212> PRT

<213> Mus musculus

<400> 127

Met Glu Gln Val Asn Glu Leu Lys Glu Lys Gly Asn Lys Ala Leu Ser
 1 5 10 15
 Ala Gly Asn Ile Asp Asp Ala Leu Gln Cys Tyr Ser Glu Ala Ile Lys
 20 25 30
 Leu Asp Pro Gln Asn His Val Leu Tyr Ser Asn Arg Ser Ala Ala Tyr
 35 40 45
 Ala Lys Lys Gly Asp Tyr Gln Lys Ala Tyr Glu Asp Gly Cys Lys Thr
 50 55 60

314/2644

290	295	300	
Arg Ile Gly Asn Ser Tyr Phe Lys Glu Glu Lys Tyr Lys Asp Ala Ile			
305	310	315	320
His Phe Tyr Asn Lys Ser Leu Ala Glu His Arg Thr Pro Asp Val Leu			
	325	330	335
Lys Lys Cys Gln Gln Ala Glu Lys Ile Leu Lys Glu Gln Glu Arg Leu			
	340	345	350
Ala Tyr Ile Asn Pro Asp Leu Ala Leu Glu Glu Lys Asn Lys Gly Asn			
	355	360	365
Glu Cys Phe Gln Lys Gly Asp Tyr Pro Gln Ala Met Lys His Tyr Thr			
	370	375	380
Glu Ala Ile Lys Arg Asn Pro Arg Asp Ala Lys Leu Tyr Ser Asn Arg			
385	390	395	400
Ala Ala Cys Tyr Thr Lys Leu Leu Glu Phe Gln Leu Ala Leu Lys Asp			
	405	410	415
Cys Glu Glu Cys Ile Gln Leu Glu Pro Thr Phe Ile Lys Gly Tyr Thr			
	420	425	430
Arg Lys Ala Ala Ala Leu Glu Ala Met Lys Asp Tyr Thr Lys Ala Met			
	435	440	445
Asp Val Tyr Gln Lys Ala Leu Asp Leu Asp Ser Ser Cys Lys Glu Ala			
	450	455	460
Ala Asp Gly Tyr Gln Arg Cys Met Met Ala Gln Tyr Asn Arg His Asp			
465	470	475	480
Ser Pro Glu Asp Val Lys Arg Arg Ala Met Ala Asp Pro Glu Val Gln			
	485	490	495
Gln Ile Met Ser Asp Pro Ala Met Arg Leu Ile Leu Glu Gln Met Gln			
	500	505	510
Lys Asp Pro Gln Ala Leu Ser Glu His Leu Lys Asn Pro Val Ile Ala			
	515	520	525

Gln Lys Ile Gln Lys Leu Met Asp Val Gly Leu Ile Ala Ile Arg

530

535

540

<210> 128

<211> 11673

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (283).. (10668)

<400> 128

ggggcgctcgc gtgcacaccg gcggcgggcgg cgctcggagg cggacgacgc gctctcggcg 60
 ccgcgggccc cggttcccc cgcgctctcg ctccggcggc ccaaagtaac ttccgggagcc 120
 tcggctctccc gctaacttcc ccccgcgggc tcggttgccc ggaccgcgtc ggctcgagcc 180
 cgccgcccggc tcgccttccc cgcacgcggc tcctccgtgc cggtgccctcc gaaagtgga 240
 gagagagcgc gcggggcgcg cggcggcacg gagcgcgggc gc atg gag cgc ggc 294

Met Glu Arg Gly

1

tgc tgg gcg ccg cgg gct ctc gtc ctg gcc gtg ctg ctg ctg ctg gcg 342
 Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu Leu Leu Leu Ala

5

10

15

20

acg ctg agg gcg cgc gcg gcc acc ggc tac tac ccg cgc ttc tcg cct 390
 Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro Arg Phe Ser Pro

25

30

35

ttc ttt ttc ctg tgc acc cac cac ggg gag ctg gaa ggg gat ggg gag 438
 Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu Gly Asp Gly Glu

40

45

50

cag ggc gag gtg ctc att tcc ctg cac att gcg ggc aac ccc acc tac 486
 Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly Asn Pro Thr Tyr
 55 60 65
 tac gta ccg gga cag gaa tac cat gtt aca att tca aca agc acc ttc 534
 Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser Thr Ser Thr Phe
 70 75 80
 ttt gat ggc ttg ctg gtg acg gga ctc tat acc tcg aca agc atc cag 582
 Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser Thr Ser Ile Gln
 85 90 95 100
 tct tct cag agc att gga ggc tcc agc gcc ttt gga ttc ggg atc atg 630
 Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly Phe Gly Ile Met
 105 110 115
 tcc gac cac cag ttt ggt aac cag ttt atg tgc agt gtg gtg gcc tct 678
 Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser Val Val Ala Ser
 120 125 130
 cat gtg agt cac ctg cct aca acc aac ctc agc ttt gtc tgg att gcc 726
 His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe Val Trp Ile Ala
 135 140 145
 cca cca gct ggc aca ggc tgt gtg aat ttc atg gct act gca aca cat 774
 Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala Thr Ala Thr His
 150 155 160
 agg ggc cag gtg att ttc aaa gac gca ctg gcc cag cag ctg tgt gaa 822
 Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln Gln Leu Cys Glu
 165 170 175 180
 caa gga gct ccc aca gag gcc act gct tac tcg cac ctt gct gaa ata 870
 Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His Leu Ala Glu Ile
 185 190 195
 cac agt gac agt gtg atc cta cga gat gac ttt gac tcc tac cag caa 918
 His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp Ser Tyr Gln Gln

200	205	210	
ctg gaa ttg aac ccc aac ata tgg gtt gaa tgc agc aac tgt gag atg			966
Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser Asn Cys Glu Met			
215	220	225	
gga gag cag tgt ggc acc atc atg cat ggc aat gct gtc acc ttc tgt			1014
Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala Val Thr Phe Cys			
230	235	240	
gag ccg tac ggc cct cga gag ctg acc acc aca tgc ctg aac aca aca			1062
Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys Leu Asn Thr Thr			
245	250	255	260
aca gca tct gtc ctc cag ttt tcc att ggg tca gga tca tgt cga ttt			1110
Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly Ser Cys Arg Phe			
265	270	275	
agt tac tct gac ccc agc atc act gtg tca tac gcc aag aac aat acc			1158
Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala Lys Asn Asn Thr			
280	285	290	
gct gat tgg att cag ctg gag aaa att aga gcc cct tcc aat gtg agc			1206
Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro Ser Asn Val Ser			
295	300	305	
aca gtc atc cac atc ctg tac ctc ccc gag gaa gcc aaa ggg gag agc			1254
Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala Lys Gly Glu Ser			
310	315	320	
gtg cag ttc cag tgg aaa cag gac agc ctg cga gtg ggt gag gtg tat			1302
Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val Gly Glu Val Tyr			
325	330	335	340
gag gcc tgc tgg gcc ctg gat aac atc ctg gtc atc aat tca gcc cac			1350
Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile Asn Ser Ala His			
345	350	355	
aga gaa gtc gtt ctg gag gac aac ctc gac ccg gtc gac acg ggc aac			1398

Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val Asp Thr Gly Asn
 360 365 370
 tgg ctc ttc ttc cct gga gca acg gtc aag cat agc tgt cag tca gat 1446
 Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser Cys Gln Ser Asp
 375 380 385
 ggg aac tcc att tat ttc cat gga aat gaa ggc agc gag ttc aat ttt 1494
 Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser Glu Phe Asn Phe
 390 395 400
 gcc acc acc cgg gat gta gat ctt tct aca gag gat att caa gag cag 1542
 Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp Ile Gln Glu Gln
 405 410 415 420
 tgg tca gaa gaa ttt gag agc cag ccc aca gga tgg gat atc ttg gga 1590
 Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp Asp Ile Leu Gly
 425 430 435
 gca gta gtt ggt gca gac tgt gga acc gta gaa tca gga cta tca ctg 1638
 Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser Gly Leu Ser Leu
 440 445 450
 gtg ttc ctc aaa gat gga gag agg aag ctt tgc acc ccc tac atg gat 1686
 Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr Pro Tyr Met Asp
 455 460 465
 aca act ggt tat ggc aac ctg agg ttc tac ttc gtt atg gga gga atc 1734
 Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val Met Gly Gly Ile
 470 475 480
 tgt gac cct gga gtc tct cat gaa aac gat atc atc tta tat gca aag 1782
 Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile Leu Tyr Ala Lys
 485 490 495 500
 att gaa gga aga aaa gaa cac att gca ctg gac act ctt acc tat tct 1830
 Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr Leu Thr Tyr Ser
 505 510 515

tcc tat aag gtt ccg tct ttg gtt tct gtg gtc atc aac cct gaa ctt	1878
Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile Asn Pro Glu Leu	
520 525 530	
cag aca cct gcc acc aaa ttt tgt ctc agg caa aag agc cac caa ggg	1926
Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys Ser His Gln Gly	
535 540 545	
tat aat cgg aat gtc tgg gct gtg gac ttc ttc cat gtg ctg ccc gtt	1974
Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His Val Leu Pro Val	
550 555 560	
ctc cct tca aca atg tct cac atg atc cag ttt tct att aat ttg gga	2022
Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser Ile Asn Leu Gly	
565 570 575 580	
tgc ggc aca cac cag cct ggg aac agc gtc agc ttg gag ttt tct act	2070
Cys Gly Thr His Gln Pro Gly Asn Ser Val Ser Leu Glu Phe Ser Thr	
585 590 595	
aac cat gga cgg tcc tgg tcc cta ctc cac act gag tgc ttg ccg gag	2118
Asn His Gly Arg Ser Trp Ser Leu Leu His Thr Glu Cys Leu Pro Glu	
600 605 610	
atc tgt gca ggc ccc cac ctc ccc cac agc act gtc tac tcc tca gaa	2166
Ile Cys Ala Gly Pro His Leu Pro His Ser Thr Val Tyr Ser Ser Glu	
615 620 625	
aac tac agc ggg tgg aac cga atc acg att cct ctc cct aat gca gca	2214
Asn Tyr Ser Gly Trp Asn Arg Ile Thr Ile Pro Leu Pro Asn Ala Ala	
630 635 640	
ctc acc cga gac acc agg att cgc tgg aga caa aca ggc cca atc ctg	2262
Leu Thr Arg Asp Thr Arg Ile Arg Trp Arg Gln Thr Gly Pro Ile Leu	
645 650 655 660	
gga aat atg tgg gca att gat aat gtt tat ata ggt cct tcg tgt ctc	2310
Gly Asn Met Trp Ala Ile Asp Asn Val Tyr Ile Gly Pro Ser Cys Leu	

665	670	675	
aaa ttc tgt tct ggc aga gga caa tgc act cgg cat ggc tgc aag tgt			2358
Lys Phe Cys Ser Gly Arg Gly Gln Cys Thr Arg His Gly Cys Lys Cys			
680	685	690	
gac cca gga ttt tct ggc cca gct tgt gag atg gca tct cag aca ttc			2406
Asp Pro Gly Phe Ser Gly Pro Ala Cys Glu Met Ala Ser Gln Thr Phe			
695	700	705	
cca atg ttt att tcg gaa agc ttt ggc agt gcc aga ctt tcc tct tac			2454
Pro Met Phe Ile Ser Glu Ser Phe Gly Ser Ala Arg Leu Ser Ser Tyr			
710	715	720	
cat aac ttt tac tct atc cgt ggt gct gaa gtc agc ttt ggt tgt ggt			2502
His Asn Phe Tyr Ser Ile Arg Gly Ala Glu Val Ser Phe Gly Cys Gly			
725	730	735	740
gtc tta gcc agt ggt aag gct ctg gtt ttc aac aaa gat ggg agg cgg			2550
Val Leu Ala Ser Gly Lys Ala Leu Val Phe Asn Lys Asp Gly Arg Arg			
745	750	755	
cag cta atc acg tcc ttt ctg gac agc tcg cag tcc agg ttt ctt cag			2598
Gln Leu Ile Thr Ser Phe Leu Asp Ser Ser Gln Ser Arg Phe Leu Gln			
760	765	770	
ttt aca ctg agg ctg ggg agc aag tct gtg ctg agc acg tgc aga gcc			2646
Phe Thr Leu Arg Leu Gly Ser Lys Ser Val Leu Ser Thr Cys Arg Ala			
775	780	785	
cct gac cag ccg ggg gag gga gtc ctg ctg cac tat tca tat gac aac			2694
Pro Asp Gln Pro Gly Glu Gly Val Leu Leu His Tyr Ser Tyr Asp Asn			
790	795	800	
ggg ata aca tgg aaa ctc ctg gag cac tat tcc tac gtc aac tac cac			2742
Gly Ile Thr Trp Lys Leu Leu Glu His Tyr Ser Tyr Val Asn Tyr His			
805	810	815	820
gag ccc aga ata atc tct gta gag cta ccg gat gat gca aga cag ttt			2790

Glu Pro Arg Ile Ile Ser Val Glu Leu Pro Asp Asp Ala Arg Gln Phe
 825 830 835
 gga atc cag ttc aga tgg tgg cag cct tac cat tct tcc caa gga gaa :2838
 Gly Ile Gln Phe Arg Trp Trp Gln Pro Tyr His Ser Ser Gln Gly Glu
 840 845 850
 gac gtg tgg gcc att gat gag att gtc atg acc tca gtc ctg ttc aac :2886
 Asp Val Trp Ala Ile Asp Glu Ile Val Met Thr Ser Val Leu Phe Asn
 855 860 865
 agc atc agt ctc gac ttt acc aat ctt gtg gaa gtc act caa tcc ctg :2934
 Ser Ile Ser Leu Asp Phe Thr Asn Leu Val Glu Val Thr Gln Ser Leu
 870 875 880
 gga ttc tac ctt ggc aat gtt caa cca tac tgt ggc cat gac tgg acg :2982
 Gly Phe Tyr Leu Gly Asn Val Gln Pro Tyr Cys Gly His Asp Trp Thr
 885 890 895 900
 ctt tgt ttt acg gga gat tct aaa ctt gcc tca agc atg cgc tat gtg :3030
 Leu Cys Phe Thr Gly Asp Ser Lys Leu Ala Ser Ser Met Arg Tyr Val
 905 910 915
 gaa aca cag tcc atg cag atc gga gca tcc tat atg att cag ttc agc :3078
 Glu Thr Gln Ser Met Gln Ile Gly Ala Ser Tyr Met Ile Gln Phe Ser
 920 925 930
 cta gtg atg gga tgt ggc cag aaa tac act cct cac atg gac aac cag :3126
 Leu Val Met Gly Cys Gly Gln Lys Tyr Thr Pro His Met Asp Asn Gln
 935 940 945
 gtg aag ctg gag tac tca gcc aac cac ggc ctt aca tgg cac ctt gta :3174
 Val Lys Leu Glu Tyr Ser Ala Asn His Gly Leu Thr Trp His Leu Val
 950 955 960
 caa gaa gaa tgc ctt ccc agt atg cca agc tgc cag gaa ttt aca tct :3222
 Gln Glu Glu Cys Leu Pro Ser Met Pro Ser Cys Gln Glu Phe Thr Ser
 965 970 975 980

gcc agc att tac cat gcc agc gag ttc aca cag tgg aga aga gtc act 3270
 Ala Ser Ile Tyr His Ala Ser Glu Phe Thr Gln Trp Arg Arg Val Thr
 985 990 995
 gtt gtt ctt ccc cag aaa aca tgg tcc ggt gcc acc cgc ttc cgt tgg 3318
 Val Val Leu Pro Gln Lys Thr Trp Ser Gly Ala Thr Arg Phe Arg Trp
 1000 1005 1010
 agt cag agc tat tac aca gcc cag gat gag tgg gct tta gac aac att 3366
 Ser Gln Ser Tyr Tyr Thr Ala Gln Asp Glu Trp Ala Leu Asp Asn Ile
 1015 1020 1025
 tac att ggg cag cag tgc ccc aac atg tgc agt ggg cat ggc tca tgt 3414
 Tyr Ile Gly Gln Gln Cys Pro Asn Met Cys Ser Gly His Gly Ser Cys
 1030 1035 1040
 gac cat ggc gtg tgc agg tgt gac cag gga tac cag ggc act gaa tgc 3462
 Asp His Gly Val Cys Arg Cys Asp Gln Gly Tyr Gln Gly Thr Glu Cys
 1045 1050 1055 1060
 cac cca gaa gct gca ctt cct tcc acg att atg tca gat ttt gag aac 3510
 His Pro Glu Ala Ala Leu Pro Ser Thr Ile Met Ser Asp Phe Glu Asn
 1065 1070 1075
 ccg agc agt tgg gaa tca gac tgg cag gaa gtt att ggg gga gaa gtt 3558
 Pro Ser Ser Trp Glu Ser Asp Trp Gln Glu Val Ile Gly Gly Glu Val
 1080 1085 1090
 gta aag cct gag caa ggc tgt gga gtc gtg tct tct gga tct tct ctg 3606
 Val Lys Pro Glu Gln Gly Cys Gly Val Val Ser Ser Gly Ser Ser Leu
 1095 1100 1105
 tac ttc agc aag gct ggg aag agg cag ctg gtg agc tgg gac ctg gac 3654
 Tyr Phe Ser Lys Ala Gly Lys Arg Gln Leu Val Ser Trp Asp Leu Asp
 1110 1115 1120
 aca tcc tgg gtg gac ttt gtc cag ttc tac atc cag ata gga gga gag 3702
 Thr Ser Trp Val Asp Phe Val Gln Phe Tyr Ile Gln Ile Gly Gly Glu

1125	1130	1135	1140	
agt gct gca tgc aac aag cct gac agc aga gag gag ggc att ctg ctc				3750
Ser Ala Ala Cys Asn Lys Pro Asp Ser Arg Glu Glu Gly Ile Leu Leu				
	1145	1150	1155	
cag tat agc aac aac ggg ggc atc cag tgg cac ctg ctg gca gag atg				3798
Gln Tyr Ser Asn Asn Gly Gly Ile Gln Trp His Leu Leu Ala Glu Met				
	1160	1165	1170	
tac ttc tca gac ttc agc aaa ccc aga ttt gtc tac ctg gag ctc cca				3846
Tyr Phe Ser Asp Phe Ser Lys Pro Arg Phe Val Tyr Leu Glu Leu Pro				
	1175	1180	1185	
gct gct ggg aag acc cct tgt acc agg ttc cgc tgg tgg aag cct gtg				3894
Ala Ala Gly Lys Thr Pro Cys Thr Arg Phe Arg Trp Trp Lys Pro Val				
	1190	1195	1200	
ttc tcg ggg gag gac tat gac cag tgg gcc gtt gat gat atc atc att				3942
Phe Ser Gly Glu Asp Tyr Asp Gln Trp Ala Val Asp Asp Ile Ile Ile				
	1205	1210	1215	1220
ctg tca gag aag cag aag cag gtt atc cca gtt gtc aac cca act ttg				3990
Leu Ser Glu Lys Gln Lys Gln Val Ile Pro Val Val Asn Pro Thr Leu				
	1225	1230	1235	
ccc cag aac ttc tat gag aag cca gct ttc gat tac cct atg aac caa				4038
Pro Gln Asn Phe Tyr Glu Lys Pro Ala Phe Asp Tyr Pro Met Asn Gln				
	1240	1245	1250	
atg agt gtg tgg cta atg ttg gcc aat gaa ggc atg gct aaa aac gac				4086
Met Ser Val Trp Leu Met Leu Ala Asn Glu Gly Met Ala Lys Asn Asp				
	1255	1260	1265	
agc ttc tgt gcg acc acg ccg tca gcc atg gtg ttt gga aag tca gat				4134
Ser Phe Cys Ala Thr Thr Pro Ser Ala Met Val Phe Gly Lys Ser Asp				
	1270	1275	1280	
gga gac cgg ttt gca gta act cga gat ctg acc ctg aaa cct gga tat				4182

Gly Asp Arg Phe Ala Val Thr Arg Asp Leu Thr Leu Lys Pro Gly Tyr
 1285 1290 1295 1300
 gtg ctg cag ttc aag cta aac ata ggc tgc acc agc cag ttc agc agc 4230
 Val Leu Gln Phe Lys Leu Asn Ile Gly Cys Thr Ser Gln Phe Ser Ser
 1305 1310 1315
 act gcc ccg gtt ctc ctg cag tat tca cat gat gcc ggc atg tcg tgg 4278
 Thr Ala Pro Val Leu Leu Gln Tyr Ser His Asp Ala Gly Met Ser Trp
 1320 1325 1330
 ttt ctg ttg aag gaa gga tgc ttc cca gcg tca gca gcc aaa gga tgt 4326
 Phe Leu Leu Lys Glu Gly Cys Phe Pro Ala Ser Ala Ala Lys Gly Cys
 1335 1340 1345
 gaa ggg aac tcc agg gaa ttg agt gag cct act gtc tat tat act ggg 4374
 Glu Gly Asn Ser Arg Glu Leu Ser Glu Pro Thr Val Tyr Tyr Thr Gly
 1350 1355 1360
 gac ttc gaa gaa tgg act aga atc acc att gcc att cca agg tcc ctt 4422
 Asp Phe Glu Glu Trp Thr Arg Ile Thr Ile Ala Ile Pro Arg Ser Leu
 1365 1370 1375 1380
 gca tcc agc aag acc aga ttc cga tgg atc caa gag agc agc tct cag 4470
 Ala Ser Ser Lys Thr Arg Phe Arg Trp Ile Gln Glu Ser Ser Ser Gln
 1385 1390 1395
 aag aat gtg ccc ccg ttt ggc tta gat ggg gtg tac ata tct gag cct 4518
 Lys Asn Val Pro Pro Phe Gly Leu Asp Gly Val Tyr Ile Ser Glu Pro
 1400 1405 1410
 tgt ccc agt tac tgc agt ggc cat gga gac tgc atc tcg ggg gtg tgt 4566
 Cys Pro Ser Tyr Cys Ser Gly His Gly Asp Cys Ile Ser Gly Val Cys
 1415 1420 1425
 ttt tgt gac ctg ggg tac aca gct gca caa gga acc tgt gtg tca aac 4614
 Phe Cys Asp Leu Gly Tyr Thr Ala Ala Gln Gly Thr Cys Val Ser Asn
 1430 1435 1440

acc cct aac cac agt gag atg ttc gac agg ttt gag ggg aag cta agc 4662
 Thr Pro Asn His Ser Glu Met Phe Asp Arg Phe Glu Gly Lys Leu Ser
 1445 1450 1455 1460
 cca ctg tgg tac aaa atc acc ggg ggt cag gtt ggc acg ggc tgt ggc 4710
 Pro Leu Trp Tyr Lys Ile Thr Gly Gly Gln Val Gly Thr Gly Cys Gly
 1465 1470 1475
 acc ctc aat gac ggc agg tcc ctc tac ttt aat ggc ctt ggg aaa agg 4758
 Thr Leu Asn Asp Gly Arg Ser Leu Tyr Phe Asn Gly Leu Gly Lys Arg
 1480 1485 1490
 gaa gcc agg aca gtc cca ctg gac acc agg aat atc agt ctt gtt cag 4806
 Glu Ala Arg Thr Val Pro Leu Asp Thr Arg Asn Ile Ser Leu Val Gln
 1495 1500 1505
 ttt tat ata caa att gga agt aaa aca tca ggg att acg tac atc acc 4854
 Phe Tyr Ile Gln Ile Gly Ser Lys Thr Ser Gly Ile Thr Tyr Ile Thr
 1510 1515 1520
 cca cgg gct aga tat gag ggg ctt gtt gtt cag tat tcc aat gat aat 4902
 Pro Arg Ala Arg Tyr Glu Gly Leu Val Val Gln Tyr Ser Asn Asp Asn
 1525 1530 1535 1540
 ggg ata ctt tgg cat ttg ctg aga gag ttg gat ttc atg tca ttc ctg 4950
 Gly Ile Leu Trp His Leu Leu Arg Glu Leu Asp Phe Met Ser Phe Leu
 1545 1550 1555
 gag cca cag atc att tcc att gac ctg ccc cgg gaa gca aag aca cct 4998
 Glu Pro Gln Ile Ile Ser Ile Asp Leu Pro Arg Glu Ala Lys Thr Pro
 1560 1565 1570
 gcc aca gct ttc cgg tgg tgg cag ccg cag cat ggg aag cat tcg gcc 5046
 Ala Thr Ala Phe Arg Trp Trp Gln Pro Gln His Gly Lys His Ser Ala
 1575 1580 1585
 cag tgg gct ttg ggt gat gtc ctt ata gga gtg aat gac agc tct caa 5094
 Gln Trp Ala Leu Gly Asp Val Leu Ile Gly Val Asn Asp Ser Ser Gln

1590	1595	1600	
act gga ttt caa gat aaa ttg gat ggc tcc ata gac ttg caa gcc aac			5142
Thr Gly Phe Gln Asp Lys Leu Asp Gly Ser Ile Asp Leu Gln Ala Asn			
1605	1610	1615	1620
tgg tat cga atc cag gga ggc caa gtt gat atc gac tgc ctc tct atg			5190
Trp Tyr Arg Ile Gln Gly Gly Gln Val Asp Ile Asp Cys Leu Ser Met			
	1625	1630	1635
gac act gcc ctt ata ttc act gaa aac ata gga aac cct cgc tat gct			5238
Asp Thr Ala Leu Ile Phe Thr Glu Asn Ile Gly Asn Pro Arg Tyr Ala			
	1640	1645	1650
gag acc tgg gac ttc cat gtg tca gag tca agc ttc tta cag tgg gaa			5286
Glu Thr Trp Asp Phe His Val Ser Glu Ser Ser Phe Leu Gln Trp Glu			
	1655	1660	1665
atg aac atg ggc tgc agc aag cct ttc agt ggt gcc cac ggc ata cag			5334
Met Asn Met Gly Cys Ser Lys Pro Phe Ser Gly Ala His Gly Ile Gln			
	1670	1675	1680
ctc cag tac tct ctg aac aac ggc aag gac tgg cag ctt gtc acc gaa			5382
Leu Gln Tyr Ser Leu Asn Asn Gly Lys Asp Trp Gln Leu Val Thr Glu			
1685	1690	1695	1700
gag tgt gtc cct cca acc att ggg tgc gtg cac tac aca gag agt tca			5430
Glu Cys Val Pro Pro Thr Ile Gly Cys Val His Tyr Thr Glu Ser Ser			
	1705	1710	1715
act tac aca tca gaa aga ttc cag aac tgg agg cgg gtc acg gtc tac			5478
Thr Tyr Thr Ser Glu Arg Phe Gln Asn Trp Arg Arg Val Thr Val Tyr			
	1720	1725	1730
ctg cca ctc gcc acc aat tct ccc agg act cgg ttc aga tgg att cag			5526
Leu Pro Leu Ala Thr Asn Ser Pro Arg Thr Arg Phe Arg Trp Ile Gln			
	1735	1740	1745
acc aac tat act gtt gga gca gat tcc tgg gct att gat aat gtc atc			5574

Thr Asn Tyr Thr Val Gly Ala Asp Ser Trp Ala Ile Asp Asn Val Ile
 1750 1755 1760
 ctg gcc tcg ggc tgt cct tgg atg tgc tca gga cga ggg atc tgt gat 5622
 Leu Ala Ser Gly Cys Pro Trp Met Cys Ser Gly Arg Gly Ile Cys Asp
 1765 1770 1775 1780
 tcg ggg cgc tgt gtg tgt gac cgg ggc ttc ggt gga ccc ttc tgt gtt 5670
 Ser Gly Arg Cys Val Cys Asp Arg Gly Phe Gly Gly Pro Phe Cys Val
 1785 1790 1795
 cct gtt gtt cct ctt ccc tcc att cta aaa gat gat ttc aat ggg aac 5718
 Pro Val Val Pro Leu Pro Ser Ile Leu Lys Asp Asp Phe Asn Gly Asn
 1800 1805 1810
 tta cat cct gac ctt tgg cct gaa gtg tac ggg gca gag agg ggc aat 5766
 Leu His Pro Asp Leu Trp Pro Glu Val Tyr Gly Ala Glu Arg Gly Asn
 1815 1820 1825
 ctg aat ggc gaa acc atc aaa tcc gga aca tgt ctg atc ttt aaa ggg 5814
 Leu Asn Gly Glu Thr Ile Lys Ser Gly Thr Cys Leu Ile Phe Lys Gly
 1830 1835 1840
 gag gga cta aga atg ctt att tcc aga gat cta gat tgt acc aat act 5862
 Glu Gly Leu Arg Met Leu Ile Ser Arg Asp Leu Asp Cys Thr Asn Thr
 1845 1850 1855 1860
 atg tat gtc cag ttc tct ctc cga ttt ata gcg aaa ggt acc cca gag 5910
 Met Tyr Val Gln Phe Ser Leu Arg Phe Ile Ala Lys Gly Thr Pro Glu
 1865 1870 1875
 agg tct cac tcc atc ctt cta cag ttc tct gtc agt gga gga gtc acc 5958
 Arg Ser His Ser Ile Leu Leu Gln Phe Ser Val Ser Gly Gly Val Thr
 1880 1885 1890
 tgg cac ctg atg gat gaa ttc tac ttc cct caa acg acc agc ata ctt 6006
 Trp His Leu Met Asp Glu Phe Tyr Phe Pro Gln Thr Thr Ser Ile Leu
 1895 1900 1905

ttc atc aat gtt ccc tta cca tac ggt gcc caa acc aac gct aca aga	6054
Phe Ile Asn Val Pro Leu Pro Tyr Gly Ala Gln Thr Asn Ala Thr Arg	
1910 1915 1920	
ttc aga ctc tgg caa ccg tac aat aat ggt aag aaa gaa gaa atc tgg	6102
Phe Arg Leu Trp Gln Pro Tyr Asn Asn Gly Lys Lys Glu Glu Ile Trp	
1925 1930 1935 1940	
atc att gat gac ttt att att gat gga aac aat ttg aac aac ccc gtg	6150
Ile Ile Asp Asp Phe Ile Ile Asp Gly Asn Asn Leu Asn Asn Pro Val	
1945 1950 1955	
ctg ctg ctg gac acg ttc gac ttt ggg ccc agg gaa gac aat tgg ttt	6198
Leu Leu Leu Asp Thr Phe Asp Phe Gly Pro Arg Glu Asp Asn Trp Phe	
1960 1965 1970	
ttc tat ccg ggt ggt aat atc gga ctt tac tgc ccg tat tct tca aag	6246
Phe Tyr Pro Gly Gly Asn Ile Gly Leu Tyr Cys Pro Tyr Ser Ser Lys	
1975 1980 1985	
gga gct cct gag gag gat tcg gcc atg gtg ttt gtt tca aac gaa gtt	6294
Gly Ala Pro Glu Glu Asp Ser Ala Met Val Phe Val Ser Asn Glu Val	
1990 1995 2000	
gga gaa cac tcc att acc aca cga gac cta agt gtg aac gag aac acc	6342
Gly Glu His Ser Ile Thr Thr Arg Asp Leu Ser Val Asn Glu Asn Thr	
2005 2010 2015 2020	
atc att caa ttt gag atc aat gtt ggc tgc tcc act gat agt tct tct	6390
Ile Ile Gln Phe Glu Ile Asn Val Gly Cys Ser Thr Asp Ser Ser Ser	
2025 2030 2035	
gct gat ccg gtc aga ctg gaa ttc tca agg gac ttt gga gcc acc tgg	6438
Ala Asp Pro Val Arg Leu Glu Phe Ser Arg Asp Phe Gly Ala Thr Trp	
2040 2045 2050	
cac ctg ctg ctg cct ctc tgc tac cac agc agc agc ctc gtc agc tcc	6486
His Leu Leu Leu Pro Leu Cys Tyr His Ser Ser Ser Leu Val Ser Ser	

2055	2060	2065	
tta tgc tcc act gag cat cac ccg agc agc acc tac tac gcg ggg acc			6534
Leu Cys Ser Thr Glu His His Pro Ser Ser Thr Tyr Tyr Ala Gly Thr			
2070	2075	2080	
acc cag ggc tgg cgg cgg gag gtc gtg cac ttc gga aag ctg cac ctt			6582
Thr Gln Gly Trp Arg Arg Glu Val Val His Phe Gly Lys Leu His Leu			
2085	2090	2095	2100
tgt gga tct gtg cgt ttc cgt tgg tac cag gga ttt tat cct gct ggc			6630
Cys Gly Ser Val Arg Phe Arg Trp Tyr Gln Gly Phe Tyr Pro Ala Gly			
2105	2110	2115	
tct cag ccg gtc aca tgg gcc att gac aat gtc tac att ggt ccc cag			6678
Ser Gln Pro Val Thr Trp Ala Ile Asp Asn Val Tyr Ile Gly Pro Gln			
2120	2125	2130	
tgt gaa gag atg tgc tat ggg cac ggg agc tgc atc aat gga acc aag			6726
Cys Glu Glu Met Cys Tyr Gly His Gly Ser Cys Ile Asn Gly Thr Lys			
2135	2140	2145	
tgt ata tgt gac ccg ggc tac tct ggg cca acc tgt aaa ata agc acc			6774
Cys Ile Cys Asp Pro Gly Tyr Ser Gly Pro Thr Cys Lys Ile Ser Thr			
2150	2155	2160	
aaa aat cct gat ttt ctc aaa gac gac ttt gaa ggt caa ctg gaa tcc			6822
Lys Asn Pro Asp Phe Leu Lys Asp Asp Phe Glu Gly Gln Leu Glu Ser			
2165	2170	2175	2180
gat cga ttc tta ctg atg agc ggt ggg aag ccg tct cgt aag tgt ggc			6870
Asp Arg Phe Leu Leu Met Ser Gly Gly Lys Pro Ser Arg Lys Cys Gly			
2185	2190	2195	
atc ctt tcc agt ggg aac aac ctc ttc ttc aat gag gac ggc ttg cgc			6918
Ile Leu Ser Ser Gly Asn Asn Leu Phe Phe Asn Glu Asp Gly Leu Arg			
2200	2205	2210	
atg cta gta aca cgg gac ctg gat tta tca cat gca agg ttt gtg cag			6966

Met Leu Val Thr Arg Asp Leu Asp Leu Ser His Ala Arg Phe Val Gln
2215 2220 2225
ttc ttc atg aga ctg gga tgt ggt aaa ggt gtt cca gac ccc agg agc 7014
Phe Phe Met Arg Leu Gly Cys Gly Lys Gly Val Pro Asp Pro Arg Ser
2230 2235 2240
cag ccc gtg ctt ctg cag tac tcc ctc aat ggc ggc ctc tcc tgg agt 7062
Gln Pro Val Leu Leu Gln Tyr Ser Leu Asn Gly Gly Leu Ser Trp Ser
2245 2250 2255 2260
ctt ctt caa gag ttc ctc ttc agc aac tcc agc aat gtg ggc agg tac 7110
Leu Leu Gln Glu Phe Leu Phe Ser Asn Ser Ser Asn Val Gly Arg Tyr
2265 2270 2275
att gcc ctg gaa atg ccc ctg aaa gcc cgt tct ggt tcg aca cgc ctc 7158
Ile Ala Leu Glu Met Pro Leu Lys Ala Arg Ser Gly Ser Thr Arg Leu
2280 2285 2290
cgc tgg tgg cag cca tct gaa aat ggg cac ttc tat agc ccc tgg gtg 7206
Arg Trp Trp Gln Pro Ser Glu Asn Gly His Phe Tyr Ser Pro Trp Val
2295 2300 2305
atc gac cag att ctt att gga gga aat atc tct ggt aat aca gtc tta 7254
Ile Asp Gln Ile Leu Ile Gly Gly Asn Ile Ser Gly Asn Thr Val Leu
2310 2315 2320
gaa gat gat ttc tca act ctg gac agc aga aag tgg ctg ctt cac cca 7302
Glu Asp Asp Phe Ser Thr Leu Asp Ser Arg Lys Trp Leu Leu His Pro
2325 2330 2335 2340
gga ggc acc aag atg cct gtg tgt ggc tcc aca ggc gat gcc ctg gtc 7350
Gly Gly Thr Lys Met Pro Val Cys Gly Ser Thr Gly Asp Ala Leu Val
2345 2350 2355
ttt att gaa aag gcc agc acc cgt tac gtg gtc acg aca gac atc gct 7398
Phe Ile Glu Lys Ala Ser Thr Arg Tyr Val Val Thr Thr Asp Ile Ala
2360 2365 2370

gtg aat gag gac tca ttc cta cag ata gac ttt gct gcc tcc tgc tca	7446
Val Asn Glu Asp Ser Phe Leu Gln Ile Asp Phe Ala Ala Ser Cys Ser	
2375	2380
2385	
gtc aca gac tcc tgc tat gct att gaa ctg gag tac tcg gtg gat ctc	7494
Val Thr Asp Ser Cys Tyr Ala Ile Glu Leu Glu Tyr Ser Val Asp Leu	
2390	2395
2400	
ggt ctg tcg tgg cac ccg ctg gtg agg gac tgc ctg cct acc aat gtt	7542
Gly Leu Ser Trp His Pro Leu Val Arg Asp Cys Leu Pro Thr Asn Val	
2405	2410
2415	2420
gag tgt agt cgt tac cac ctg cag cgg atc ctg gtg tca gat act ttc	7590
Glu Cys Ser Arg Tyr His Leu Gln Arg Ile Leu Val Ser Asp Thr Phe	
2425	2430
2435	
aac aag tgg acc aga atc act ctg ccc ctg cct tcc tac acc agg tct	7638
Asn Lys Trp Thr Arg Ile Thr Leu Pro Leu Pro Ser Tyr Thr Arg Ser	
2440	2445
2450	
caa gcc act cgt ttc cgc tgg cat cag cca gcg cct ttt gac aag cag	7686
Gln Ala Thr Arg Phe Arg Trp His Gln Pro Ala Pro Phe Asp Lys Gln	
2455	2460
2465	
cag acc tgg gca ata gat aat gtc tat att ggg gat ggt tgc cta gac	7734
Gln Thr Trp Ala Ile Asp Asn Val Tyr Ile Gly Asp Gly Cys Leu Asp	
2470	2475
2480	
atg tgc agt ggc cac ggg aga tgc gtc cag gga agc tgt gtc tgt gat	7782
Met Cys Ser Gly His Gly Arg Cys Val Gln Gly Ser Cys Val Cys Asp	
2485	2490
2495	2500
gaa cag tgg gga ggc ctg tac tgt gat gag cct gag acc tcc ctt ccc	7830
Glu Gln Trp Gly Gly Leu Tyr Cys Asp Glu Pro Glu Thr Ser Leu Pro	
2505	2510
2515	
acc cag ctc aaa gac aac ttc aac cga gcc ccc tcc aac cag aac tgg	7878
Thr Gln Leu Lys Asp Asn Phe Asn Arg Ala Pro Ser Asn Gln Asn Trp	

2520	2525	2530	
ctg act gtg agc ggt ggg aag ctg agt aca gtg tgt ggg gct gtg gct			7926
Leu Thr Val Ser Gly Gly Lys Leu Ser Thr Val Cys Gly Ala Val Ala			
2535	2540	2545	
tcc ggc ctg gct ctc cat ttc agt ggg ggc tgc agc cga ttg tta gtc			7974
Ser Gly Leu Ala Leu His Phe Ser Gly Gly Cys Ser Arg Leu Leu Val			
2550	2555	2560	
act gtg gat ctg aac ctc acc aat gct gag ttt atc cag ttt tac ttt			8022
Thr Val Asp Leu Asn Leu Thr Asn Ala Glu Phe Ile Gln Phe Tyr Phe			
2565	2570	2575	2580
atg tat gga tgc ctc att acg ccg agc aac cgt aac cag gga gtc ctg			8070
Met Tyr Gly Cys Leu Ile Thr Pro Ser Asn Arg Asn Gln Gly Val Leu			
2585	2590	2595	
ctg gag tac tct gtc aat gga ggc atc acc tgg aac ttg ctg atg gag			8118
Leu Glu Tyr Ser Val Asn Gly Gly Ile Thr Trp Asn Leu Leu Met Glu			
2600	2605	2610	
att ttc tat gac cag tac agc aaa cct gga ttt gtg aat atc ctt ctc			8166
Ile Phe Tyr Asp Gln Tyr Ser Lys Pro Gly Phe Val Asn Ile Leu Leu			
2615	2620	2625	
cct cct gat gct aaa gag att gcc act cgc ttc cga tgg tgg cag cca			8214
Pro Pro Asp Ala Lys Glu Ile Ala Thr Arg Phe Arg Trp Trp Gln Pro			
2630	2635	2640	
cga cat gat ggc ctt gac cag aat gac tgg gcc att gac aat gtc ctc			8262
Arg His Asp Gly Leu Asp Gln Asn Asp Trp Ala Ile Asp Asn Val Leu			
2645	2650	2655	2660
atc tcg ggc tct gcg gac cag agg aca gtc atg ctg gac acc ttt agc			8310
Ile Ser Gly Ser Ala Asp Gln Arg Thr Val Met Leu Asp Thr Phe Ser			
2665	2670	2675	
agc gcc cca gta cca cag cat gag cgc tcc ccc gca gac gct ggc cct			8358

Ser Ala Pro Val Pro Gln His Glu Arg Ser Pro Ala Asp Ala Gly Pro
 2680 2685 2690
 gtt gga aga att gct ttt gaa atg ttc tta gaa gac aaa act tca gtg 8406
 Val Gly Arg Ile Ala Phe Glu Met Phe Leu Glu Asp Lys Thr Ser Val
 2695 2700 2705
 aat gag aat tgg ctc ttc cat gat gac tgt aca gtg gaa aga ttc tgt 8454
 Asn Glu Asn Trp Leu Phe His Asp Asp Cys Thr Val Glu Arg Phe Cys
 2710 2715 2720
 gac tcg cca gat ggt gtc atg ctc tgt ggc agc cat gat gga cga gag 8502
 Asp Ser Pro Asp Gly Val Met Leu Cys Gly Ser His Asp Gly Arg Glu
 2725 2730 2735 2740
 gtg tat gca gtg act cat gac ctg acg ccc act gag aac tgg atc atg 8550
 Val Tyr Ala Val Thr His Asp Leu Thr Pro Thr Glu Asn Trp Ile Met
 2745 2750 2755
 cag ttc aag atc tct gtt gga tgc aaa gtg cct gaa aaa att gcc cag 8598
 Gln Phe Lys Ile Ser Val Gly Cys Lys Val Pro Glu Lys Ile Ala Gln
 2760 2765 2770
 aat caa att cac gtg cag ttt tct act gac ttt ggc gtg agc tgg agt 8646
 Asn Gln Ile His Val Gln Phe Ser Thr Asp Phe Gly Val Ser Trp Ser
 2775 2780 2785
 tat tta gtc cct cag tgc tta ccc gcc gac cca aag tgt tct gga agc 8694
 Tyr Leu Val Pro Gln Cys Leu Pro Ala Asp Pro Lys Cys Ser Gly Ser
 2790 2795 2800
 gtt tct caa ccg tct gtg ttc ttc cca act gaa ggg tgg aaa agg atc 8742
 Val Ser Gln Pro Ser Val Phe Phe Pro Thr Glu Gly Trp Lys Arg Ile
 2805 2810 2815 2820
 acc tac ccg ctt cct gaa agc tta acg ggg aat cct gta aga ttt agg 8790
 Thr Tyr Pro Leu Pro Glu Ser Leu Thr Gly Asn Pro Val Arg Phe Arg
 2825 2830 2835

ttc tac caa aag tac tca gat gtg cag tgg gca att gac aat ttc tac 8838
 Phe Tyr Gln Lys Tyr Ser Asp Val Gln Trp Ala Ile Asp Asn Phe Tyr
 2840 2845 2850
 ctt ggc cct gga tgt ttg gac aac tgt gga ggc cac gga gac tgc cta 8886
 Leu Gly Pro Gly Cys Leu Asp Asn Cys Gly Gly His Gly Asp Cys Leu
 2855 2860 2865
 aag gaa cag tgt atc tgt gac cca ggc tac tca ggg cca aac tgc tac 8934
 Lys Glu Gln Cys Ile Cys Asp Pro Gly Tyr Ser Gly Pro Asn Cys Tyr
 2870 2875 2880
 tta act cac agc ctg aag act ttc ctg aag gag cgc ttt gac agt gag 8982
 Leu Thr His Ser Leu Lys Thr Phe Leu Lys Glu Arg Phe Asp Ser Glu
 2885 2890 2895 2900
 gag atc aag cct gac tta tgg atg tcc ttg gaa ggc gga agc act tgt 9030
 Glu Ile Lys Pro Asp Leu Trp Met Ser Leu Glu Gly Gly Ser Thr Cys
 2905 2910 2915
 aca gag tgc ggg gtc ctc gcc gag aac act gca ctc tat ttt ggg gga 9078
 Thr Glu Cys Gly Val Leu Ala Glu Asn Thr Ala Leu Tyr Phe Gly Gly
 2920 2925 2930
 tcc act gtg aga caa gct att act caa gac tta gat ctc aga ggt gca 9126
 Ser Thr Val Arg Gln Ala Ile Thr Gln Asp Leu Asp Leu Arg Gly Ala
 2935 2940 2945
 aaa ttc ctg cag tac tgg gga cgt atc ggc agt gag aac aac atg aca 9174
 Lys Phe Leu Gln Tyr Trp Gly Arg Ile Gly Ser Glu Asn Asn Met Thr
 2950 2955 2960
 tct tgc cat cgg cct gtc tgc cgg aag gaa ggc gtg ctg ctg gac ttc 9222
 Ser Cys His Arg Pro Val Cys Arg Lys Glu Gly Val Leu Leu Asp Phe
 2965 2970 2975 2980
 tct acg gat gga gga atc act tgg acc ttg ctt cac gag atg gat ttc 9270
 Ser Thr Asp Gly Gly Ile Thr Trp Thr Leu Leu His Glu Met Asp Phe

2985	2990	2995	
cag aaa tac att tct gtg agg cac gac tac atc ctc ctg cct gag ggg			9318
Gln Lys Tyr Ile Ser Val Arg His Asp Tyr Ile Leu Leu Pro Glu Gly			
3000	3005	3010	
gcc ctc acc aac aca act cga ctt cgc tgg tgg cag cct ttt gtc atc			9366
Ala Leu Thr Asn Thr Thr Arg Leu Arg Trp Trp Gln Pro Phe Val Ile			
3015	3020	3025	
agc aat ggg ctc gtg gtt tcc ggg gtg gag cgt gcg cag tgg gca ctg			9414
Ser Asn Gly Leu Val Val Ser Gly Val Glu Arg Ala Gln Trp Ala Leu			
3030	3035	3040	
gac aac att ctg att ggt gga gca gaa atc aat cca agc caa ctg gtg			9462
Asp Asn Ile Leu Ile Gly Gly Ala Glu Ile Asn Pro Ser Gln Leu Val			
3045	3050	3055	3060
gac act ttc gat gac gaa ggc tcc tcc cat gaa gaa aac tgg agt ttt			9510
Asp Thr Phe Asp Asp Glu Gly Ser Ser His Glu Glu Asn Trp Ser Phe			
3065	3070	3075	
tac cct aat gca gta agg aca gca gga ttc tgt ggc aac cca tcc ttc			9558
Tyr Pro Asn Ala Val Arg Thr Ala Gly Phe Cys Gly Asn Pro Ser Phe			
3080	3085	3090	
cac ctc tac tgg cca aat aaa aag aag gac aag acc cac aat gca ctc			9606
His Leu Tyr Trp Pro Asn Lys Lys Lys Asp Lys Thr His Asn Ala Leu			
3095	3100	3105	
tcc tcc cga gag ctc att ata cag cca gga tac atg atg caa ttt aaa			9654
Ser Ser Arg Glu Leu Ile Ile Gln Pro Gly Tyr Met Met Gln Phe Lys			
3110	3115	3120	
att gtg gtg ggt tgt gaa gcc act tca tgt ggt gac ctt cat tcc gtg			9702
Ile Val Val Gly Cys Glu Ala Thr Ser Cys Gly Asp Leu His Ser Val			
3125	3130	3135	3140
atg ctg gag tac acc aag gat gca agg tcc gat tcc tgg cag ctc gtg			9750

Met Leu Glu Tyr Thr Lys Asp Ala Arg Ser Asp Ser Trp Gln Leu Val
3145 3150 3155
cag acc cag tgc cta cct tcc tct tcc aat agc att ggc tgc tcc ccg 9798
Gln Thr Gln Cys Leu Pro Ser Ser Ser Asn Ser Ile Gly Cys Ser Pro
3160 3165 3170
ttc cag ttc cat gaa gcc acc att tat aat gct gtc aac agc tca agc 9846
Phe Gln Phe His Glu Ala Thr Ile Tyr Asn Ala Val Asn Ser Ser Ser
3175 3180 3185
tgg aag agg atc acc atc cag ctc cca gac cac gtc tcg tca agt gcc 9894
Trp Lys Arg Ile Thr Ile Gln Leu Pro Asp His Val Ser Ser Ser Ala
3190 3195 3200
aca cag ttc cgc tgg atc cag aag gga gaa gaa acc gag aag caa agc 9942
Thr Gln Phe Arg Trp Ile Gln Lys Gly Glu Glu Thr Glu Lys Gln Ser
3205 3210 3215 3220
tgg gcc atc gac cac gtg tac atc gga gag gct tgt ccc aag ctc tgc 9990
Trp Ala Ile Asp His Val Tyr Ile Gly Glu Ala Cys Pro Lys Leu Cys
3225 3230 3235
agc ggg cat ggc tac tgc acc aca ggg gcc gtc tgc atc tgc gat gaa 10038
Ser Gly His Gly Tyr Cys Thr Thr Gly Ala Val Cys Ile Cys Asp Glu
3240 3245 3250
agc ttc caa ggt gac gac tgc tct gtc ttc agt cac gag ctt cct agt 10086
Ser Phe Gln Gly Asp Asp Cys Ser Val Phe Ser His Glu Leu Pro Ser
3255 3260 3265
tac att aaa gat aat ttt gaa tca gca aga gtc act gaa gcc aac tgg 10134
Tyr Ile Lys Asp Asn Phe Glu Ser Ala Arg Val Thr Glu Ala Asn Trp
3270 3275 3280
gaa acc atc cag ggt gga gtg atc gga agt ggc tgt ggg cag ctg gcg 10182
Glu Thr Ile Gln Gly Gly Val Ile Gly Ser Gly Cys Gly Gln Leu Ala
3285 3290 3295 3300

ccc tat gcc cat gga gat tgc ctc tac ttt aat ggt tgt cag ata agg 10230
 Pro Tyr Ala His Gly Asp Ser Leu Tyr Phe Asn Gly Cys Gln Ile Arg
 3305 3310 3315
 caa gct gcc acc aag cca ctg gac ctc act cga gca agc aaa att atg 10278
 Gln Ala Ala Thr Lys Pro Leu Asp Leu Thr Arg Ala Ser Lys Ile Met
 3320 3325 3330
 ttt gtc ttg caa att ggg agc cca gcc cag aca gac agt tgc aac agc 10326
 Phe Val Leu Gln Ile Gly Ser Pro Ala Gln Thr Asp Ser Cys Asn Ser
 3335 3340 3345
 gac ctc agc ggc ccc cac acc gtg gac aaa gca gta ctg ctg cag tac 10374
 Asp Leu Ser Gly Pro His Thr Val Asp Lys Ala Val Leu Leu Gln Tyr
 3350 3355 3360
 agt gtc aac aat ggc atc acc tgg cac gtc atc gct cag cac cag ccg 10422
 Ser Val Asn Asn Gly Ile Thr Trp His Val Ile Ala Gln His Gln Pro
 3365 3370 3375 3380
 aag gac ttc aca caa gct cag cgg gtg tct tac aac gtc ccc ctg gaa 10470
 Lys Asp Phe Thr Gln Ala Gln Arg Val Ser Tyr Asn Val Pro Leu Glu
 3385 3390 3395
 gct cgg atg aaa gga gtt cta ctg cgc tgg tgg cag cca cgc cac aat 10518
 Ala Arg Met Lys Gly Val Leu Leu Arg Trp Trp Gln Pro Arg His Asn
 3400 3405 3410
 gga aca ggt cat gat caa tgg gct ttg gac cat gtg gag gtc gtc cta 10566
 Gly Thr Gly His Asp Gln Trp Ala Leu Asp His Val Glu Val Val Leu
 3415 3420 3425
 gta agc act cgc aaa caa aat tac atg atg aat ttt tca cgg caa cat 10614
 Val Ser Thr Arg Lys Gln Asn Tyr Met Met Asn Phe Ser Arg Gln His
 3430 3435 3440
 ggg ctc agg cac ttc tac aac aga aga cga agg tgc ctt agg cga tac 10662
 Gly Leu Arg His Phe Tyr Asn Arg Arg Arg Arg Ser Leu Arg Arg Tyr

3445 3450 3455 3460
 cca tga agaatccaag tttatttccc tttccagcgt acaatgtgtc ccttcctggt 10718
 Pro
 tttttgaaac acctctcact gcatctgata tcaggaaaca aagatgaagg acttggcgaa 10778
 cagaaagccc ttcgagatct tgtgtacccc accttcccac actgtgagct aatgatgtgt 10838
 ggtttctctg cacataagta aatgtcttca cgtcagtgcg tccgtggaaa ttgtgatctg 10898
 ttgtaatatc agttacagtg gcagtattga gaataagaaa tagtttaaca ggaaaaaacg 10958
 ttttaagcaca aacattttta agatcttatg ttttaagtgg catttttagca cagtatttaa 11018
 cattgtttgt caccgagcta ttttaagtaga ctgtatttca gctctgtctc ttgtttaata 11078
 tgaataagtt ctgctcggtt gtcccttatg tattcttctc taccgataaa cacactgaaa 11138
 ctgtatctac ttgctgtgtt gcaatatatt gctgctggac ttgacctac ttgtattatg 11198
 cagaaagita atgcagatac ctattcaaga tgataactgt aaagacactg ctgctcctt 11258
 aatatgctcc ttaacacgta tgttgatgta gcatcatttt gtggatagga aaaaaaatgt 11318
 ttgaccttca gatattttct acctaaaaaa ttgtggatga acgccctatc tccctcccac 11378
 agtgagtcce cattaccttg tctaaaacaa ttttttaatg tgttctgttg ccgttttact 11438
 gacagtaact gccatttcgt gtctgtggta acaaagtgac ttgtaaaatg gtggatgttt 11498
 ccctcactgt gttctcttcg tgggttggtt ccttgtgggt catagtcata ccttctgatg 11558
 aggtggagcc aacaccagca aagtatgatg gccctgtagc ctctgactag tcctgaaaca 11618
 gaaggctgca ctctaggctg aacctatgta aaagcccatg cttaaataaa aaatg 11673

<210> 129

<211> 3461

<212> PRT

<213> Mus musculus

<400> 129

Met Glu Arg Gly Cys Trp Ala Pro Arg Ala Leu Val Leu Ala Val Leu

1

5

10

15

Leu Leu Leu Ala Thr Leu Arg Ala Arg Ala Ala Thr Gly Tyr Tyr Pro

20	25	30
Arg Phe Ser Pro Phe Phe Phe Leu Cys Thr His His Gly Glu Leu Glu		
35	40	45
Gly Asp Gly Glu Gln Gly Glu Val Leu Ile Ser Leu His Ile Ala Gly		
50	55	60
Asn Pro Thr Tyr Tyr Val Pro Gly Gln Glu Tyr His Val Thr Ile Ser		
65	70	75
Thr Ser Thr Phe Phe Asp Gly Leu Leu Val Thr Gly Leu Tyr Thr Ser		
85	90	95
Thr Ser Ile Gln Ser Ser Gln Ser Ile Gly Gly Ser Ser Ala Phe Gly		
100	105	110
Phe Gly Ile Met Ser Asp His Gln Phe Gly Asn Gln Phe Met Cys Ser		
115	120	125
Val Val Ala Ser His Val Ser His Leu Pro Thr Thr Asn Leu Ser Phe		
130	135	140
Val Trp Ile Ala Pro Pro Ala Gly Thr Gly Cys Val Asn Phe Met Ala		
145	150	155
Thr Ala Thr His Arg Gly Gln Val Ile Phe Lys Asp Ala Leu Ala Gln		
165	170	175
Gln Leu Cys Glu Gln Gly Ala Pro Thr Glu Ala Thr Ala Tyr Ser His		
180	185	190
Leu Ala Glu Ile His Ser Asp Ser Val Ile Leu Arg Asp Asp Phe Asp		
195	200	205
Ser Tyr Gln Gln Leu Glu Leu Asn Pro Asn Ile Trp Val Glu Cys Ser		
210	215	220
Asn Cys Glu Met Gly Glu Gln Cys Gly Thr Ile Met His Gly Asn Ala		
225	230	235
Val Thr Phe Cys Glu Pro Tyr Gly Pro Arg Glu Leu Thr Thr Thr Cys		
245	250	255

Leu Asn Thr Thr Thr Ala Ser Val Leu Gln Phe Ser Ile Gly Ser Gly
 260 265 270
 Ser Cys Arg Phe Ser Tyr Ser Asp Pro Ser Ile Thr Val Ser Tyr Ala
 275 280 285
 Lys Asn Asn Thr Ala Asp Trp Ile Gln Leu Glu Lys Ile Arg Ala Pro
 290 295 300
 Ser Asn Val Ser Thr Val Ile His Ile Leu Tyr Leu Pro Glu Glu Ala
 305 310 315 320
 Lys Gly Glu Ser Val Gln Phe Gln Trp Lys Gln Asp Ser Leu Arg Val
 325 330 335
 Gly Glu Val Tyr Glu Ala Cys Trp Ala Leu Asp Asn Ile Leu Val Ile
 340 345 350
 Asn Ser Ala His Arg Glu Val Val Leu Glu Asp Asn Leu Asp Pro Val
 355 360 365
 Asp Thr Gly Asn Trp Leu Phe Phe Pro Gly Ala Thr Val Lys His Ser
 370 375 380
 Cys Gln Ser Asp Gly Asn Ser Ile Tyr Phe His Gly Asn Glu Gly Ser
 385 390 395 400
 Glu Phe Asn Phe Ala Thr Thr Arg Asp Val Asp Leu Ser Thr Glu Asp
 405 410 415
 Ile Gln Glu Gln Trp Ser Glu Glu Phe Glu Ser Gln Pro Thr Gly Trp
 420 425 430
 Asp Ile Leu Gly Ala Val Val Gly Ala Asp Cys Gly Thr Val Glu Ser
 435 440 445
 Gly Leu Ser Leu Val Phe Leu Lys Asp Gly Glu Arg Lys Leu Cys Thr
 450 455 460
 Pro Tyr Met Asp Thr Thr Gly Tyr Gly Asn Leu Arg Phe Tyr Phe Val
 465 470 475 480
 Met Gly Gly Ile Cys Asp Pro Gly Val Ser His Glu Asn Asp Ile Ile

	485	490	495
Leu Tyr Ala Lys Ile Glu Gly Arg Lys Glu His Ile Ala Leu Asp Thr			
500	505	510	
Leu Thr Tyr Ser Ser Tyr Lys Val Pro Ser Leu Val Ser Val Val Ile			
515	520	525	
Asn Pro Glu Leu Gln Thr Pro Ala Thr Lys Phe Cys Leu Arg Gln Lys			
530	535	540	
Ser His Gln Gly Tyr Asn Arg Asn Val Trp Ala Val Asp Phe Phe His			
545	550	555	560
Val Leu Pro Val Leu Pro Ser Thr Met Ser His Met Ile Gln Phe Ser			
565	570	575	
Ile Asn Leu Gly Cys Gly Thr His Gln Pro Gly Asn Ser Val Ser Leu			
580	585	590	
Glu Phe Ser Thr Asn His Gly Arg Ser Trp Ser Leu Leu His Thr Glu			
595	600	605	
Cys Leu Pro Glu Ile Cys Ala Gly Pro His Leu Pro His Ser Thr Val			
610	615	620	
Tyr Ser Ser Glu Asn Tyr Ser Gly Trp Asn Arg Ile Thr Ile Pro Leu			
625	630	635	640
Pro Asn Ala Ala Leu Thr Arg Asp Thr Arg Ile Arg Trp Arg Gln Thr			
645	650	655	
Gly Pro Ile Leu Gly Asn Met Trp Ala Ile Asp Asn Val Tyr Ile Gly			
660	665	670	
Pro Ser Cys Leu Lys Phe Cys Ser Gly Arg Gly Gln Cys Thr Arg His			
675	680	685	
Gly Cys Lys Cys Asp Pro Gly Phe Ser Gly Pro Ala Cys Glu Met Ala			
690	695	700	
Ser Gln Thr Phe Pro Met Phe Ile Ser Glu Ser Phe Gly Ser Ala Arg			
705	710	715	720

Leu Ser Ser Tyr His Asn Phe Tyr Ser Ile Arg Gly Ala Glu Val Ser
 725 730 735
 Phe Gly Cys Gly Val Leu Ala Ser Gly Lys Ala Leu Val Phe Asn Lys
 740 745 750
 Asp Gly Arg Arg Gln Leu Ile Thr Ser Phe Leu Asp Ser Ser Gln Ser
 755 760 765
 Arg Phe Leu Gln Phe Thr Leu Arg Leu Gly Ser Lys Ser Val Leu Ser
 770 775 780
 Thr Cys Arg Ala Pro Asp Gln Pro Gly Glu Gly Val Leu Leu His Tyr
 785 790 795 800
 Ser Tyr Asp Asn Gly Ile Thr Trp Lys Leu Leu Glu His Tyr Ser Tyr
 805 810 815
 Val Asn Tyr His Glu Pro Arg Ile Ile Ser Val Glu Leu Pro Asp Asp
 820 825 830
 Ala Arg Gln Phe Gly Ile Gln Phe Arg Trp Trp Gln Pro Tyr His Ser
 835 840 845
 Ser Gln Gly Glu Asp Val Trp Ala Ile Asp Glu Ile Val Met Thr Ser
 850 855 860
 Val Leu Phe Asn Ser Ile Ser Leu Asp Phe Thr Asn Leu Val Glu Val
 865 870 875 880
 Thr Gln Ser Leu Gly Phe Tyr Leu Gly Asn Val Gln Pro Tyr Cys Gly
 885 890 895
 His Asp Trp Thr Leu Cys Phe Thr Gly Asp Ser Lys Leu Ala Ser Ser
 900 905 910
 Met Arg Tyr Val Glu Thr Gln Ser Met Gln Ile Gly Ala Ser Tyr Met
 915 920 925
 Ile Gln Phe Ser Leu Val Met Gly Cys Gly Gln Lys Tyr Thr Pro His
 930 935 940
 Met Asp Asn Gln Val Lys Leu Glu Tyr Ser Ala Asn His Gly Leu Thr

945	950	955	960
Trp His Leu Val Gln Glu Glu Cys Leu Pro Ser Met Pro Ser Cys Gln			
	965	970	975
Glu Phe Thr Ser Ala Ser Ile Tyr His Ala Ser Glu Phe Thr Gln Trp			
	980	985	990
Arg Arg Val Thr Val Val Leu Pro Gln Lys Thr Trp Ser Gly Ala Thr			
	995	1000	1005
Arg Phe Arg Trp Ser Gln Ser Tyr Tyr Thr Ala Gln Asp Glu Trp Ala			
1010	1015	1020	
Leu Asp Asn Ile Tyr Ile Gly Gln Gln Cys Pro Asn Met Cys Ser Gly			
025	1030	1035	1040
His Gly Ser Cys Asp His Gly Val Cys Arg Cys Asp Gln Gly Tyr Gln			
	1045	1050	1055
Gly Thr Glu Cys His Pro Glu Ala Ala Leu Pro Ser Thr Ile Met Ser			
	1060	1065	1070
Asp Phe Glu Asn Pro Ser Ser Trp Glu Ser Asp Trp Gln Glu Val Ile			
	1075	1080	1085
Gly Gly Glu Val Val Lys Pro Glu Gln Gly Cys Gly Val Val Ser Ser			
1090	1095	1100	
Gly Ser Ser Leu Tyr Phe Ser Lys Ala Gly Lys Arg Gln Leu Val Ser			
105	1110	1115	1120
Trp Asp Leu Asp Thr Ser Trp Val Asp Phe Val Gln Phe Tyr Ile Gln			
	1125	1130	1135
Ile Gly Gly Glu Ser Ala Ala Cys Asn Lys Pro Asp Ser Arg Glu Glu			
	1140	1145	1150
Gly Ile Leu Leu Gln Tyr Ser Asn Asn Gly Gly Ile Gln Trp His Leu			
	1155	1160	1165
Leu Ala Glu Met Tyr Phe Ser Asp Phe Ser Lys Pro Arg Phe Val Tyr			
1170	1175	1180	

Leu Glu Leu Pro Ala Ala Gly Lys Thr Pro Cys Thr Arg Phe Arg Trp
 185 1190 1195 1200
 Trp Lys Pro Val Phe Ser Gly Glu Asp Tyr Asp Gln Trp Ala Val Asp
 1205 1210 1215
 Asp Ile Ile Ile Leu Ser Glu Lys Gln Lys Gln Val Ile Pro Val Val
 1220 1225 1230
 Asn Pro Thr Leu Pro Gln Asn Phe Tyr Glu Lys Pro Ala Phe Asp Tyr
 1235 1240 1245
 Pro Met Asn Gln Met Ser Val Trp Leu Met Leu Ala Asn Glu Gly Met
 1250 1255 1260
 Ala Lys Asn Asp Ser Phe Cys Ala Thr Thr Pro Ser Ala Met Val Phe
 265 1270 1275 1280
 Gly Lys Ser Asp Gly Asp Arg Phe Ala Val Thr Arg Asp Leu Thr Leu
 1285 1290 1295
 Lys Pro Gly Tyr Val Leu Gln Phe Lys Leu Asn Ile Gly Cys Thr Ser
 1300 1305 1310
 Gln Phe Ser Ser Thr Ala Pro Val Leu Leu Gln Tyr Ser His Asp Ala
 1315 1320 1325
 Gly Met Ser Trp Phe Leu Leu Lys Glu Gly Cys Phe Pro Ala Ser Ala
 1330 1335 1340
 Ala Lys Gly Cys Glu Gly Asn Ser Arg Glu Leu Ser Glu Pro Thr Val
 345 1350 1355 1360
 Tyr Tyr Thr Gly Asp Phe Glu Glu Trp Thr Arg Ile Thr Ile Ala Ile
 1365 1370 1375
 Pro Arg Ser Leu Ala Ser Ser Lys Thr Arg Phe Arg Trp Ile Gln Glu
 1380 1385 1390
 Ser Ser Ser Gln Lys Asn Val Pro Pro Phe Gly Leu Asp Gly Val Tyr
 1395 1400 1405
 Ile Ser Glu Pro Cys Pro Ser Tyr Cys Ser Gly His Gly Asp Cys Ile

1410	1415	1420	
Ser Gly Val Cys Phe Cys Asp Leu Gly Tyr Thr Ala Ala Gln Gly Thr			
425	1430	1435	1440
Cys Val Ser Asn Thr Pro Asn His Ser Glu Met Phe Asp Arg Phe Glu			
1445	1450	1455	
Gly Lys Leu Ser Pro Leu Trp Tyr Lys Ile Thr Gly Gly Gln Val Gly			
1460	1465	1470	
Thr Gly Cys Gly Thr Leu Asn Asp Gly Arg Ser Leu Tyr Phe Asn Gly			
1475	1480	1485	
Leu Gly Lys Arg Glu Ala Arg Thr Val Pro Leu Asp Thr Arg Asn Ile			
1490	1495	1500	
Ser Leu Val Gln Phe Tyr Ile Gln Ile Gly Ser Lys Thr Ser Gly Ile			
505	1510	1515	1520
Thr Tyr Ile Thr Pro Arg Ala Arg Tyr Glu Gly Leu Val Val Gln Tyr			
1525	1530	1535	
Ser Asn Asp Asn Gly Ile Leu Trp His Leu Leu Arg Glu Leu Asp Phe			
1540	1545	1550	
Met Ser Phe Leu Glu Pro Gln Ile Ile Ser Ile Asp Leu Pro Arg Glu			
1555	1560	1565	
Ala Lys Thr Pro Ala Thr Ala Phe Arg Trp Trp Gln Pro Gln His Gly			
1570	1575	1580	
Lys His Ser Ala Gln Trp Ala Leu Gly Asp Val Leu Ile Gly Val Asn			
585	1590	1595	1600
Asp Ser Ser Gln Thr Gly Phe Gln Asp Lys Leu Asp Gly Ser Ile Asp			
1605	1610	1615	
Leu Gln Ala Asn Trp Tyr Arg Ile Gln Gly Gly Gln Val Asp Ile Asp			
1620	1625	1630	
Cys Leu Ser Met Asp Thr Ala Leu Ile Phe Thr Glu Asn Ile Gly Asn			
1635	1640	1645	

Pro Arg Tyr Ala Glu Thr Trp Asp Phe His Val Ser Glu Ser Ser Phe
 1650 1655 1660
 Leu Gln Trp Glu Met Asn Met Gly Cys Ser Lys Pro Phe Ser Gly Ala
 665 1670 1675 1680
 His Gly Ile Gln Leu Gln Tyr Ser Leu Asn Asn Gly Lys Asp Trp Gln
 1685 1690 1695
 Leu Val Thr Glu Glu Cys Val Pro Pro Thr Ile Gly Cys Val His Tyr
 1700 1705 1710
 Thr Glu Ser Ser Thr Tyr Thr Ser Glu Arg Phe Gln Asn Trp Arg Arg
 1715 1720 1725
 Val Thr Val Tyr Leu Pro Leu Ala Thr Asn Ser Pro Arg Thr Arg Phe
 1730 1735 1740
 Arg Trp Ile Gln Thr Asn Tyr Thr Val Gly Ala Asp Ser Trp Ala Ile
 745 1750 1755 1760
 Asp Asn Val Ile Leu Ala Ser Gly Cys Pro Trp Met Cys Ser Gly Arg
 1765 1770 1775
 Gly Ile Cys Asp Ser Gly Arg Cys Val Cys Asp Arg Gly Phe Gly Gly
 1780 1785 1790
 Pro Phe Cys Val Pro Val Val Pro Leu Pro Ser Ile Leu Lys Asp Asp
 1795 1800 1805
 Phe Asn Gly Asn Leu His Pro Asp Leu Trp Pro Glu Val Tyr Gly Ala
 1810 1815 1820
 Glu Arg Gly Asn Leu Asn Gly Glu Thr Ile Lys Ser Gly Thr Cys Leu
 825 1830 1835 1840
 Ile Phe Lys Gly Glu Gly Leu Arg Met Leu Ile Ser Arg Asp Leu Asp
 1845 1850 1855
 Cys Thr Asn Thr Met Tyr Val Gln Phe Ser Leu Arg Phe Ile Ala Lys
 1860 1865 1870
 Gly Thr Pro Glu Arg Ser His Ser Ile Leu Leu Gln Phe Ser Val Ser

1875	1880	1885	
Gly Gly Val Thr Trp His Leu Met Asp Glu Phe Tyr Phe Pro Gln Thr			
1890	1895	1900	
Thr Ser Ile Leu Phe Ile Asn Val Pro Leu Pro Tyr Gly Ala Gln Thr			
905	1910	1915	1920
Asn Ala Thr Arg Phe Arg Leu Trp Gln Pro Tyr Asn Asn Gly Lys Lys			
	1925	1930	1935
Glu Glu Ile Trp Ile Ile Asp Asp Phe Ile Ile Asp Gly Asn Asn Leu			
	1940	1945	1950
Asn Asn Pro Val Leu Leu Leu Asp Thr Phe Asp Phe Gly Pro Arg Glu			
	1955	1960	1965
Asp Asn Trp Phe Phe Tyr Pro Gly Gly Asn Ile Gly Leu Tyr Cys Pro			
1970	1975	1980	
Tyr Ser Ser Lys Gly Ala Pro Glu Glu Asp Ser Ala Met Val Phe Val			
985	1990	1995	2000
Ser Asn Glu Val Gly Glu His Ser Ile Thr Thr Arg Asp Leu Ser Val			
	2005	2010	2015
Asn Glu Asn Thr Ile Ile Gln Phe Glu Ile Asn Val Gly Cys Ser Thr			
	2020	2025	2030
Asp Ser Ser Ser Ala Asp Pro Val Arg Leu Glu Phe Ser Arg Asp Phe			
	2035	2040	2045
Gly Ala Thr Trp His Leu Leu Leu Pro Leu Cys Tyr His Ser Ser Ser			
2050	2055	2060	
Leu Val Ser Ser Leu Cys Ser Thr Glu His His Pro Ser Ser Thr Tyr			
065	2070	2075	2080
Tyr Ala Gly Thr Thr Gln Gly Trp Arg Arg Glu Val Val His Phe Gly			
	2085	2090	2095
Lys Leu His Leu Cys Gly Ser Val Arg Phe Arg Trp Tyr Gln Gly Phe			
2100	2105	2110	

Tyr Pro Ala Gly Ser Gln Pro Val Thr Trp Ala Ile Asp Asn Val Tyr
 2115 2120 2125
 Ile Gly Pro Gln Cys Glu Glu Met Cys Tyr Gly His Gly Ser Cys Ile
 2130 2135 2140
 Asn Gly Thr Lys Cys Ile Cys Asp Pro Gly Tyr Ser Gly Pro Thr Cys
 145 2150 2155 2160
 Lys Ile Ser Thr Lys Asn Pro Asp Phe Leu Lys Asp Asp Phe Glu Gly
 2165 2170 2175
 Gln Leu Glu Ser Asp Arg Phe Leu Leu Met Ser Gly Gly Lys Pro Ser
 2180 2185 2190
 Arg Lys Cys Gly Ile Leu Ser Ser Gly Asn Asn Leu Phe Phe Asn Glu
 2195 2200 2205
 Asp Gly Leu Arg Met Leu Val Thr Arg Asp Leu Asp Leu Ser His Ala
 2210 2215 2220
 Arg Phe Val Gln Phe Phe Met Arg Leu Gly Cys Gly Lys Gly Val Pro
 225 2230 2235 2240
 Asp Pro Arg Ser Gln Pro Val Leu Leu Gln Tyr Ser Leu Asn Gly Gly
 2245 2250 2255
 Leu Ser Trp Ser Leu Leu Gln Glu Phe Leu Phe Ser Asn Ser Ser Asn
 2260 2265 2270
 Val Gly Arg Tyr Ile Ala Leu Glu Met Pro Leu Lys Ala Arg Ser Gly
 2275 2280 2285
 Ser Thr Arg Leu Arg Trp Trp Gln Pro Ser Glu Asn Gly His Phe Tyr
 2290 2295 2300
 Ser Pro Trp Val Ile Asp Gln Ile Leu Ile Gly Gly Asn Ile Ser Gly
 305 2310 2315 2320
 Asn Thr Val Leu Glu Asp Asp Phe Ser Thr Leu Asp Ser Arg Lys Trp
 2325 2330 2335
 Leu Leu His Pro Gly Gly Thr Lys Met Pro Val Cys Gly Ser Thr Gly

2340	2345	2350
Asp Ala Leu Val Phe Ile Glu Lys Ala Ser Thr Arg Tyr Val Val Thr		
2355	2360	2365
Thr Asp Ile Ala Val Asn Glu Asp Ser Phe Leu Gln Ile Asp Phe Ala		
2370	2375	2380
Ala Ser Cys Ser Val Thr Asp Ser Cys Tyr Ala Ile Glu Leu Glu Tyr		
385	2390	2395
Ser Val Asp Leu Gly Leu Ser Trp His Pro Leu Val Arg Asp Cys Leu		
2405	2410	2415
Pro Thr Asn Val Glu Cys Ser Arg Tyr His Leu Gln Arg Ile Leu Val		
2420	2425	2430
Ser Asp Thr Phe Asn Lys Trp Thr Arg Ile Thr Leu Pro Leu Pro Ser		
2435	2440	2445
Tyr Thr Arg Ser Gln Ala Thr Arg Phe Arg Trp His Gln Pro Ala Pro		
2450	2455	2460
Phe Asp Lys Gln Gln Thr Trp Ala Ile Asp Asn Val Tyr Ile Gly Asp		
465	2470	2475
Gly Cys Leu Asp Met Cys Ser Gly His Gly Arg Cys Val Gln Gly Ser		
2485	2490	2495
Cys Val Cys Asp Glu Gln Trp Gly Gly Leu Tyr Cys Asp Glu Pro Glu		
2500	2505	2510
Thr Ser Leu Pro Thr Gln Leu Lys Asp Asn Phe Asn Arg Ala Pro Ser		
2515	2520	2525
Asn Gln Asn Trp Leu Thr Val Ser Gly Gly Lys Leu Ser Thr Val Cys		
2530	2535	2540
Gly Ala Val Ala Ser Gly Leu Ala Leu His Phe Ser Gly Gly Cys Ser		
545	2550	2555
Arg Leu Leu Val Thr Val Asp Leu Asn Leu Thr Asn Ala Glu Phe Ile		
2565	2570	2575

Gln Phe Tyr Phe Met Tyr Gly Cys Leu Ile Thr Pro Ser Asn Arg Asn
 2580 2585 2590
 Gln Gly Val Leu Leu Glu Tyr Ser Val Asn Gly Gly Ile Thr Trp Asn
 2595 2600 2605
 Leu Leu Met Glu Ile Phe Tyr Asp Gln Tyr Ser Lys Pro Gly Phe Val
 2610 2615 2620
 Asn Ile Leu Leu Pro Pro Asp Ala Lys Glu Ile Ala Thr Arg Phe Arg
 625 2630 2635 2640
 Trp Trp Gln Pro Arg His Asp Gly Leu Asp Gln Asn Asp Trp Ala Ile
 2645 2650 2655
 Asp Asn Val Leu Ile Ser Gly Ser Ala Asp Gln Arg Thr Val Met Leu
 2660 2665 2670
 Asp Thr Phe Ser Ser Ala Pro Val Pro Gln His Glu Arg Ser Pro Ala
 2675 2680 2685
 Asp Ala Gly Pro Val Gly Arg Ile Ala Phe Glu Met Phe Leu Glu Asp
 2690 2695 2700
 Lys Thr Ser Val Asn Glu Asn Trp Leu Phe His Asp Asp Cys Thr Val
 705 2710 2715 2720
 Glu Arg Phe Cys Asp Ser Pro Asp Gly Val Met Leu Cys Gly Ser His
 2725 2730 2735
 Asp Gly Arg Glu Val Tyr Ala Val Thr His Asp Leu Thr Pro Thr Glu
 2740 2745 2750
 Asn Trp Ile Met Gln Phe Lys Ile Ser Val Gly Cys Lys Val Pro Glu
 2755 2760 2765
 Lys Ile Ala Gln Asn Gln Ile His Val Gln Phe Ser Thr Asp Phe Gly
 2770 2775 2780
 Val Ser Trp Ser Tyr Leu Val Pro Gln Cys Leu Pro Ala Asp Pro Lys
 785 2790 2795 2800
 Cys Ser Gly Ser Val Ser Gln Pro Ser Val Phe Phe Pro Thr Glu Gly

2805	2810	2815
Trp Lys Arg Ile Thr Tyr Pro Leu Pro Glu Ser Leu Thr Gly Asn Pro		
2820	2825	2830
Val Arg Phe Arg Phe Tyr Gln Lys Tyr Ser Asp Val Gln Trp Ala Ile		
2835	2840	2845
Asp Asn Phe Tyr Leu Gly Pro Gly Cys Leu Asp Asn Cys Gly Gly His		
2850	2855	2860
Gly Asp Cys Leu Lys Glu Gln Cys Ile Cys Asp Pro Gly Tyr Ser Gly		
865	2870	2875
Pro Asn Cys Tyr Leu Thr His Ser Leu Lys Thr Phe Leu Lys Glu Arg		2880
2885	2890	2895
Phe Asp Ser Glu Glu Ile Lys Pro Asp Leu Trp Met Ser Leu Glu Gly		
2900	2905	2910
Gly Ser Thr Cys Thr Glu Cys Gly Val Leu Ala Glu Asn Thr Ala Leu		
2915	2920	2925
Tyr Phe Gly Gly Ser Thr Val Arg Gln Ala Ile Thr Gln Asp Leu Asp		
2930	2935	2940
Leu Arg Gly Ala Lys Phe Leu Gln Tyr Trp Gly Arg Ile Gly Ser Glu		
945	2950	2955
Asn Asn Met Thr Ser Cys His Arg Pro Val Cys Arg Lys Glu Gly Val		2960
2965	2970	2975
Leu Leu Asp Phe Ser Thr Asp Gly Gly Ile Thr Trp Thr Leu Leu His		
2980	2985	2990
Glu Met Asp Phe Gln Lys Tyr Ile Ser Val Arg His Asp Tyr Ile Leu		
2995	3000	3005
Leu Pro Glu Gly Ala Leu Thr Asn Thr Thr Arg Leu Arg Trp Trp Gln		
3010	3015	3020
Pro Phe Val Ile Ser Asn Gly Leu Val Val Ser Gly Val Glu Arg Ala		
025	3030	3035
		3040

Gln Trp Ala Leu Asp Asn Ile Leu Ile Gly Gly Ala Glu Ile Asn Pro
 3045 3050 3055
 Ser Gln Leu Val Asp Thr Phe Asp Asp Glu Gly Ser Ser His Glu Glu
 3060 3065 3070
 Asn Trp Ser Phe Tyr Pro Asn Ala Val Arg Thr Ala Gly Phe Cys Gly
 3075 3080 3085
 Asn Pro Ser Phe His Leu Tyr Trp Pro Asn Lys Lys Lys Asp Lys Thr
 3090 3095 3100
 His Asn Ala Leu Ser Ser Arg Glu Leu Ile Ile Gln Pro Gly Tyr Met
 105 3110 3115 3120
 Met. Gln Phe Lys Ile Val Val Gly Cys Glu Ala Thr Ser Cys Gly Asp
 3125 3130 3135
 Leu His Ser Val Met Leu Glu Tyr Thr Lys Asp Ala Arg Ser Asp Ser
 3140 3145 3150
 Trp Gln Leu Val Gln Thr Gln Cys Leu Pro Ser Ser Ser Asn Ser Ile
 3155 3160 3165
 Gly Cys Ser Pro Phe Gln Phe His Glu Ala Thr Ile Tyr Asn Ala Val
 3170 3175 3180
 Asn Ser Ser Ser Trp Lys Arg Ile Thr Ile Gln Leu Pro Asp His Val
 185 3190 3195 3200
 Ser Ser Ser Ala Thr Gln Phe Arg Trp Ile Gln Lys Gly Glu Glu Thr
 3205 3210 3215
 Glu Lys Gln Ser Trp Ala Ile Asp His Val Tyr Ile Gly Glu Ala Cys
 3220 3225 3230
 Pro Lys Leu Cys Ser Gly His Gly Tyr Cys Thr Thr Gly Ala Val Cys
 3235 3240 3245
 Ile Cys Asp Glu Ser Phe Gln Gly Asp Asp Cys Ser Val Phe Ser His
 3250 3255 3260
 Glu Leu Pro Ser Tyr Ile Lys Asp Asn Phe Glu Ser Ala Arg Val Thr

265 3270 3275 3280
 Glu Ala Asn Trp Glu Thr Ile Gln Gly Gly Val Ile Gly Ser Gly Cys
 3285 3290 3295
 Gly Gln Leu Ala Pro Tyr Ala His Gly Asp Ser Leu Tyr Phe Asn Gly
 3300 3305 3310
 Cys Gln Ile Arg Gln Ala Ala Thr Lys Pro Leu Asp Leu Thr Arg Ala
 3315 3320 3325
 Ser Lys Ile Met Phe Val Leu Gln Ile Gly Ser Pro Ala Gln Thr Asp
 3330 3335 3340
 Ser Cys Asn Ser Asp Leu Ser Gly Pro His Thr Val Asp Lys Ala Val
 345 3350 3355 3360
 Leu Leu Gln Tyr Ser Val Asn Asn Gly Ile Thr Trp His Val Ile Ala
 3365 3370 3375
 Gln His Gln Pro Lys Asp Phe Thr Gln Ala Gln Arg Val Ser Tyr Asn
 3380 3385 3390
 Val Pro Leu Glu Ala Arg Met Lys Gly Val Leu Leu Arg Trp Trp Gln
 3395 3400 3405
 Pro Arg His Asn Gly Thr Gly His Asp Gln Trp Ala Leu Asp His Val
 3410 3415 3420
 Glu Val Val Leu Val Ser Thr Arg Lys Gln Asn Tyr Met Met Asn Phe
 425 3430 3435 3440
 Ser Arg Gln His Gly Leu Arg His Phe Tyr Asn Arg Arg Arg Arg Ser
 3445 3450 3455
 Leu Arg Arg Tyr Pro
 3460

<210> 130

<211> 483

<212> DNA

<213> Mus musculus

<400> 130

```

cttctctcac agaggcacc agagcagaca cccgccgctc agcgacgact gcccgccgc 60
cacgatgcta ggtaacaagc gaatggggct gtgtggactg accctcgctc tctctctgct 120
cgtgtgtttg ggcattctgg ctgaggggta cccctccaag ccggacaatc cgggcgagga 180
cgcgccacga gaggacatgg ccagatacta ctccgctctg cgacactaca tcaatctcat 240
caccagacag agatatggca agagatccag ccctgagaca ctgatttcag acctcttaat 300
gaaggaaagc acagaaaacg cccccagAAC aaggcttgaa gacccttcca tgttgtgatg 360
ggaaatgaaa ctgtttctcc cgacttttcc aagtttccac cctcatctca tctcatcccc 420
tgaaaccagt ctgcctgtcc caccaatgca tgccaccact aggcctggact ccgccccatt 480
tcc 483

```

<210> 131

<211> 3141

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (493).. (2118)

<400> 131

```

ggtgaagaga ggggaggaag gagtgaaggg caggaagtga agttagagca ttaaaggacg 60
cctgctcatg aagaccctcc caggctataa cgggcgcctt ggtgaatgca atggccatcg 120
gctgtgggag ttctgacaaa ggatagatgc aacctgggtgc gcatttcttt ctttcttctt 180
tttttctctg gtgcgccttt caaaaggatc gctcggagta ctctgtaaag aaacagctgc 240
aggtggccag ggacggaaga ctagtaaaga ggctactgcg gaaatttaag ctacagagga 300
gagcagtggc tggaaccatt ctttttagta gccgcgtcct gcttctcatt ttccgcatgt 360

```

aaaactgctg cgtgtgcat ccactctgcc cccacagagc ctgcagtggg gtgaaatgtc 420
 aggaacaagc cccggagaag gagtgagaga gagagccagg ctgctgatga ctccgaggga 480
 ggaaccctgg ac atg tgc tgt agt gag agg ctg ttg ggt ctc ccc cag ccg 531

Met Cys Cys Ser Glu Arg Leu Leu Gly Leu Pro Gln Pro

1 5 10

gta gag atg gaa gca ccg gac gag gcc gaa gga ctc ccc agc aag cag 579
 Val Glu Met Glu Ala Pro Asp Glu Ala Glu Gly Leu Pro Ser Lys Gln

15 20 25

aaa gag atg cca cca ccc ccg cca ccc tca ccg ccc tct gag cca gct 627
 Lys Glu Met Pro Pro Pro Pro Pro Ser Pro Pro Ser Glu Pro Ala

30 35 40 45

cag aag ctg cca cct caa ggc gct ggg agc cac tcc ctc acc gtc aga 675
 Gln Lys Leu Pro Pro Gln Gly Ala Gly Ser His Ser Leu Thr Val Arg

50 55 60

agc agc ctg tgc ctg ttt gct gcc tct cag ttc ctg ctt gcc tgt ggg 723
 Ser Ser Leu Cys Leu Phe Ala Ala Ser Gln Phe Leu Leu Ala Cys Gly

65 70 75

gtg ctc tgg ctc agt ggc cat ggc cac tcc tgg ctg cag aac acc aca 771
 Val Leu Trp Leu Ser Gly His Gly His Ser Trp Leu Gln Asn Thr Thr

80 85 90

gac ctc atc tcc tcc tcg ctc aca gtg ttg aac cat ctg gga cct gtg 819
 Asp Leu Ile Ser Ser Ser Leu Thr Val Leu Asn His Leu Gly Pro Val

95 100 105

gcc tgg ctg ggt tct ggg acc tgg ggg ata cca agt ctg ctg cta gtc 867
 Ala Trp Leu Gly Ser Gly Thr Trp Gly Ile Pro Ser Leu Leu Leu Val

110 115 120 125

tct ctg act gtg agc ctg gtc atc gtc acc acc ctg gtg tgg cac ctc 915
 Ser Leu Thr Val Ser Leu Val Ile Val Thr Thr Leu Val Trp His Leu

130 135 140

ctc aag gca ccc cca gag cca cct gcc cca ctg ccc cca gag gac agg 963
 Leu Lys Ala Pro Pro Glu Pro Pro Ala Pro Leu Pro Pro Glu Asp Arg
 145 150 155
 cgt caa tca gtg agc cgg cag cct tcc ttc acc tac tca gag tgg atg 1011
 Arg Gln Ser Val Ser Arg Gln Pro Ser Phe Thr Tyr Ser Glu Trp Met
 160 165 170
 gag gag aag gta gag gat gac ttc ctg gac ctg gac gcg gtg ccc gag 1059
 Glu Glu Lys Val Glu Asp Asp Phe Leu Asp Leu Asp Ala Val Pro Glu
 175 180 185
 aca cct gig ttt gac tgt gtg atg gac atc aag cct gag act gat cct 1107
 Thr Pro Val Phe Asp Cys Val Met Asp Ile Lys Pro Glu Thr Asp Pro
 190 195 200 205
 gcc tca ttg act gtc aag tcc atg ggt cta cag gag agg aga gga tcc 1155
 Ala Ser Leu Thr Val Lys Ser Met Gly Leu Gln Glu Arg Arg Gly Ser
 210 215 220
 aat gtc tcc ttg acc ctg gac atg tgt act cct ggc tgc aat gag gag 1203
 Asn Val Ser Leu Thr Leu Asp Met Cys Thr Pro Gly Cys Asn Glu Glu
 225 230 235
 ggc ttc ggc tac ctg gtg tct cca cga gaa gag tca gcc cat gag tat 1251
 Gly Phe Gly Tyr Leu Val Ser Pro Arg Glu Glu Ser Ala His Glu Tyr
 240 245 250
 ctg ctc agc gcc tcc cgt gtc ctc cgg gca gaa gag cta cat gaa aag 1299
 Leu Leu Ser Ala Ser Arg Val Leu Arg Ala Glu Glu Leu His Glu Lys
 255 260 265
 gct ctg gac cct ttc ttg ctg cag gcg gaa ttc ttt gaa atc ccc atg 1347
 Ala Leu Asp Pro Phe Leu Leu Gln Ala Glu Phe Phe Glu Ile Pro Met
 270 275 280 285
 aac ttt gtg gat cca aaa gag tat gac atc cca ggg ctg gtg cgg aag 1395
 Asn Phe Val Asp Pro Lys Glu Tyr Asp Ile Pro Gly Leu Val Arg Lys

290	295	300	
aat cgg tac aaa acc atc ctt ccc aat cct cac agc agg gta cgt ctg			1443
Asn Arg Tyr Lys Thr Ile Leu Pro Asn Pro His Ser Arg Val Arg Leu			
305	310	315	
acg tca cca gac cct gaa gat cct ctg agt tcc tac atc aat gcc aac			1491
Thr Ser Pro Asp Pro Glu Asp Pro Leu Ser Ser Tyr Ile Asn Ala Asn			
320	325	330	
tac atc cgg ggc tac agt ggg gag gag aag gtg tac atc gcc acg cag			1539
Tyr Ile Arg Gly Tyr Ser Gly Glu Glu Lys Val Tyr Ile Ala Thr Gln			
335	340	345	
gga ccc atc gtc agc act gtg gcc gac ttt tgg cgc atg gtg tgg cag			1587
Gly Pro Ile Val Ser Thr Val Ala Asp Phe Trp Arg Met Val Trp Gln			
350	355	360	365
gag cgc aca ccc atc atc gtc atg atc acc aac atc gag gag atg aac			1635
Glu Arg Thr Pro Ile Ile Val Met Ile Thr Asn Ile Glu Glu Met Asn			
370	375	380	
gag aag tgc aca gaa tac tgg cca gaa gag cag gtg gtc cat gac ggc			1683
Glu Lys Cys Thr Glu Tyr Trp Pro Glu Glu Gln Val Val His Asp Gly			
385	390	395	
gtg gag atc acc gtg cag aaa gtc atc cac acg gag gac tac cgg ctg			1731
Val Glu Ile Thr Val Gln Lys Val Ile His Thr Glu Asp Tyr Arg Leu			
400	405	410	
cga ctc atc tcc ctc agg aga ggg act gaa gag cga acg ttg aag cat			1779
Arg Leu Ile Ser Leu Arg Arg Gly Thr Glu Glu Arg Thr Leu Lys His			
415	420	425	
tac tgg ttc aca tcc tgg cct gac cag aag acc ccc gac cgg gct ccc			1827
Tyr Trp Phe Thr Ser Trp Pro Asp Gln Lys Thr Pro Asp Arg Ala Pro			
430	435	440	445
cca ctc ctg cac ctg gta cgg gaa gtg gag gag gca gcc caa caa gag			1875

Pro Leu Leu His Leu Val Arg Glu Val Glu Glu Ala Ala Gln Gln Glu
 450 455 460
 gga ccc cat tgt tcc cca atc atc gtt cac tgc agt gca ggg att ggg 1923
 Gly Pro His Cys Ser Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly
 465 470 475
 aga act ggc tgc ttc att gcc acc agc atc tgc tgc cag cag ctg cga 1971
 Arg Thr Gly Cys Phe Ile Ala Thr Ser Ile Cys Cys Gln Gln Leu Arg
 480 485 490
 cgt gag ggc gtg gtg gac atc ctg aag acc acg tgc cag ctc cgt cag 2019
 Arg Glu Gly Val Val Asp Ile Leu Lys Thr Thr Cys Gln Leu Arg Gln
 495 500 505
 gac agg ggt ggc atg atc cag aca tgc gaa cag tac cag ttt gtg cac 2067
 Asp Arg Gly Gly Met Ile Gln Thr Cys Glu Gln Tyr Gln Phe Val His
 510 515 520 525
 cac gcc atg agc ctc tat gag aag cag ctg tcc ctc cag tcc tca gag 2115
 His Ala Met Ser Leu Tyr Glu Lys Gln Leu Ser Leu Gln Ser Ser Glu
 530 535 540
 tga ccacgctctt cctctgagat ccactgggta ctgccaagcc tgaggctggg 2168
 tctttacccc aactacccaa gatcttgcc tgggtcctgg gcctattccc tggccctccc 2228
 cctcatcctc cctctcttc agtctgttcc ccactatttg tcttggcctg gtccctaccc 2288
 caagcctagc tctcctactg tataactgc agagtgggg agggcaggg aggaatgtgc 2348
 caggccaggc ctggggcccc tgggcctgac ccacaccata tagacctgag ggcctcagtt 2408
 ttaaccatgg ttccacagct acttgggtcca aaatgtttcc atgccacacc ccaagtgtcc 2468
 taccataatg tgttctgtct gtccatctat cacagctatt tgtaccaaac actgtgtccc 2528
 ctccagccagg aaaggagcac tgaactaagc tctcaccctc cagccctcac ccacatcccc 2588
 acaccagact cccaccctgc tccccaggca gagatactga ccttcctctg gcccacttgg 2648
 ctccctctgca aaggcagagt gcattttgct accaggatgt ggatggcaga gaccaggcag 2708
 gggagcaca gatgggtgac agagagatcc cagctaagac agttcctggg caaagatgag 2768
 tatctccagt ctatgtggca ctggagagga agaggacaga tatagtgggg aaccccaaag 2828

atctgagccc tgaggggggc ctccaagagt aggatgtgga cagctccaga cctgtgagac 2888
 atcittctgt gtcactatgg gaaaccgcaa gtgtctccct acatgttgct ctgtgtgtgt 2948
 tcccttgicc atgcgtgtgt tgagagccca tgaacagggc atgcatgact ctttggcaac 3008
 atgtgttalc ttggagccac gtgtttttat tgctgacttt aaatatttat tccacggcaa 3068
 acggagacat ttggtgtctt tttttaatcc gctcgtggtc attgaataga gcaataaaca 3128
 gagcattttg agc 3141

<210> 132

<211> 541

<212> PRT

<213> Mus musculus

<400> 132

Met Cys Cys Ser Glu Arg Leu Leu Gly Leu Pro Gln Pro Val Glu Met

1 5 10 15

Glu Ala Pro Asp Glu Ala Glu Gly Leu Pro Ser Lys Gln Lys Glu Met

20 25 30

Pro Pro Pro Pro Pro Pro Ser Pro Pro Ser Glu Pro Ala Gln Lys Leu

35 40 45

Pro Pro Gln Gly Ala Gly Ser His Ser Leu Thr Val Arg Ser Ser Leu

50 55 60

Cys Leu Phe Ala Ala Ser Gln Phe Leu Leu Ala Cys Gly Val Leu Trp

65 70 75 80

Leu Ser Gly His Gly His Ser Trp Leu Gln Asn Thr Thr Asp Leu Ile

85 90 95

Ser Ser Ser Leu Thr Val Leu Asn His Leu Gly Pro Val Ala Trp Leu

100 105 110

Gly Ser Gly Thr Trp Gly Ile Pro Ser Leu Leu Leu Val Ser Leu Thr

115 120 125

Val Ser Leu Val Ile Val Thr Thr Leu Val Trp His Leu Leu Lys Ala
 130 135 140
 Pro Pro Glu Pro Pro Ala Pro Leu Pro Pro Glu Asp Arg Arg Gln Ser
 145 150 155 160
 Val Ser Arg Gln Pro Ser Phe Thr Tyr Ser Glu Trp Met Glu Glu Lys
 165 170 175
 Val Glu Asp Asp Phe Leu Asp Leu Asp Ala Val Pro Glu Thr Pro Val
 180 185 190
 Phe Asp Cys Val Met Asp Ile Lys Pro Glu Thr Asp Pro Ala Ser Leu
 195 200 205
 Thr Val Lys Ser Met Gly Leu Gln Glu Arg Arg Gly Ser Asn Val Ser
 210 215 220
 Leu Thr Leu Asp Met Cys Thr Pro Gly Cys Asn Glu Glu Gly Phe Gly
 225 230 235 240
 Tyr Leu Val Ser Pro Arg Glu Glu Ser Ala His Glu Tyr Leu Leu Ser
 245 250 255
 Ala Ser Arg Val Leu Arg Ala Glu Glu Leu His Glu Lys Ala Leu Asp
 260 265 270
 Pro Phe Leu Leu Gln Ala Glu Phe Phe Glu Ile Pro Met Asn Phe Val
 275 280 285
 Asp Pro Lys Glu Tyr Asp Ile Pro Gly Leu Val Arg Lys Asn Arg Tyr
 290 295 300
 Lys Thr Ile Leu Pro Asn Pro His Ser Arg Val Arg Leu Thr Ser Pro
 305 310 315 320
 Asp Pro Glu Asp Pro Leu Ser Ser Tyr Ile Asn Ala Asn Tyr Ile Arg
 325 330 335
 Gly Tyr Ser Gly Glu Glu Lys Val Tyr Ile Ala Thr Gln Gly Pro Ile
 340 345 350
 Val Ser Thr Val Ala Asp Phe Trp Arg Met Val Trp Gln Glu Arg Thr

355	360	365
Pro Ile Ile Val Met Ile Thr Asn Ile Glu Glu Met Asn Glu Lys Cys		
370	375	380
Thr Glu Tyr Trp Pro Glu Glu Gln Val Val His Asp Gly Val Glu Ile		
385	390	395
Thr Val Gln Lys Val Ile His Thr Glu Asp Tyr Arg Leu Arg Leu Ile		
405	410	415
Ser Leu Arg Arg Gly Thr Glu Glu Arg Thr Leu Lys His Tyr Trp Phe		
420	425	430
Thr Ser Trp Pro Asp Gln Lys Thr Pro Asp Arg Ala Pro Pro Leu Leu		
435	440	445
His Leu Val Arg Glu Val Glu Glu Ala Ala Gln Gln Glu Gly Pro His		
450	455	460
Cys Ser Pro Ile Ile Val His Cys Ser Ala Gly Ile Gly Arg Thr Gly		
465	470	475
Cys Phe Ile Ala Thr Ser Ile Cys Cys Gln Gln Leu Arg Arg Glu Gly		
485	490	495
Val Val Asp Ile Leu Lys Thr Thr Cys Gln Leu Arg Gln Asp Arg Gly		
500	505	510
Gly Met Ile Gln Thr Cys Glu Gln Tyr Gln Phe Val His His Ala Met		
515	520	525
Ser Leu Tyr Glu Lys Gln Leu Ser Leu Gln Ser Ser Glu		
530	535	540

<210> 133

<211> 715

<212> DNA

<213> Mus musculus

<400> 133

attcggatcc atgtgaagtt cagcgtcagc ctgtcgtccg tgtggcagtg gaggccaaga 60
 acccagctga cctgcccaag ctggctggagg ggctgaagcg gctggctaag tctgacccta 120
 tggctgcagtg catcattgag gagctctggag aacatattat tgcctggcgcc ggtgagctgc 180
 acctggagat ctgccttaag gacctggagg aggacctatgc ctgcatcccc atcaagaaat 240
 ctgaccctgt tgtgtcatat cgggagacag tcagtgagga atccaacgtg ctgtgtctgt 300
 ccaagtcccc caataagcac aaccggctgt acatgaaggc caggcccttc cctgatggcc 360
 tggcagagga catcgataag ggtgaggtgt ctgcccgcca gaggtcaag gcacttgccc 420
 gctacctggc cgaaaagttt aattgggacg tttctgaagc ccgcaagatc tggctgtttg 480
 gcccctaattg gaatggcccc aaaattttta ccgggattac caagggggtg caagtaccct 540
 aaattggctc aggaacatt ttgtggcttg ctccaattgg ggcattaaag agggggcctc 600
 tctttgggaa acacatgcgt ggtttccggt ttaatgtcca taatgtacc tccagccgat 660
 gcaattaccg gggaagggtc cagataatcc ccacagaagc cgctgcctgt atcca 715

<210> 134

<211> 12410

<212> DNA

<213> Mus musculus

<400> 134

gagctcagga ttagcatggg ggcacagtga ggctctcgct gtttgggcta ggcataggta 60
 tcttcagatt cttatagggc gcctgaagcc gcccagagcg acagtgtctc cacattctga 120
 gcacctagaa ggagaatcag gaccgtccta acctaaaggac actcctctgc tccctggcag 180
 accttattgg ctcaagggga gcatctttc cagggtttct ctgtctttct ggggtccagc 240
 gtgcccacct gccacaaaac ctgagacca aacgcctcaa ggatcgcagc ctgttgggaa 300
 tctgggctcc acccgaagac agcgtcggg gagacccgac cggccaggcc ttctgagccc 360
 gccagtcct accccggttg cccccgccc agagcaagcc gtagccccgc cccgccggac 420
 ccgctctgcg cgtgcgcagt cccgccccgc ccgcgctgcg ggcgactagt gacgtcaccg 480
 gccccgaagc gccctccggc ggcggcgcgc tccaccccag caggcgggtc gtgaacagcc 540

cgaggggcgg cgggccgcgg gagccctcag agccgcttcc cctggcgccc gctccggggc 600
cgcggcggat gggcgggccgc gggccgcggg gcgacaggcg gggaacgggt gcgagccggg 660
accgggaggg gcggccgcgc caaggggccc cggggcgggc gggcggggcg cgggccggcg 720
gtttgggagg gcgccccgcg tccgagaggc gagccggggc ctgacggcg gcgggttccg 780
cgtcgcccci gccgcgcat ggcgagagacc aaaatcatct accacatgga cgaggaggag 840
acgccgtacc tggtaagct gcccgtagct cccgagcgcg tcacgctggc cgacttcaag 900
aacgtgctca gcaaccggcc ggtgcacgcc tacaaattct tcttcaagtc catggaccag 960
gacttcgggt cagtggggcg cgcggccttg gcagggggcg tggcctctc ccgcgcctgt 1020
gtgcacgagc tggcacctgt ccgcgccggc tgggccttcg ggtctgggga cgtcagagag 1080
cgccccgct gccggcaacc ctgctgcgca tctacagaca ggtgtaggta gagtttctgc 1140
gccagtgac cctgagtgtg gcaaactggg ggtccgaacc actgaactacc ctctgggtag 1200
gccagacagt tctttctgac ggacaggcga gggcccaggc tttctgacca ccatccactg 1260
gtgctcctgt gccagctgg tccatgittg gttccgaaga ccactcttaa agccaactcc 1320
cttctctctg gtttaagcaca gagccgatg cgttctcct ctgtggatgg aaaccgggg 1380
ctcaggactg ccctggaggg ttttcagttt atccgggagg tggggggggg ggtgggatca 1440
cggagaagga ttgggggttt gtggctccta gcaccagtg gatcccccg catgagatgg 1500
gggtaatgtg aaatagggtg ctcataaggc accccgcctg tttcttgaa catagaaaag 1560
ttgtgaagcc tgaanaacaga ctcttcagg tccctctaga gtccctgtg gcaagacaga 1620
gaggtcaagg gtcactggaa accaagaagc ttcattccgt gtaccctccc cccttggtc 1680
ctggctcctg tgcctctgac ctttctgaac cacacaacat ttgcattcct gggaggtgct 1740
cggttcatct cctgacttga gtcaattct aatgtagtgt ttttcttagc tgaatggctg 1800
tggtggtctc aggagaaggg acttctatt tgagataagc tggcctctg gacgctgagc 1860
cagggactga cagtacaaca gaggcctgac cagggcatag ccacagaaaa cttgagtccc 1920
atggccttgg cagtgaattg ggggggtggg gaggccaggg tagcatgtt agccctgtg 1980
ggtggagcag gtgtgcttgg tgccttgtg tgtggctcca tctcagggt ttgacattga 2040
ggcgatttcc tggattccat ggttgcaggg tccctgggca gcccatcggc caggtaagc 2100
ttggacttct tcttggccct gggcgcttag acaggactga acctggttt gatgactaaa 2160
ctctcttgcc tactcagtc ttgtgcccc accaccagga aaaggcagag gagagagtgt 2220
ccctcacagc ttgagggcgg gtgctctcca ttgcccagga gactagaggg tcttgcctta 2280

gaggtcggtc ticcctgact ctccctgacig ggccacctct gtggctctcta atctgaggga 2340
cagggtatct ctggatccaa atatiggtac atttiggttt ttgttgaccc aagtcacaaa 2400
tgttctcaca aacttgttac accctagcgt gtaagtggta aggaggcaga cctgggttgc 2460
tttctgctat acactctggg tctctcctga gggctacctgt cccctttactc tgatattcat 2520
gttgggtaga tagcatcagc tcacataggt ttctcactgt ctgtgccctgt ggcaggtttg 2580
ggggacctgc aggtgtccta gctaaggaga taggatagca gataggggtc ttgaagcagg 2640
agtagttcct tcgggtgggt ttgaagtggc tgggacatgg ggctctggagc tagcagagag 2700
cctagaggta caagtgggt gttctggggg tgtagaagaa ttagggggca gacgaaacta 2760
gagatagagt tggggttaca cagaaagact tgtcagtagg cctcaccatg actttgatgg 2820
tctagtggac ttgggagcct agacaaggag cctgccccg tctcaactgc atcctttctt 2880
tccttaccta agttctacct acagagctcc aaggatacca agagaaagta gcttaatgtt 2940
gggagaaggg agtttgtttg agagctagtt tggctgagct ggacaagtg cctcagggtt 3000
ggccgcagac tagagctctgt gaggcatact ctagtgagtc tagctccaaa ccaaggctgc 3060
ctactttgta aatagcagag ttgcccctgg actgggctca gtcccagtg tgtatttcta 3120
gccaacaagg taaaggctta ttctgtgccc acttaatggg agcttcttgt tgttctgacc 3180
ctggacccca aggcttagta gcagcaggac ttctagattc tgggtgggcc catggagggt 3240
tctgggtgtg ggccctggta taaatggagg tctatggtag aggaattgag tacattggct 3300
tttggggcct ctgtctactg ggaacatact gctgatatca gtctggctga tgcgataccg 3360
agtttattgc ctggcagttg ctgcagcccc atctcttgag aaagagctac gtgagctaga 3420
gggaagcagg caagggttaag ggctaggagc cctggaatct ggggtcctct gtacattggc 3480
aaatgttctg agggctccct gtgcccctgg cgagctgcct ggggtcagtg acttagcctt 3540
tctgtgccct cctagtattt attatgagag tctaggtaat tatcatgcat tccctgagct 3600
gtggggaagg actctatgtt ctggggctca atgccccatg ggatgagttg gtagaagagt 3660
ggccagctat ggtctggggc ctgtgcacac ctgccagttc aagttcatgg gtagtaaac 3720
tccttaggct aagagtcag tccacaacaa tgcttggtag gaattggatg ctcactcctg 3780
ggagcataca gaagccccct gaagctcaag atatctccat gacctgtgcc tacttgctct 3840
gccagtctct ggctctgtgt gtatgggaat ggggctatct cagggtggg ccactagaga 3900
ggtagtctgt gtgttactgt aatctcctga aaccctgggt ccttttaggc taagctatgc 3960
aggggtccaa aggccttact ttagagcaga ttctctcttg aggtggatca ctgggggtgg 4020

ctggttagagt ccaatggcca caaggatctc tccaggaatt ctaaggttgg ggcaaaatgc 4080
tcacaggagt gtcctgagtc actgtgcaga gtcagtggag acacattaag gtcagctttc 4140
ctcttgagag gatagacata caaggctcag ggtggtaggg atgtttgggt gtgcctcatt 4200
ctgttcttgt tatacagtcg ccagcagctg tgggttagcat cacataacct tggccaccat 4260
tcctgcttcc actatgggta ttgtgatgtt tgccttttgc ctagccaatg gtggggaagg 4320
gccagggtta gccctaggat ctgggggcaa acacatccct tcaggactgt ccttttccct 4380
ttggccagtc ttcttgctct tgaccctagg taggaaagca ggacttgtgt tgctctgtctg 4440
ggaggaaggc ctttccctgc taagaagcag ggccctttga accatagagg tatgtccttt 4500
cctagggttt gggaggcaca aagaccgcga agctgcccatt attaccttaa gggtctgact 4560
gagtaggctc tggctgtctg gaatgggaca cagtgcctgt ttgaggagcc aggcagcccc 4620
tattgtgggt gctaggaatt gctcatatgt ttcccatgg gtgagtcagg gagggttgga 4680
gcttgggtgt gccaatggga aaggcttttg gtgagtcac ttggggctga ggctagggga 4740
taaggtaggg gttcttttct gggtagatta ctgaggctt ttagcagcct caggtcttcc 4800
tgtgatgaca gactctcttg ttggctacct tggcccaggc ttgtaaaagg agcaaccaca 4860
gagctgtaac tgaaattgga agaaatagat attaaggag tcctgagaag tgattctgtt 4920
cgctgggtgg gtcccatggg cacatggaca cagcagtaag gtcaggaaag tggctggaca 4980
ctttcacttt caggctgtcc agcctctgcc attacctcag cgccaggctc ctagcaagtg 5040
ggtggacaaa ggccttattc cctagagagg atgggatgtt gccctgctag agcttccctgc 5100
aacctgggtg tggccactgg ttctggagca gcaagcagag gtgcctctcc ccctggcact 5160
gggcccattt agtcacaagc ctgcttccct ccagggtgac ttccaggacc agcctgtttt 5220
ccagctccac tcaatcaagt tttaggtagt gaaatccac tatgttaggc ggagctaaga 5280
gctaggtgaa gttgaggag tggagaatct agggcctgaa gagccccctc aagcctgccc 5340
tgactgtgtt ccgtgccttg tgaacactgc cccaggtc tggcttccct cccagttctc 5400
attccctgcc ttttgtatct tgcttgggtg agcttggctc ctttctagcc catctgacca 5460
gggaagcagc atgaggacaa aacagagatg gctgtgggtc ataggtacag ccaaggcttg 5520
gctagctctg tccctaaatg cccttccagg tcttcagata gaaaccaagc aaactccctg 5580
atagttgggg ctgatcttgc gcatgagatc cacittatct ttctggctgg gtagatggtt 5640
ttgagggcag caagagctgg gtatccttct ggccctctca catctataga aggggatggc 5700
agtctttgta ccaggaagtc cagccttctc tgggctgggg gaacttcagg agcccaaggg 5760

cttggagcac cgtgagaigc tcatcatatt aacgagcgcc cgtgagtgct ccagagaggc 5820
ccagaggggtg tgtgctgaga agacaaggac aggaggcagt gggcctgatg taagcagagt 5880
gcacaaaatg cggttcctct gcagcccaat ctgaatgcag gcttaggagg ccaggctccc 5940
ttctggaacg agttggaatt ggagcttttg tggtagatgg tgggatttgg ggtgaggggc 6000
agagaagagc catagtctgt cccaagcacc tggctaggta gagctgctct ccctaaaatt 6060
ttgaaggctg agaagagtic ccaaaggagc cccaagtgtg gtatatgtg gtgagggagc 6120
ttttgggtcc catgaggaa gcatacaaag ctagagacag gcctgatata aaccccaggg 6180
ccaaggaagc cgaagaactg gggatttccc aggaacctc aaccttgct gactaccaa 6240
gggctggagg ctgactctgg acgtgaacaa gatttctagg atgtccttc atgaacattt 6300
ctctacattt ctctacceca gtgctaaggg tcagggtttt gggattggca gagagcagca 6360
gagtccttag gaagagaatg tggtaggtaa acctcagtg gtgacatctg cagcctagca 6420
ggtgctccat tgctacgtcc aagagtagaa agtgtctctt aatgtccttc atggatccag 6480
gtgaggtagc atcgggctt tgtttgacca cagggtggtg aaggaggaga tcttcgatga 6540
caatgccaaag ttgccctgct tcaatggccg ggtgggttcc tgggtgagtc tatgggtggc 6600
cccagcagaa tgggtgaagg gggctctccc tgggagaagt aaagtaactg gacaaaggta 6660
ggcagcagt ggggtgcctgt ggggggtggtc ttgacgcaga tggccatcca aggcctcact 6720
cttcctttac agctggicct ggctgagggc gctcactcgg atgcagggtc ccagggcact 6780
gacagccaca cggacctgcc cccacctt gagaggacag gcggcattgg ggactccagg 6840
ccccctcct tccagtaagg ccccttgcgg gggcagagct ctgccattgc tagatacttg 6900
ctaccaaga cccacctggg aagagtgaac ctaacaacat agcaggggcc tacagttgtt 6960
tgggaggcac cttctagaac tagggtcttg cctgggggtt tggggacctg gaatcatttg 7020
aggtaatggc tgtcggcaac ctggtctgcc caattccacc tgcctcttat ctatgcagac 7080
caaatgttgg cagtagccgg gacggaatgg acaatgagac aggcacagag tctatggtca 7140
gtcaccggcg ggagcgagcc cgacgtcgaa accgcgatga ggttactatg gctgtgtctc 7200
cccagatctg gaaccaggc ttcccttggg ttccctttgg tatacgccaa gcctggaata 7260
ttccacatat tcttccaagc agtgatcctt gggtagaggt cccaacctgg tacttctagc 7320
ccctgtggcc ccagagttac tgcataaact tggaaatgca caggccaccc gcattctgtt 7380
aggactgaag tcccacagtc gtaccaccc tactgtcccc acagctgccc ggaccaatgg 7440
gcacccgaga ggggatcgcc ggcgggacct gggactacct ccagacagt catctactgt 7500

actgagcagt gagctigaat ctagcagctt tattgactca gatgaggagg acaatacgag 7560
ccgggtgggtg acgtgtgcac atgtcagtac gtgctggaga ttgttagttg agcgiccag 7620
ctggttatac atgcttgtgc ttttctgact cctgcctcag gctgagcagc tccacagagc 7680
agagcaactc ctcctcggcta gtctcggaagc acaaatgccg tcgtcggaag cagcgcttga 7740
ggcagacaga ccgggtaggc agcagggtggg tgggggtgct gctctgaatg gtgcccacac 7800
agcccc tcac tgggtccctc cgcaggcatc ctcttcagc agcatcacag actccacat 7860
gtccctgaac atcatcaccg tcactctcaa catgggtgag gccttgtggg ctctgggggg 7920
ctgctggggg tgggtacagc ctcgaggagct ttggggggct gctcacgggc cctcctgcag 7980
agaggcacca ctccctgggc atcagcatcg tgggccagag caacgaccgg ggtgatggcg 8040
gcatctacat tggatccatc atgaaggcg gggccgtggc tgctgatggc cgcatlgagc 8100
cgggcgacat gtgtctgcag gtgggagcca tgaggggact gtggggacaa gatgcacca 8160
catcccacca ccaaccctg accccacaaa ccccgtaggt gaacgatgtc aactttgaga 8220
acatgagcaa tgacgacgt gtacgggtgc ttcgggagat cgtgtcccag acagggtgag 8280
gtgggagcca agtgggggtg ggagtggcac aggatgggag gggctgtgcg ggcctcactt 8340
acaacatggt ctgtcaact ctgtaggccc atcagtcica cagtggccaa gtgctgggac 8400
ccaaccctc ggagctactt caccatccca aggggtgagt taccatgga aagggtgggt 8460
agggtgggtt tcctgtgttc agtctggggg tctatcttgt ctgcctctgt gctgcccc 8520
tacttaccac ctgtaatccg ttgctgtgga aactatgcag ctgaccagt gcgaccatc 8580
gaccggctg cctggctgtc ccacacagca gcactgacgg gtgcccctgcc ccgctatggt 8640
acgagtcctt gctccagcg catcacagc accagctctt cctcactaac cagctcagt 8700
cctggcgccc cagtaagtg gcagttcaca ggaccccc tccccaaagg aaactgaggt 8760
tgaaggacaa tggtcagttc tagctttgag ctctgggtgt catcagagct attacaggg 8820
cccattacat atgaaggttt tgtttgttc caacacctt acaaatgtgt acacaaagat 8880
acatgtacat atccctccag gccctggccat actggctac tgcattgaatt gagggctctg 8940
ccaggcctgt gtggaggggg aattgggagg acatggcagc ctctgctttg ctctctgcta 9000
cctcaacata gctaacagct tgttctctcc ggggaggggg ggggggtgcc ttgcctatgt 9060
ggacttgac tgtgggacgg ggaagaatct cccggctcta gctcaagttt cgatgagggg 9120
catctcccaa ggatgggaga taagaggttt gacctgccc cctgctctca acccatgga 9180
ggttcacgct gtgagcctgg gctcaggga gtgtgctctg cagagcttga ggaggcgccg 9240

ctgactgtga agagtgacat gagtgccatt gtccgcgtca tgcagttgcc agactcagga 9300
ctggagatcc gggaccgcat gtggcctaag atcaccattg ccaatgctgt catttggtgag 9360
tccctggctg tgtgggaagg ggcccgtctc ttcctcattc tgcgtaggt tcccagggt 9420
caattacctt gactttgatg gacctgtgcc caggggcgga tgtggtggac tggctgtaca 9480
cacacgtgga gggcttcaag gagcgaaggg aggcaagaaa gtaatgccagc agtatgctga 9540
agcacggitt cctgaggcac accgtgaaca agatcacctt ttctgagcag tgctactatg 9600
tctttggcga cctgtgcagt agtgagtagg ggtagggttg ggtagggtt gctgtggcct 9660
cattcatttg ccttcactta cccctccctc cctcccttcc tgccagacct cgcacccctg 9720
aacctcaaca gtggctccag tggagcctca gatcaggaca cactggcccc actgccccac 9780
ccatcagtac cctggccctt gggtaagggc taccctacc agtaccagg acccccgccc 9840
tgcttccac ctgcttacca ggacctggc ttcatgtgcg gcagcggcag tgctgggagc 9900
cagcagagtg aaggtagag gtgtggcaac cctcctccc actccctccc actcccacgc 9960
tctgtctggg cccaacggtt cctctgtgc tctgtctgtg tgittgagtc ctggigggt 10020
ccatcgcaag agtcagtgtg tgggacaggg aggggctgat gtgggtagaa gccgcttaga 10080
gaataggaag acagcctggt gtgctagggt gcagaggcaa gaggccagga gatgatatg 10140
caagaatgaa agtaaccact gatagcaggt aggggcactc tctaggcccc aagctagggg 10200
gagaatgggc ttttatcagc tatggagcct gcatcccaac agagtgccag ataagcagta 10260
tcaagcaaca ctgittaaagc atatcagtgt taaagcatat ccccagggga tattgaagac 10320
cttggaaggg gtgggttgtc cctcaggag gagatggact tgatgtggag gtcttttagac 10380
agagtggggc cacacttgtg ctacagggtc cagagaaaga ctcaggagag gttgggccag 10440
agggtgccaa agcccaaggg gaagctatcg agtgaatcct gaccatggac aggccttgc 10500
atgtaccag gctcagcttg gcccaaaatc gtctatttag ccattggtga gcactggact 10560
ggtgtgtgac ttgtgctatc ccttgctttg tgctagcaa gccttagact gaaggactag 10620
cagagtggac tctcgggccg gtaagccagc tccctctgtg tccctctcag catgtcccca 10680
gccagcacgt gttttcaggt tcccactact ttcaggacag gggctaacca aattagatga 10740
ccagggtcct gggttgggtg gaccctggtt ggtctttggg tgtgaacca ggatggctaa 10800
tggaatgct gggcacacag gcccttcgct ggtttttagt ttctcagctg taacattaac 10860
ccttggttca agcatgggg ttaggtgtgg ggtgccaggc tggccctgt tgtccctgct 10920
gtctgccact gcccttagct tctgcctct cagctgttcc tggatatctg atggctgcca 10980

ttcccc tacc atctccaggc ttaccaggtc ctgccctggc tgtctgggag cagctgggtg 11040
 ccctggaagt ggccaggcct cgtgctgact ctgttgtccc ctccccccc cctagggagc 11100
 aagagcagtg ggtccacacg gagcagccat cggaccccag gccgagagga gcgccgggca 11160
 actggagctg ggggtagtg cagtgaatca gaccacacag taccaagtgg gtctggtagc 11220
 accggctggt gggagcggcc tgtcagccag cttagccgtg gcagtagccc tcgaagtcag 11280
 gcttcagctg ttgccccagg gctcccccca ctgcaccccc ttacaaaggc ctatgcagta 11340
 gtgggtgggc cacctggagg gccacctgtc cgggagctgg ctgctgtccc tccagaactt 11400
 acaggtagcc gccagtcctt ccaaaaggcc atgggaaacc cctgtgagtt ctttgtggac 11460
 atcatgtgat gatcaaccaa tgtcttcagc gctgccctgtg gctgagctctg agctcctgct 11520
 gtgccaggag ctctgcgctg gccgtgggtg tggccagcca ggatagatca gctgtggggt 11580
 ctgggccagg gcagagggag caggctccag aggaggggca gagggcagcc ataccaccag 11640
 gatattggct tgacattttg tctgtctctt gggctgtctga tgggtgtaca gctcaagtat 11700
 ctatagagtc ttgtaaggag acatctctga ctttaagtcc tcagcacaag tctcagggac 11760
 cacctcctgg ttcccttctt tggaaagtac ctccatttag aacaagaaag gctctcttgg 11820
 gctcttggta ccccttggcc caaagcctca cagaactgtg cacagggaca caggctgact 11880
 gtcgctaagt tcatgggcct cacctgtcag gccaaagggtg gatTTTTgag ggtagacag 11940
 aaccttcaaa cctctctggc tgcccagggtg gggctctaact tatttattta ttgctagcct 12000
 gcctgtctta aggggtggcag ctggttaccc aaaggggcag ttgtcatgcc cttttcccca 12060
 cctgctactt ggcacatgac aacacagttt gtactgaagg tatgtgaagg gtagctagta 12120
 ggagagacag gagagagacc tggcacctag ccactgtctc agtctcagtg gtgggtgaca 12180
 gigaacacaa gagctgcaga ggtagggacc tgttctgttt ctgttctggg ggctgcccac 12240
 catcacgtgc cactgccatc ccggcacagc ggccccacac atctacacta gacactgtgt 12300
 caaagtctga gtgactgggt agttgacata gagctgcttc tgtgtaaatg ctgcttctgt 12360
 gtaaattgta ttttaaacac taaaaaagcg tttaatttta tgggaaaaaa 12410

<210> 135

<211> 1480

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (101).. (1060)

<400> 135

```

gaagagtact gccttgtcct ttggcgtgtg catcggtcct gctctcaccg gcagcctgcg 60
ctctactgcc tgcctccagtc cactcctgac cgacagcatc atg gct acg aga ggc 115
                                         Met Ala Thr Arg Gly
                                         1           5

act gtg act gac ttc cct gga ttt gat ggc agg gct gat gca gaa gtc 163
Thr Val Thr Asp Phe Pro Gly Phe Asp Gly Arg Ala Asp Ala Glu Val
                10                15                20

ctt cgg aag gcc atg aaa ggc ttg ggt acc gat gag gac agc atc ctg 211
Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Ile Leu
                25                30                35

aac ctg ttg aca tcc cga agc aat gct cag cgc cag gaa att gct cag 259
Asn Leu Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ala Gln
                40                45                50

gag ttt aag act ctg ttt ggc agg gac ctt gtg gat gac ctg aag tct 307
Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val Asp Asp Leu Lys Ser
                55                60                65

gaa ctg act gga aag ttt gag aag tta att gtg gct atg atg aag ccc 355
Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Met Met Lys Pro
                70                75                80                85

tca cga ctc tac gat gcc tac gag ctg aag cat gct ctt aag gga gct 403
Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala
                90                95                100

ggc aca gac gag aaa gta ttg acc gag att att gct tca agg aca cct 451

```

Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro	
105	110
gaa gaa ctc agt gcc ata aaa caa gtt tat gaa gaa gaa tat ggt tcc	499
Glu Glu Leu Ser Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser	
120	125
aac ctg gaa gat gat gtg gtg ggg gat act tca ggg tac tac cag agg	547
Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg	
135	140
atg ttg gtg gtc ctc ctt cag gcg aat aga gac cct gat act gca att	595
Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Thr Ala Ile	
150	155
gat gat gct caa gtt gaa ctg gat gct cag gca ttg ttc cag gct gga	643
Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala Leu Phe Gln Ala Gly	
170	175
gag ctg aag tgg ggg aca gat gaa gaa aaa ttc atc acc atc ttt ggg	691
Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly	
185	190
aca cgc agt gtg tct cat tta aga aga gtg ttt gac aag tac atg acc	739
Thr Arg Ser Val Ser His Leu Arg Arg Val Phe Asp Lys Tyr Met Thr	
200	205
ata tca gga ttt cag att gag gaa acc att gat cga gag acc tcg ggg	787
Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly	
215	220
aac ttg gag cag ctg ctc ctg gct gtc gtg aag tct att cgg agc ata	835
Asn Leu Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile	
230	235
cct gcc tac ctt gca gag acc ctc tac tat gcc atg aag ggt gct ggg	883
Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly	
250	255
	260

acg gac gat cac acc ctc atc aga gtc gtg gtg tcg agg agt gag att 931
 Thr Asp Asp His Thr Leu Ile Arg Val Val Val Ser Arg Ser Glu Ile
 265 270 275
 gac ctg ttt aac ata agg aag gag ttt agg aag aac ttc gcc acc tcc 979
 Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser
 280 285 290
 ctg tat tct atg atc aag ggc gac aca tct gga gac tat aag aag gcc 1027
 Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala
 295 300 305
 ctg ctg ctg ctc tgc ggg ggc gag gat gac tga gagccgcctg gagcgccctg 1080
 Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
 310 315 320
 tgcctgctgc ccaccatcag ctttcctcag caccacactt gcttgcatte tgtgcctgcc 1140
 gcgctgcctt acactagtat gctaattgacc aaagggtgtct tagatgaaag cagtgtcccg 1200
 ccttctgat gtctgtcta cagtaggtag tgacctccc atatctctca gtccaatgtc 1260
 tgagttatta atattgtcta tgaattgcct tttatatacct ttttttaaag cttcatttat 1320
 attaatgtaa taaccctatt atcttgattg gaaccttagc ggtgaaattg tgaactcttg 1380
 gaaatgctgt caatcaagct tactgtcta gcagacctgc aaaattatga tggtagtatc 1440
 caaaacattg gcgacaaata aaaacattcc cttccctcca 1480

<210> 136

<211> 319

<212> PRT

<213> Mus musculus

<400> 136

Met Ala Thr Arg Gly Thr Val Thr Asp Phe Pro Gly Phe Asp Gly Arg

1

5

10

15

Ala Asp Ala Glu Val Leu Arg Lys Ala Met Lys Gly Leu Gly Thr Asp

20	25	30
Glu Asp Ser Ile Leu Asn Leu Leu Thr Ser Arg Ser Asn Ala Gln Arg		
35	40	45
Gln Glu Ile Ala Gln Glu Phe Lys Thr Leu Phe Gly Arg Asp Leu Val		
50	55	60
Asp Asp Leu Lys Ser Glu Leu Thr Gly Lys Phe Glu Lys Leu Ile Val		
65	70	75
Ala Met Met Lys Pro Ser Arg Leu Tyr Asp Ala Tyr Glu Leu Lys His		
85	90	95
Ala Leu Lys Gly Ala Gly Thr Asp Glu Lys Val Leu Thr Glu Ile Ile		
100	105	110
Ala Ser Arg Thr Pro Glu Glu Leu Ser Ala Ile Lys Gln Val Tyr Glu		
115	120	125
Glu Glu Tyr Gly Ser Asn Leu Glu Asp Asp Val Val Gly Asp Thr Ser		
130	135	140
Gly Tyr Tyr Gln Arg Met Leu Val Val Leu Leu Gln Ala Asn Arg Asp		
145	150	155
Pro Asp Thr Ala Ile Asp Asp Ala Gln Val Glu Leu Asp Ala Gln Ala		
165	170	175
Leu Phe Gln Ala Gly Glu Leu Lys Trp Gly Thr Asp Glu Glu Lys Phe		
180	185	190
Ile Thr Ile Phe Gly Thr Arg Ser Val Ser His Leu Arg Arg Val Phe		
195	200	205
Asp Lys Tyr Met Thr Ile Ser Gly Phe Gln Ile Glu Glu Thr Ile Asp		
210	215	220
Arg Glu Thr Ser Gly Asn Leu Glu Gln Leu Leu Leu Ala Val Val Lys		
225	230	235
Ser Ile Arg Ser Ile Pro Ala Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala		
245	250	255

Met Lys Gly Ala Gly Thr Asp Asp His Thr Leu Ile Arg Val Val Val
 260 265 270
 Ser Arg Ser Glu Ile Asp Leu Phe Asn Ile Arg Lys Glu Phe Arg Lys
 275 280 285
 Asn Phe Ala Thr Ser Leu Tyr Ser Met Ile Lys Gly Asp Thr Ser Gly
 290 295 300
 Asp Tyr Lys Lys Ala Leu Leu Leu Leu Cys Gly Gly Glu Asp Asp
 305 310 315

<210> 137

<211> 2029

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (70).. (1251)

<400> 137

tgacagaagg catacaaaact caactgaagg aagattcctg gattctgtga aggaggattt 60

caaatcaag atg gtt gat aca aag gca gag aaa gat tgt gac gtg ctg gtc 111

Met Val Asp Thr Lys Ala Glu Lys Asp Cys Asp Val Leu Val

1

5

10

ggt ttt aaa gct gtg tat cgg atc aac ttt gct gtg gcc atc ttt ttc 159

Gly Phe Lys Ala Val Tyr Arg Ile Asn Phe Ala Val Ala Ile Phe Phe

15

20

25

30

ttt gcc ttc ttt ttg ctc atg tta aaa gtt aaa aca agt aaa gat ccc 207

Phe Ala Phe Phe Leu Leu Met Leu Lys Val Lys Thr Ser Lys Asp Pro

	35	40	45	
aga gca gca gtg cac aac ggg ttt tgg ttc ttc aaa atc gct gcc att				255
Arg Ala Ala Val His Asn Gly Phe Trp Phe Phe Lys Ile Ala Ala Ile				
	50	55	60	
att ggt atc atg att gga tct ttc tac atc cct ggg ggc agt ttt act				303
Ile Gly Ile Met Ile Gly Ser Phe Tyr Ile Pro Gly Gly Ser Phe Thr				
	65	70	75	
gaa gtc tgg ttt gtt gct gga atg ttg ggg gcc tct ttc ttc att atc				351
Glu Val Trp Phe Val Ala Gly Met Leu Gly Ala Ser Phe Phe Ile Ile				
	80	85	90	
atc cag ctg gtg ctc ttg gta gac atg gct cac tct tgg aat gaa tta				399
Ile Gln Leu Val Leu Leu Val Asp Met Ala His Ser Trp Asn Glu Leu				
	95	100	105	110
tgg gta aat cga atg gag gaa gga aac cca agg ctc tgg tat gct gcc				447
Trp Val Asn Arg Met Glu Glu Gly Asn Pro Arg Leu Trp Tyr Ala Ala				
	115	120	125	
ttg ctg tcc ttt aca agc ctc ttt tac atc ctc tcc atc gtc ttt gct				495
Leu Leu Ser Phe Thr Ser Leu Phe Tyr Ile Leu Ser Ile Val Phe Ala				
	130	135	140	
gcg ctg ctc tac gtc ttc tac acc aag cct gac gac tgc aca gaa aac				543
Ala Leu Leu Tyr Val Phe Tyr Thr Lys Pro Asp Asp Cys Thr Glu Asn				
	145	150	155	
aag gtc ttc atc agc ctc aac ctg att ttt tgt gtt gca gtt tct att				591
Lys Val Phe Ile Ser Leu Asn Leu Ile Phe Cys Val Ala Val Ser Ile				
	160	165	170	
gtg tcc atc ctc cct aaa gtt cag gaa cat cag cct cgc tct ggc ctc				639
Val Ser Ile Leu Pro Lys Val Gln Glu His Gln Pro Arg Ser Gly Leu				
	175	180	185	190
ctg cag tcc tcc atc atc act ctg tac acc ctt tac ctc acg tgg tca				687

Leu Gln Ser Ser Ile Ile Thr Leu Tyr Thr Leu Tyr Leu Thr Trp Ser
 195 200 205
 gcc atg acc aat gaa cct gag cgg tcc tgc aat ccc tcc tta atg agc 735
 Ala Met Thr Asn Glu Pro Glu Arg Ser Cys Asn Pro Ser Leu Met Ser
 210 215 220
 atc atc aca cac tta act tca cca act gtg tct cct gca aat tca act 783
 Ile Ile Thr His Leu Thr Ser Pro Thr Val Ser Pro Ala Asn Ser Thr
 225 230 235
 act ctt gct cct gcc tat cgt ccg ccg tca cag agt ggg cac ttt atg 831
 Thr Leu Ala Pro Ala Tyr Arg Pro Pro Ser Gln Ser Gly His Phe Met
 240 245 250
 aat ttg gat gat att tgg gga ctg att atc ttt gtt ttc tgc ctt ata 879
 Asn Leu Asp Asp Ile Trp Gly Leu Ile Ile Phe Val Phe Cys Leu Ile
 255 260 265 270
 tat tct agc ttc cgt act tcg agc aac agc caa gtt aac aag ctg acc 927
 Tyr Ser Ser Phe Arg Thr Ser Ser Asn Ser Gln Val Asn Lys Leu Thr
 275 280 285
 ctc tct ggg agt gac agt gtt atc ctt ggt gat acc acc aat gga gcc 975
 Leu Ser Gly Ser Asp Ser Val Ile Leu Gly Asp Thr Thr Asn Gly Ala
 290 295 300
 aat gat gaa gag gat gga cag cca cgg agg gct gta gac aat gag aag 1023
 Asn Asp Glu Glu Asp Gly Gln Pro Arg Arg Ala Val Asp Asn Glu Lys
 305 310 315
 gag ggg gtg cag tat agc tac tcc ttt ttc cac ttg atg ctc tgc tgt 1071
 Glu Gly Val Gln Tyr Ser Tyr Ser Phe Phe His Leu Met Leu Cys Cys
 320 325 330
 gcc tcc ttg tac atc atg atg acc ata acc agc tgg tac agc cct gat 1119
 Ala Ser Leu Tyr Ile Met Met Thr Ile Thr Ser Trp Tyr Ser Pro Asp
 335 340 345 350

```

gcc aaa ttc cag aag gta tcc agc aag tgg cta gct gtg tgg ttc aaa 1167
Ala Lys Phe Gln Lys Val Ser Ser Lys Trp Leu Ala Val Trp Phe Lys
          355                      360                      365
atg ggc tcc agc tgg ttg tgc ctc ctc ctt tac ctc tgg act ctt gtg 1215
Met Gly Ser Ser Trp Leu Cys Leu Leu Leu Tyr Leu Trp Thr Leu Val
          370                      375                      380
gct ccc ctg gtc ctc aca ggt cgg gac ttc agc tga gctcagtgtg 1261
Ala Pro Leu Val Leu Thr Gly Arg Asp Phe Ser
          385                      390
tcaaggacac tgataaagct gaccagagtc tccttttctg aaaatgcata tccattttgc 1321
gtttcatcaa cgagactatt aagtgaacgc ttgacagatt tggctgtatt caggttttata 1381
tcaaaaggca agattgagta atgcttgatg cagaatctga gctttcatat atatataat 1441
atatataat atatatacac acacacacac acacataat atgtttatit gtaaggctat 1501
agcaciaaagg gaacattttt gigtittaac atgaactaca gctgtgctgt gaagagaatt 1561
ctttataaag acctgtagat tcctacaact ttggtttaag ttttaagtta gaagattgtt 1621
ggatatttaa ggctatitit aatttctatt acagtctcct taaaaccaa aaaggaatgc 1681
attaatccac atttcccttc ttacagagggt tagtgtcctg gctcttggca aggaattatg 1741
tatttaggtc agtccccaga aatgcagcgc tcatacagct gagagaaggc tattattgag 1801
ttcctttact tactttttat actacactga tgctgcttga tagaagtctg tgggctttgt 1861
cagatatgtc acccaagtaa atgctttgta gatctgatta aaatgaaaag ctcacttgag 1921
aaacactgca gagttatgta atgatcttgt tgtgagtgtg tgaaagtcaa aggcattgtca 1981
gtttattaca ttgcaacat aaaagtactt aattaaaata gaaaaaaaa 2029

```

<210> 138

<211> 393

<212> PRT

<213> Mus musculus

<400> 138

Met Val Asp Thr Lys Ala Glu Lys Asp Cys Asp Val Leu Val Gly Phe
 1 5 10 15
 Lys Ala Val Tyr Arg Ile Asn Phe Ala Val Ala Ile Phe Phe Phe Ala
 20 25 30
 Phe Phe Leu Leu Met Leu Lys Val Lys Thr Ser Lys Asp Pro Arg Ala
 35 40 45
 Ala Val His Asn Gly Phe Trp Phe Phe Lys Ile Ala Ala Ile Ile Gly
 50 55 60
 Ile Met Ile Gly Ser Phe Tyr Ile Pro Gly Gly Ser Phe Thr Glu Val
 65 70 75 80
 Trp Phe Val Ala Gly Met Leu Gly Ala Ser Phe Phe Ile Ile Ile Gln
 85 90 95
 Leu Val Leu Leu Val Asp Met Ala His Ser Trp Asn Glu Leu Trp Val
 100 105 110
 Asn Arg Met Glu Glu Gly Asn Pro Arg Leu Trp Tyr Ala Ala Leu Leu
 115 120 125
 Ser Phe Thr Ser Leu Phe Tyr Ile Leu Ser Ile Val Phe Ala Ala Leu
 130 135 140
 Leu Tyr Val Phe Tyr Thr Lys Pro Asp Asp Cys Thr Glu Asn Lys Val
 145 150 155 160
 Phe Ile Ser Leu Asn Leu Ile Phe Cys Val Ala Val Ser Ile Val Ser
 165 170 175
 Ile Leu Pro Lys Val Gln Glu His Gln Pro Arg Ser Gly Leu Leu Gln
 180 185 190
 Ser Ser Ile Ile Thr Leu Tyr Thr Leu Tyr Leu Thr Trp Ser Ala Met
 195 200 205
 Thr Asn Glu Pro Glu Arg Ser Cys Asn Pro Ser Leu Met Ser Ile Ile
 210 215 220
 Thr His Leu Thr Ser Pro Thr Val Ser Pro Ala Asn Ser Thr Thr Leu

225 230 235 240
 Ala Pro Ala Tyr Arg Pro Pro Ser Gln Ser Gly His Phe Met Asn Leu
 245 250 255
 Asp Asp Ile Trp Gly Leu Ile Ile Phe Val Phe Cys Leu Ile Tyr Ser
 260 265 270
 Ser Phe Arg Thr Ser Ser Asn Ser Gln Val Asn Lys Leu Thr Leu Ser
 275 280 285
 Gly Ser Asp Ser Val Ile Leu Gly Asp Thr Thr Asn Gly Ala Asn Asp
 290 295 300
 Glu Glu Asp Gly Gln Pro Arg Arg Ala Val Asp Asn Glu Lys Glu Gly
 305 310 315 320
 Val Gln Tyr Ser Tyr Ser Phe Phe His Leu Met Leu Cys Cys Ala Ser
 325 330 335
 Leu Tyr Ile Met Met Thr Ile Thr Ser Trp Tyr Ser Pro Asp Ala Lys
 340 345 350
 Phe Gln Lys Val Ser Ser Lys Trp Leu Ala Val Trp Phe Lys Met Gly
 355 360 365
 Ser Ser Trp Leu Cys Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro
 370 375 380
 Leu Val Leu Thr Gly Arg Asp Phe Ser
 385 390

<210> 139

<211> 3512

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1).. (2304)

<400> 139

```

atg agt ggg gac cac ctc cac aac gat tcc cag atc gaa gcg gat ttc      48
Met Ser Gly Asp His Leu His Asn Asp Ser Gln Ile Glu Ala Asp Phe
   1             5             10             15
cga ttg aat gat tct cac aaa cac aaa gat aaa cac aaa gat cga gaa      96
Arg Leu Asn Asp Ser His Lys His Lys Asp Lys His Lys Asp Arg Glu
          20             25             30
cac cgg cat aag gag cac aag aag gat aag gat aag gac cgg gaa aag      144
His Arg His Lys Glu His Lys Lys Asp Lys Asp Lys Asp Arg Glu Lys
          35             40             45
tct aag cat agc aac agt gaa cat aaa gat tct gaa aag aaa cac aaa      192
Ser Lys His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys
          50             55             60
gag aaa gag aaa acc aaa cac aaa gat ggc agc tca gaa aaa cat aaa      240
Glu Lys Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys
          65             70             75             80
gac aaa cat aaa gac aga gac aag gaa aga cga aag gag gaa aag att      288
Asp Lys His Lys Asp Arg Asp Lys Glu Arg Arg Lys Glu Glu Lys Ile
          85             90             95
aga gct gct ggg gat gca aaa ata aag aag gaa aag gaa aat ggc ttc      336
Arg Ala Ala Gly Asp Ala Lys Ile Lys Lys Glu Lys Glu Asn Gly Phe
          100            105            110
tct agt ccg cca cga att aaa gat gac cct gag gat gat ggc tat ttt      384
Ser Ser Pro Pro Arg Ile Lys Asp Asp Pro Glu Asp Asp Gly Tyr Phe
          115            120            125
gct cct cca aaa gag gat att aag cca ttg aag agg ctt cga gat gaa      432
Ala Pro Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Leu Arg Asp Glu

```

130	135	140	
gat gat gct gat tat aaa cct aag aaa att aag aca gaa gat atc aag			480
Asp Asp Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Ile Lys			
145	150	155	160
aag gag aag aaa aga aaa tca gaa gag gaa gag gat ggt aaa ctt aaa			528
Lys Glu Lys Lys Arg Lys Ser Glu Glu Glu Glu Asp Gly Lys Leu Lys			
	165	170	175
aag ccc aag aat aaa gat aaa gat aaa aaa gtt gct gag cca gat aat			576
Lys Pro Lys Asn Lys Asp Lys Asp Lys Lys Val Ala Glu Pro Asp Asn			
	180	185	190
aag aaa aag aag ccg aaa aag gaa gag gaa cag aag tgg aaa tgg tgg			624
Lys Lys Lys Lys Pro Lys Lys Glu Glu Glu Gln Lys Trp Lys Trp Trp			
	195	200	205
gaa gaa gaa cgt tat cca gaa ggc atc aaa tgg aaa ttc cta gag cat			672
Glu Glu Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His			
	210	215	220
aaa ggg cct gtc ttc gct cca cca tat gag cct ctg cca gag agt gtc			720
Lys Gly Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Ser Val			
225	230	235	240
aag ttt tac tat gat ggt aaa gtt atg aag ctg agt cct aaa gca gaa			768
Lys Phe Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu			
	245	250	255
gaa gta gct aca ttc ttt gca aaa atg ctt gac cac gaa tat act act			816
Glu Val Ala Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr			
	260	265	270
aag gaa ata ttc agg aaa aat ttc ttt aaa gat tgg aga aag gaa atg			864
Lys Glu Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met			
	275	280	285
act aat gac gga aaa aat acg att acc aac cta agc aaa tgc gac ttt			912

Thr Asn Asp Gly Lys Asn Thr Ile Thr Asn Leu Ser Lys Cys Asp Phe
 290 295 300
 aca cag atg agc cag tat ttc aaa gcg cag tca gaa gct cgg aaa cag 960
 Thr Gln Met Ser Gln Tyr Phe Lys Ala Gln Ser Glu Ala Arg Lys Gln
 305 310 315 320
 atg agc aag gaa gaa aaa ttg aaa atc aaa gaa gaa aat gaa aag tta 1008
 Met Ser Lys Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu
 325 330 335
 ttg aaa gaa tac ggc ttt tgt gta atg gat aat cat aga gag cgg att 1056
 Leu Lys Glu Tyr Gly Phe Cys Val Met Asp Asn His Arg Glu Arg Ile
 340 345 350
 gcc aac ttc aag ata gag cct ccg ggg ctt ttc cga ggc cga ggg aac 1104
 Ala Asn Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn
 355 360 365
 cac ccc aag atg ggt atg ctg aag aga agg atc atg cct gag gac atc 1152
 His Pro Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile
 370 375 380
 atc atc aac tgt agc aaa gac gca aag gtt cct tct ccc cct cct gga 1200
 Ile Ile Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Pro Gly
 385 390 395 400
 cat aaa tgg aag gaa gtc cga cat gat aac aag gtt act tgg ctg gtc 1248
 His Lys Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val
 405 410 415
 tcc tgg aca gag aat atc caa ggt tct atc aaa tat atc atg ctg aat 1296
 Ser Trp Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn
 420 425 430
 ccc agt tca cga atc aag ggt gag aaa gac tgg cag aag tat gag act 1344
 Pro Ser Ser Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr
 435 440 445

gcg cgg cgt ctg aag aag tgt gtg gac aag atc cga aat cag tat cgg 1392
 Ala Arg Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg
 450 455 460
 gaa gac tgg aag tcc aaa gag atg aaa gtt cgt cag aga gct gta gca 1440
 Glu Asp Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala
 465 470 475 480
 ctg tac ttc att gat aag ctt gct ctg aga gca ggc aat gag aag gaa 1488
 Leu Tyr Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu
 485 490 495
 gaa gga gag acg gca gac act gtg ggc tgc tgt tca ctt aga gtg gaa 1536
 Glu Gly Glu Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu
 500 505 510
 cac atc aat tta cac cca gaa ttg gat ggt cag gag tat gtg gtg gaa 1584
 His Ile Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu
 515 520 525
 ttt gac ttt cct ggg aag gac tca atc aga tac tat aac aaa gtc cca 1632
 Phe Asp Phe Pro Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro
 530 535 540
 gtt gag aaa cga gtt ttt aaa aac tta caa ctg ttt atg gag aac aag 1680
 Val Glu Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys
 545 550 555 560
 cag cct gag gac gat ctt ttt gat cga ctt aat act ggt att cta aat 1728
 Gln Pro Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn
 565 570 575
 aaa cat ctt cag gat ctc atg gag ggc ttg act gcc aag gtg ttc cgt 1776
 Lys His Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg
 580 585 590
 acc tac aat gcc tcc atc aca cta cag cag cag ctt aaa gag ctc aca 1824
 Thr Tyr Asn Ala Ser Ile Thr Leu Gln Gln Gln Leu Lys Glu Leu Thr

595	600	605	
gcc cct gat gag aat gta cca gcg aag att cta tct tat aac cgt gcc	1872		
Ala Pro Asp Glu Asn Val Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala			
610	615	620	
aat cga gct gtt gca att ctt tgt aac cac cag agg gcg cca cca aag	1920		
Asn Arg Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys			
625	630	635	640
acc ttt gag aag tca atg atg aac ttg cag tct aag att gat gcc aag	1968		
Thr Phe Glu Lys Ser Met Met Asn Leu Gln Ser Lys Ile Asp Ala Lys			
645	650	655	
aaa gat cag tta gca gat gct cga agg gac ctg aaa agt gct aag gct	2016		
Lys Asp Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala			
660	665	670	
gat gcc aaa gtc atg aag gat gca aag acc aag aag gta gta gag tca	2064		
Asp Ala Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser			
675	680	685	
aaa aag aag gct gta cag aga cta gaa gag cag ttg atg aag ctg gaa	2112		
Lys Lys Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu			
690	695	700	
gtt caa gcc aca gat cga gag gag aac aaa caa att gcc ttg ggg acc	2160		
Val Gln Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr			
705	710	715	720
tcc aaa ctc aat tat ctg gac cct agg atc aca gtg gct tgg tgc aaa	2208		
Ser Lys Leu Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys			
725	730	735	
aag tgg ggg gtc cca att gag aag att tac aac aaa acc cag agg gag	2256		
Lys Trp Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu			
740	745	750	
aag ttt gct tgg gcc att gat atg act gat gag gac tac gag ttt tga	2304		

Lys Phe Ala Trp Ala Ile Asp Met Thr Asp Glu Asp Tyr Glu Phe

755

760

765

ccagtc t cgg caggggttct gtgaaaagga acagtgtggt ttggggaaga tggataaact 2364
 gagcctcact tccccacaca cccgagggag agaggccaca agtcttaaca aaccaacatc 2424
 ttgcaaaaa gatagacctg gagatactat aaggagagc tgagccagtt gtcctatgga 2484
 caacttattt aaaaatattt cagatatcaa aattctagct gtatgatttg ttttgaattt 2544
 tgtttttact ttcaagagag caagtggatg ggaatttgtc agcatcctgc caggcaaatt 2604
 cagtttgcct gcaatgtttg gattctctca gctactgtat gtgaagtctg attatatgga 2664
 tgcgttttta cagttagggt ttgcaataa cttctatatt ttaatagaaa caaatccta 2724
 aactccctcc tctccctat ttcaggaatt taaaattaag tagaacaaaa caaaaaccca 2784
 gcgcacctat tacagctgtc attctatcgt catgggaatc agttttcatt aaacttgaag 2844
 cagttgtgac attggcagtg ttttggttca gacacctatt cacagaaaag catgatggga 2904
 aaatatctcc tgacttgagt gttccttttt aaatgtgaat ttttatttcg ttttaattat 2964
 tttaaaatat ttaagccttc ttcttgatct taaagatcgt gtagcttggg gttggggagg 3024
 gatgaagggc gagtgagtct aaggataatg taataatcag tgactgaaac cattttccca 3084
 tcatcctttg ttctgacctt tctttgtacc ctttaagaga tccatctttt tcttggaac 3144
 cccagtcctt catttgaaag atgttattgt ataaaaactt ccacaggica ataaatttag 3204
 aggaaaatga gcatttggc caagaaaaac aaaaaccaa acaaaacaaa aaaggaaaaa 3264
 taatcaagat tttagggctt ttattttttc ttttgaatt gtgtaaaaaa tggaaaaaaa 3324
 aacataaaaa gaaaatttt aatgtgaaga cttttttttt gctataatca ttagtttttag 3384
 aggcattgtt agttagtgtg tgtgcagagt ccattcccac atctttcctc aagtatcttc 3444
 tatttttatt atgaattccc ttttaatcaa ctgtaggita tttaaaataa actcctacaa 3504
 cttacgg 3512

<210> 140

<211> 767

<212> PRT

<213> Mus musculus

<400> 140

```

Met Ser Gly Asp His Leu His Asn Asp Ser Gln Ile Glu Ala Asp Phe
  1             5             10             15
Arg Leu Asn Asp Ser His Lys His Lys Asp Lys His Lys Asp Arg Glu
      20             25             30
His Arg His Lys Glu His Lys Lys Asp Lys Asp Lys Asp Arg Glu Lys
      35             40             45
Ser Lys His Ser Asn Ser Glu His Lys Asp Ser Glu Lys Lys His Lys
      50             55             60
Glu Lys Glu Lys Thr Lys His Lys Asp Gly Ser Ser Glu Lys His Lys
      65             70             75             80
Asp Lys His Lys Asp Arg Asp Lys Glu Arg Arg Lys Glu Glu Lys Ile
      85             90             95
Arg Ala Ala Gly Asp Ala Lys Ile Lys Lys Glu Lys Glu Asn Gly Phe
      100            105            110
Ser Ser Pro Pro Arg Ile Lys Asp Asp Pro Glu Asp Asp Gly Tyr Phe
      115            120            125
Ala Pro Pro Lys Glu Asp Ile Lys Pro Leu Lys Arg Leu Arg Asp Glu
      130            135            140
Asp Asp Ala Asp Tyr Lys Pro Lys Lys Ile Lys Thr Glu Asp Ile Lys
      145            150            155            160
Lys Glu Lys Lys Arg Lys Ser Glu Glu Glu Glu Asp Gly Lys Leu Lys
      165            170            175
Lys Pro Lys Asn Lys Asp Lys Asp Lys Lys Val Ala Glu Pro Asp Asn
      180            185            190
Lys Lys Lys Lys Pro Lys Lys Glu Glu Glu Gln Lys Trp Lys Trp Trp
      195            200            205
Glu Glu Glu Arg Tyr Pro Glu Gly Ile Lys Trp Lys Phe Leu Glu His
      210            215            220

```

Lys Gly Pro Val Phe Ala Pro Pro Tyr Glu Pro Leu Pro Glu Ser Val			
225	230	235	240
Lys Phe Tyr Tyr Asp Gly Lys Val Met Lys Leu Ser Pro Lys Ala Glu			
	245	250	255
Glu Val Ala Thr Phe Phe Ala Lys Met Leu Asp His Glu Tyr Thr Thr			
	260	265	270
Lys Glu Ile Phe Arg Lys Asn Phe Phe Lys Asp Trp Arg Lys Glu Met			
	275	280	285
Thr Asn Asp Gly Lys Asn Thr Ile Thr Asn Leu Ser Lys Cys Asp Phe			
	290	295	300
Thr Gln Met Ser Gln Tyr Phe Lys Ala Gln Ser Glu Ala Arg Lys Gln			
305	310	315	320
Met Ser Lys Glu Glu Lys Leu Lys Ile Lys Glu Glu Asn Glu Lys Leu			
	325	330	335
Leu Lys Glu Tyr Gly Phe Cys Val Met Asp Asn His Arg Glu Arg Ile			
	340	345	350
Ala Asn Phe Lys Ile Glu Pro Pro Gly Leu Phe Arg Gly Arg Gly Asn			
	355	360	365
His Pro Lys Met Gly Met Leu Lys Arg Arg Ile Met Pro Glu Asp Ile			
	370	375	380
Ile Ile Asn Cys Ser Lys Asp Ala Lys Val Pro Ser Pro Pro Pro Gly			
385	390	395	400
His Lys Trp Lys Glu Val Arg His Asp Asn Lys Val Thr Trp Leu Val			
	405	410	415
Ser Trp Thr Glu Asn Ile Gln Gly Ser Ile Lys Tyr Ile Met Leu Asn			
	420	425	430
Pro Ser Ser Arg Ile Lys Gly Glu Lys Asp Trp Gln Lys Tyr Glu Thr			
	435	440	445
Ala Arg Arg Leu Lys Lys Cys Val Asp Lys Ile Arg Asn Gln Tyr Arg			

450	455	460
Glu Asp Trp Lys Ser Lys Glu Met Lys Val Arg Gln Arg Ala Val Ala		
465	470	475
Leu Tyr Phe Ile Asp Lys Leu Ala Leu Arg Ala Gly Asn Glu Lys Glu		480
	485	490
Glu Gly Glu Thr Ala Asp Thr Val Gly Cys Cys Ser Leu Arg Val Glu		495
	500	505
His Ile Asn Leu His Pro Glu Leu Asp Gly Gln Glu Tyr Val Val Glu		510
	515	520
Phe Asp Phe Pro Gly Lys Asp Ser Ile Arg Tyr Tyr Asn Lys Val Pro		525
	530	535
Val Glu Lys Arg Val Phe Lys Asn Leu Gln Leu Phe Met Glu Asn Lys		540
545	550	555
Gln Pro Glu Asp Asp Leu Phe Asp Arg Leu Asn Thr Gly Ile Leu Asn		560
	565	570
Lys His Leu Gln Asp Leu Met Glu Gly Leu Thr Ala Lys Val Phe Arg		575
	580	585
Thr Tyr Asn Ala Ser Ile Thr Leu Gln Gln Gln Leu Lys Glu Leu Thr		590
	595	600
Ala Pro Asp Glu Asn Val Pro Ala Lys Ile Leu Ser Tyr Asn Arg Ala		605
	610	615
Asn Arg Ala Val Ala Ile Leu Cys Asn His Gln Arg Ala Pro Pro Lys		620
625	630	635
Thr Phe Glu Lys Ser Met Met Asn Leu Gln Ser Lys Ile Asp Ala Lys		640
	645	650
Lys Asp Gln Leu Ala Asp Ala Arg Arg Asp Leu Lys Ser Ala Lys Ala		655
	660	665
Asp Ala Lys Val Met Lys Asp Ala Lys Thr Lys Lys Val Val Glu Ser		670
	675	680
		685

Lys Lys Lys Ala Val Gln Arg Leu Glu Glu Gln Leu Met Lys Leu Glu
 690 695 700
 Val Gln Ala Thr Asp Arg Glu Glu Asn Lys Gln Ile Ala Leu Gly Thr
 705 710 715 720
 Ser Lys Leu Asn Tyr Leu Asp Pro Arg Ile Thr Val Ala Trp Cys Lys
 725 730 735
 Lys Trp Gly Val Pro Ile Glu Lys Ile Tyr Asn Lys Thr Gln Arg Glu
 740 745 750
 Lys Phe Ala Trp Ala Ile Asp Met Thr Asp Glu Asp Tyr Glu Phe
 755 760 765

<210> 141

<211> 218

<212> DNA

<213> Mus musculus

<400> 141

atccctgctc caggacagtg tggaggtacg agaggacctt cgtctgcctg aaggaggact 60
 gggcaatgag atgtggcaga agtatgactg tggagaggag atcctgatca cagtgcctgc 120
 tgccatgaca gaggaggcag ctgttgcat caaggccatt gcggaataac cggcttccag 180
 ggtggcggtg gtgggagcag tgatccgtga gcctacag 218

<210> 142

<211> 3227

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (410).. (2455)

<400> 142

gtgctccacc ttgcacagcg ttggggggac tgaagacata agtgacgggc gggggggggg 60
 gggactatgc ggagtcccag gctgccctct tcccagagat gcgccgctat tgttatittc 120
 ttccacttcg tccccccagg atgaacttgc gtcctttctc taatccgcca tggaattctg 180
 ctccgtgctt ttagccctcc agagccaaag aaaccccgaga caacagacgc ccagacgcag 240
 cagcgtatag cagtaactcc ccagctcggt ttccgtgccg tagtttacag tatttaattt 300
 tatataatat atactattta ttatagcatt ttgataccic attccgttta cacatctcaa 360
 aagccgctta gtaattctct tattatttaa agaaccacta cactagaga atg gaa tct 418

Met Glu Ser

1

act gtg gca acg att act agt acc cta gct gct gtt act gct tcc gct 466
 Thr Val Ala Thr Ile Thr Ser Thr Leu Ala Ala Val Thr Ala Ser Ala

5

10

15

cca ccg aag tat gac aat cta tgg atg ctc atc ctg ggc ttc atc att 514
 Pro Pro Lys Tyr Asp Asn Leu Trp Met Leu Ile Leu Gly Phe Ile Ile

20

25

30

35

gca ttt gtc ttg gca ttc tcc gtg gga gcc aat gat gta gca aat tcg 562
 Ala Phe Val Leu Ala Phe Ser Val Gly Ala Asn Asp Val Ala Asn Ser

40

45

50

ttc ggt aca gct gta ggc tca ggt gta gtg acc ctg aag caa gcc tgc 610
 Phe Gly Thr Ala Val Gly Ser Gly Val Val Thr Leu Lys Gln Ala Cys

55

60

65

atc tta gct agc atc ttc gaa act gtg ggc tcc gcc ttg ctg ggg gcc 658
 Ile Leu Ala Ser Ile Phe Glu Thr Val Gly Ser Ala Leu Leu Gly Ala

70

75

80

aaa gtg agc gaa acc atc cgg aac ggc ttg ata gat gtg gag ctg tac 706
 Lys Val Ser Glu Thr Ile Arg Asn Gly Leu Ile Asp Val Glu Leu Tyr

85	90	95	
aac gaa act caa gat ctg ctc atg gct ggc tcc gtc agt gct atg ttt			754
Asn Glu Thr Gln Asp Leu Leu Met Ala Gly Ser Val Ser Ala Met Phe			
100	105	110	115
ggt tct gct gtg tgg cag ctc gtg gct tcg ttt ttg aag ctt ccg att			802
Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys Leu Pro Ile			
	120	125	130
tct ggg acc cat tgt att gtc ggt gca acc att ggt ttc tcc ctt gtg			850
Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe Ser Leu Val			
	135	140	145
gca aat ggg cag aag ggt gtc aag tgg tct gaa ctg ata aaa att gtg			898
Ala Asn Gly Gln Lys Gly Val Lys Trp Ser Glu Leu Ile Lys Ile Val			
	150	155	160
atg tcg tgg ttc gtc tct ccg ctg ctt tct ggt att atg tct gga att			946
Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met Ser Gly Ile			
	165	170	175
tta ttc ttc ctt gtt cgt gcg ttc atc ctc cgt aag gca gat ccg gtt			994
Leu Phe Phe Leu Val Arg Ala Phe Ile Leu Arg Lys Ala Asp Pro Val			
	180	185	190
cct aat ggc tta cga gct tta cca att ttt tat gcc tgc aca atc gga			1042
Pro Asn Gly Leu Arg Ala Leu Pro Ile Phe Tyr Ala Cys Thr Ile Gly			
	200	205	210
atc aac ctc ttt tcc att atg tat act gga gca ccg ttg ctg ggc ttt			1090
Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu Leu Gly Phe			
	215	220	225
gac aaa ctt cct ctg tgg ggt acc atc ctc atc tcg gtg gga tgt gca			1138
Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val Gly Cys Ala			
	230	235	240
gtt ttc tgt gcc ctt atc gtc tgg ttc ttt gta tgt ccc agg atg aag			1186

Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro Arg Met Lys
 245 250 255
 aga aaa att gaa cga gaa gta aag tct agt ccg tct gaa agt ccc tta 1234
 Arg Lys Ile Glu Arg Glu Val Lys Ser Ser Pro Ser Glu Ser Pro Leu
 260 265 270 275
 atg gaa aag aag agc aac tta aaa gaa gac cat gaa gaa aca aag atg 1282
 Met Glu Lys Lys Ser Asn Leu Lys Glu Asp His Glu Glu Thr Lys Met
 280 285 290
 gct cct gga gac gtt gag cat agg aat cct gtg tct gag gta gtg tgt 1330
 Ala Pro Gly Asp Val Glu His Arg Asn Pro Val Ser Glu Val Val Cys
 295 300 305
 gcc act ggg cca ctc cgg gct gtg gtg gag gag agg acg gtg tca ttc 1378
 Ala Thr Gly Pro Leu Arg Ala Val Val Glu Glu Arg Thr Val Ser Phe
 310 315 320
 aaa ctt ggt gac ctg gag gag gct ccg gag cga gag cgg ctt ccc atg 1426
 Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg Leu Pro Met
 325 330 335
 gac ctg aag gag gag acc agc ata gac agc acc atc aat ggt gca gtg 1474
 Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Ile Asn Gly Ala Val
 340 345 350 355
 cag ttg cct aat ggg aac ctt gtt cag ttc agt caa act gtc agc aac 1522
 Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Thr Val Ser Asn
 360 365 370
 cag atc aac tcc agt ggc cac tat cag tat cac acc gtg cac aag gat 1570
 Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val His Lys Asp
 375 380 385
 tct ggc ttg tac aag gag ctg ctc cat aag tta cat ctg gcc aag gtg 1618
 Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu Ala Lys Val
 390 395 400

gga gac tgc atg gga gat tct ggg gac aag ccc ttg aga cgc aac aac 1666
 Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg Arg Asn Asn
 405 410 415
 agc tac act tcc tac act atg gca ata tgt ggc atg ccc ctg gat tca 1714
 Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro Leu Asp Ser
 420 425 430 435
 ttc cgt gcc aaa gaa ggt gaa caa aag gga gat gaa atg gag acg ctg 1762
 Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Asp Glu Met Glu Thr Leu
 440 445 450
 aca tgg cct aat gca gat acc aag aag cgg att cga atg gac agt tac 1810
 Thr Trp Pro Asn Ala Asp Thr Lys Lys Arg Ile Arg Met Asp Ser Tyr
 455 460 465
 acc agt tac tgc aat gcc gtg tct gac ctt cac tcc gag tct gag atg 1858
 Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Glu Ser Glu Met
 470 475 480
 gac atg agt gtg aag gct gag atg ggc ctg ggt gac aga aaa gga agc 1906
 Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg Lys Gly Ser
 485 490 495
 agt ggc tct ctt gaa gaa tgg tat gac cag gat aag cct gaa gtg tcc 1954
 Ser Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro Glu Val Ser
 500 505 510 515
 ctt ctc ttc cag ttc ctg cag atc ctt aca gcc tgc ttt ggg tca ttt 2002
 Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe Gly Ser Phe
 520 525 530
 gcc cat ggt ggc aat gac gtc agc aat gcc atc ggc cct ctg gtt gct 2050
 Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro Leu Val Ala
 535 540 545
 ttg tat ctt gtt tat aaa caa gaa gcc tct aca aaa gcg gca aca ccc 2098
 Leu Tyr Leu Val Tyr Lys Gln Glu Ala Ser Thr Lys Ala Ala Thr Pro

550 555 560
 ata tgg ctt ctg ctt tat ggt ggt gtt ggc att tgc atg ggc ctg tgg 2146
 Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Met Gly Leu Trp
 565 570 575
 gtt tgg gga aga aga gtt atc cag acc atg ggg aag gac ctg acc cca 2194
 Val Trp Gly Arg Arg Val Ile Gln Thr Met Gly Lys Asp Leu Thr Pro
 580 585 590 595
 atc aca ccc tcc agt ggt ttc agt att gaa ctg gcg tct gcc tta act 2242
 Ile Thr Pro Ser Ser Gly Phe Ser Ile Glu Leu Ala Ser Ala Leu Thr
 600 605 610
 gtg gtc atc gca tca aac att ggc ctt ccc atc agc aca aca cat tgc 2290
 Val Val Ile Ala Ser Asn Ile Gly Leu Pro Ile Ser Thr Thr His Cys
 615 620 625
 aaa gtg ggc tct gtt gtg tct gtt ggc tgg ctc cga tca aag aag gct 2338
 Lys Val Gly Ser Val Val Ser Val Gly Trp Leu Arg Ser Lys Lys Ala
 630 635 640
 gtt gac tgg cga ctg ttt cga aac att ttt atg gcc tgg ttt gtc acg 2386
 Val Asp Trp Arg Leu Phe Arg Asn Ile Phe Met Ala Trp Phe Val Thr
 645 650 655
 gtc ccc atc tct ggg gtt atc agt gcc gct atc atg gca gta ttc aag 2434
 Val Pro Ile Ser Gly Val Ile Ser Ala Ala Ile Met Ala Val Phe Lys
 660 665 670 675
 tac atc atc ctg cca gtg tga cgctgggggtt gaaagctgtg tcagtgtctg 2485
 Tyr Ile Ile Leu Pro Val
 680
 ggaccattgt acacattcct gttcctagga gaacgctcac agtggttgctg aagacaggca 2545
 agggctcttaa aggagccgtg ggaaggaagt gtaattitaca ctataattgc ttttgtgcta 2605
 aatatgactt atctcaaaat tagctatgta aaatagccag gtttccattg attcattcca 2665
 aggtcccttt tctcctgggc tatgaattcc tgtacatatt tctctacitt tgtatcaggc 2725

ctcaattcca gtaigtittta atgttgctcg tgagataact taggtgggtt ctttttaaac 2785
 agccagcaga gccatttgat ggcatgtact gctttgtcgg cctcaccagc ttcttcccca 2845
 acatgcacag ggattttaaca acatgtaact gaagcttccc tccctcatag tctctcatag 2905
 aaatagtcac ggcactctgc tccctgtcac tagtggcagg ttctgttgat gtgtgacaac 2965
 ttcttagagg gccgagaatc ttgggcacag tggaaatata agtttgiagt aacctctttg 3025
 caaacagttc acggacatgt tgctaagaag caggagaca aagccccctgg cggttggtgt 3085
 tattcttctg agatttctgg cagtgtggga tgggtgaatg aagtggatg tgaactttgg 3145
 gcaaattcaa tgggacagcc ttccatgttc atctgtctac ctcttaactg aataaaaagc 3205
 ctacagtttt taaaaaaaaa aa 3227

<210> 143

<211> 681

<212> PRT

<213> Mus musculus

<400> 143

Met	Glu	Ser	Thr	Val	Ala	Thr	Ile	Thr	Ser	Thr	Leu	Ala	Ala	Val	Thr
1				5					10					15	
Ala	Ser	Ala	Pro	Pro	Lys	Tyr	Asp	Asn	Leu	Trp	Met	Leu	Ile	Leu	Gly
			20					25						30	
Phe	Ile	Ile	Ala	Phe	Val	Leu	Ala	Phe	Ser	Val	Gly	Ala	Asn	Asp	Val
		35					40						45		
Ala	Asn	Ser	Phe	Gly	Thr	Ala	Val	Gly	Ser	Gly	Val	Val	Thr	Leu	Lys
		50				55							60		
Gln	Ala	Cys	Ile	Leu	Ala	Ser	Ile	Phe	Glu	Thr	Val	Gly	Ser	Ala	Leu
		65			70					75				80	
Leu	Gly	Ala	Lys	Val	Ser	Glu	Thr	Ile	Arg	Asn	Gly	Leu	Ile	Asp	Val
				85						90				95	
Glu	Leu	Tyr	Asn	Glu	Thr	Gln	Asp	Leu	Leu	Met	Ala	Gly	Ser	Val	Ser

100	105	110
Ala Met Phe Gly Ser Ala Val Trp Gln Leu Val Ala Ser Phe Leu Lys		
115	120	125
Leu Pro Ile Ser Gly Thr His Cys Ile Val Gly Ala Thr Ile Gly Phe		
130	135	140
Ser Leu Val Ala Asn Gly Gln Lys Gly Val Lys Trp Ser Glu Leu Ile		
145	150	155
Lys Ile Val Met Ser Trp Phe Val Ser Pro Leu Leu Ser Gly Ile Met		
165	170	175
Ser Gly Ile Leu Phe Phe Leu Val Arg Ala Phe Ile Leu Arg Lys Ala		
180	185	190
Asp Pro Val Pro Asn Gly Leu Arg Ala Leu Pro Ile Phe Tyr Ala Cys		
195	200	205
Thr Ile Gly Ile Asn Leu Phe Ser Ile Met Tyr Thr Gly Ala Pro Leu		
210	215	220
Leu Gly Phe Asp Lys Leu Pro Leu Trp Gly Thr Ile Leu Ile Ser Val		
225	230	235
Gly Cys Ala Val Phe Cys Ala Leu Ile Val Trp Phe Phe Val Cys Pro		
245	250	255
Arg Met Lys Arg Lys Ile Glu Arg Glu Val Lys Ser Ser Pro Ser Glu		
260	265	270
Ser Pro Leu Met Glu Lys Lys Ser Asn Leu Lys Glu Asp His Glu Glu		
275	280	285
Thr Lys Met Ala Pro Gly Asp Val Glu His Arg Asn Pro Val Ser Glu		
290	295	300
Val Val Cys Ala Thr Gly Pro Leu Arg Ala Val Val Glu Glu Arg Thr		
305	310	315
Val Ser Phe Lys Leu Gly Asp Leu Glu Glu Ala Pro Glu Arg Glu Arg		
325	330	335

Leu Pro Met Asp Leu Lys Glu Glu Thr Ser Ile Asp Ser Thr Ile Asn
 340 345 350
 Gly Ala Val Gln Leu Pro Asn Gly Asn Leu Val Gln Phe Ser Gln Thr
 355 360 365
 Val Ser Asn Gln Ile Asn Ser Ser Gly His Tyr Gln Tyr His Thr Val
 370 375 380
 His Lys Asp Ser Gly Leu Tyr Lys Glu Leu Leu His Lys Leu His Leu
 385 390 395 400
 Ala Lys Val Gly Asp Cys Met Gly Asp Ser Gly Asp Lys Pro Leu Arg
 405 410 415
 Arg Asn Asn Ser Tyr Thr Ser Tyr Thr Met Ala Ile Cys Gly Met Pro
 420 425 430
 Leu Asp Ser Phe Arg Ala Lys Glu Gly Glu Gln Lys Gly Asp Glu Met
 435 440 445
 Glu Thr Leu Thr Trp Pro Asn Ala Asp Thr Lys Lys Arg Ile Arg Met
 450 455 460
 Asp Ser Tyr Thr Ser Tyr Cys Asn Ala Val Ser Asp Leu His Ser Glu
 465 470 475 480
 Ser Glu Met Asp Met Ser Val Lys Ala Glu Met Gly Leu Gly Asp Arg
 485 490 495
 Lys Gly Ser Ser Gly Ser Leu Glu Glu Trp Tyr Asp Gln Asp Lys Pro
 500 505 510
 Glu Val Ser Leu Leu Phe Gln Phe Leu Gln Ile Leu Thr Ala Cys Phe
 515 520 525
 Gly Ser Phe Ala His Gly Gly Asn Asp Val Ser Asn Ala Ile Gly Pro
 530 535 540
 Leu Val Ala Leu Tyr Leu Val Tyr Lys Gln Glu Ala Ser Thr Lys Ala
 545 550 555 560
 Ala Thr Pro Ile Trp Leu Leu Leu Tyr Gly Gly Val Gly Ile Cys Met

				565					570					575			
Gly	Leu	Trp	Val	Trp	Gly	Arg	Arg	Val	Ile	Gln	Thr	Met	Gly	Lys	Asp		
			580						585					590			
Leu	Thr	Pro	Ile	Thr	Pro	Ser	Ser	Gly	Phe	Ser	Ile	Glu	Leu	Ala	Ser		
			595						600					605			
Ala	Leu	Thr	Val	Val	Ile	Ala	Ser	Asn	Ile	Gly	Leu	Pro	Ile	Ser	Thr		
			610						615					620			
Thr	His	Cys	Lys	Val	Gly	Ser	Val	Val	Ser	Val	Gly	Trp	Leu	Arg	Ser		
625									630					635			640
Lys	Lys	Ala	Val	Asp	Trp	Arg	Leu	Phe	Arg	Asn	Ile	Phe	Met	Ala	Trp		
				645					650					655			
Phe	Val	Thr	Val	Pro	Ile	Ser	Gly	Val	Ile	Ser	Ala	Ala	Ile	Met	Ala		
			660						665					670			
Val	Phe	Lys	Tyr	Ile	Ile	Leu	Pro	Val									
			675						680								

<210> 144

<211> 618

<212> DNA

<213> Mus musculus

<400> 144

tgtaaagagt	gcgggaaagc	ttttaatcag	aactcacatc	tcatccagca	tatgagagtc	60
catagcggag	aaaaaccctt	cgaatgcaaa	gagtgtggaa	agaccttcgg	gactaactcc	120
agccttcgaa	ggcaccagag	aattcacgcc	ggagagaaac	ccttctgttg	cactgagtgt	180
ggcaaggcct	tcattcagag	ctcacatctg	attcaccatc	acagaatcca	tactggagaa	240
agaccttata	aatgtgaaga	gtgtggtaaa	gccttcagtc	agaactcagc	ccttattctg	300
caccagagaa	tccacactgg	agagaaaccc	tatgagtgtg	acgagtgtgg	gaagaccttc	360
cggttagct	cacagctcat	ccagcatcag	agaattcaca	cagaggaaaag	ataccacgag	420

tgcagtgagt gcggcaaagc ttcaagcaca gctccggcct catcagacat cagaaaatcc 480
 acacgggaga aaagccctat ctgtgtaatg aatgtgggaa aggctttggt cagagctcgg 540
 agcittatccc gcatcaagaa tcacacaggg gacaagccct atgagtgagt gaatgcggaa 600
 aaacgtttgc cagactca 618

<210> 145

<211> 347

<212> DNA

<213> Mus musculus

<400> 145

ggaggggctg tcggcggcgg ctgcccaagg acggtttgca ggaigctaag tgcctagagc 60
 caatcccaaa tcggcggcgc gcttcctcgc tgtcccgta cgcgcagccg agcctatcag 120
 tggtgccggg agtacctggg cggggctggc gccgagccgg ccggaggagc tgagcgtttg 180
 tcccgtagagc ggaggcctca gcaacctgct cttccgatgc tcactaccga accacgtacc 240
 cagtgtgggc ggggagcccg ggaggtgctg ctacgactct acggggccat cctgcagggt 300
 gtagactcct tgggtattaga aagcgtgatg ttgccattc tcgcaga 347

<210> 146

<211> 532

<212> DNA

<213> Mus musculus

<400> 146

catgttttcc tctttttacc cttcagtga agatgtctct gaacggacag cgcggggagt 60
 gctgggtgtg gaaccccaat accgggaagc ccatccaggg agctcccacc atccggggag 120
 accccgagtg ccatctcttc tacaacgagc agcaggagac tgggtggggc catgccccaa 180
 gtgtgcagta aaccccaccg agtcgggtccg tcggttcccc atcccgaaca ccagcagaaa 240
 tggagggcgc tagggtagcg ggtgtggagg agttcccagt tttagacacat gtatttatat 300

ttggaaagag accaacactg agctcagaag cccccctctg acccccccca gcggctgtta 360
 actgaaccctc cttgcttctg ttagagaggg gggaaggggt ggtatggagg gcactgggta 420
 caggcc tggg aatggggaaa gaaattttta tttttgaatc cctgtgtctc ttttgcttaa 480
 gattaaagga aggaaaataa aagctgctgc tgtcttactt gagtccttgg gg 532

<210> 147

<211> 878

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (55).. (771)

<400> 147

tgtccagcgg caggagagta ctgagaagcg tcggggagcg caggcccaac agcc atg 57
 Met
 1
 gcg gtg gaa gga gga atg aag tgt gtc aag ttt ttg ctc tac gtt ctc 105
 Ala Val Glu Gly Gly Met Lys Cys Val Lys Phe Leu Leu Tyr Val Leu
 5 10 15
 ctg ctg gcc ttc tgc gcc tgt gca gtg gga ttg atc gcc att ggt gta 153
 Leu Leu Ala Phe Cys Ala Cys Ala Val Gly Leu Ile Ala Ile Gly Val
 20 25 30
 gcg gtt cag gtt gtc ttg aag cag gcc att acc cat gag act act gct 201
 Ala Val Gln Val Val Leu Lys Gln Ala Ile Thr His Glu Thr Thr Ala
 35 40 45
 ggc tcg ctg ttg cct gtg gtc atc att gca gtg ggt gcc ttc ctc ttc 249
 Gly Ser Leu Leu Pro Val Val Ile Ile Ala Val Gly Ala Phe Leu Phe

50	55	60	65	
ctg gtg gcc ttt gtg ggc tgc tgt ggg gcc tgc aag gag aac tac tgt	297			
Leu Val Ala Phe Val Gly Cys Cys Gly Ala Cys Lys Glu Asn Tyr Cys				
70	75	80		
ctc atg att aca ttt gcc atc ttc ttg tct ctt atc atg ctt gtg gag	345			
Leu Met Ile Thr Phe Ala Ile Phe Leu Ser Leu Ile Met Leu Val Glu				
85	90	95		
gtg gct gtg gcc att gct ggc tat gtg ttt aga gac cag gtg aag tca	393			
Val Ala Val Ala Ile Ala Gly Tyr Val Phe Arg Asp Gln Val Lys Ser				
100	105	110		
gag ttt aat aaa agc ttc cag cag cag atg cag aat tac ctt aaa gac	441			
Glu Phe Asn Lys Ser Phe Gln Gln Gln Met Gln Asn Tyr Leu Lys Asp				
115	120	125		
aac aaa aca gcc act att ttg gac aaa ttg cag aaa gaa aat aac tgc	489			
Asn Lys Thr Ala Thr Ile Leu Asp Lys Leu Gln Lys Glu Asn Asn Cys				
130	135	140	145	
tgt gga gct tct aac tac aca gac tgg gaa aac atc ccc ggc atg gcc	537			
Cys Gly Ala Ser Asn Tyr Thr Asp Trp Glu Asn Ile Pro Gly Met Ala				
150	155	160		
aag gac aga gtc ccc gat tct tgc tgc atc aac ata act gtg ggc tgt	585			
Lys Asp Arg Val Pro Asp Ser Cys Cys Ile Asn Ile Thr Val Gly Cys				
165	170	175		
ggg aat gat ttc aag gaa tcc act atc cat acc cag ggc tgc gtg gag	633			
Gly Asn Asp Phe Lys Glu Ser Thr Ile His Thr Gln Gly Cys Val Glu				
180	185	190		
act ata gca ata tgg cta agg aag aac ata ctg ctg gtg gct gca gcg	681			
Thr Ile Ala Ile Trp Leu Arg Lys Asn Ile Leu Leu Val Ala Ala Ala				
195	200	205		
gcc ctg ggc att gct ttt gtg gag gtc ttg gga att atc ttc tcc tgc	729			

Ala Leu Gly Ile Ala Phe Val Glu Val Leu Gly Ile Ile Phe Ser Cys
 210 215 220 225
 tgt ctg gtg aag agt att cga agt ggc tat gaa gta atg tag 771
 Cys Leu Val Lys Ser Ile Arg Ser Gly Tyr Glu Val Met
 230 235
 ggggtggggg cgtttgggtct tticattggag tggattctcc aggtttttca attaaacgga 831
 ttattttttc agacctaaaa aaaaaaataa aaaaaaaaaa aaaaaaa 878

<210> 148

<211> 238

<212> PRT

<213> Mus musculus

<400> 148

Met Ala Val Glu Gly Gly Met Lys Cys Val Lys Phe Leu Leu Tyr Val
 1 5 10 15
 Leu Leu Leu Ala Phe Cys Ala Cys Ala Val Gly Leu Ile Ala Ile Gly
 20 25 30
 Val Ala Val Gln Val Val Leu Lys Gln Ala Ile Thr His Glu Thr Thr
 35 40 45
 Ala Gly Ser Leu Leu Pro Val Val Ile Ile Ala Val Gly Ala Phe Leu
 50 55 60
 Phe Leu Val Ala Phe Val Gly Cys Cys Gly Ala Cys Lys Glu Asn Tyr
 65 70 75 80
 Cys Leu Met Ile Thr Phe Ala Ile Phe Leu Ser Leu Ile Met Leu Val
 85 90 95
 Glu Val Ala Val Ala Ile Ala Gly Tyr Val Phe Arg Asp Gln Val Lys
 100 105 110
 Ser Glu Phe Asn Lys Ser Phe Gln Gln Gln Met Gln Asn Tyr Leu Lys

115	120	125
Asp Asn Lys Thr Ala Thr Ile Leu Asp Lys Leu Gln Lys Glu Asn Asn		
130	135	140
Cys Cys Gly Ala Ser Asn Tyr Thr Asp Trp Glu Asn Ile Pro Gly Met		
145	150	155
Ala Lys Asp Arg Val Pro Asp Ser Cys Cys Ile Asn Ile Thr Val Gly		
165	170	175
Cys Gly Asn Asp Phe Lys Glu Ser Thr Ile His Thr Gln Gly Cys Val		
180	185	190
Glu Thr Ile Ala Ile Trp Leu Arg Lys Asn Ile Leu Leu Val Ala Ala		
195	200	205
Ala Ala Leu Gly Ile Ala Phe Val Glu Val Leu Gly Ile Ile Phe Ser		
210	215	220
Cys Cys Leu Val Lys Ser Ile Arg Ser Gly Tyr Glu Val Met		
225	230	235

<210> 149

<211> 1589

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1).. (1458)

<400> 149

gaa ggc ctc att gtc cgg tca gct act aag gtc act gct gat gtc atc 48

Glu Gly Leu Ile Val Arg Ser Ala Thr Lys Val Thr Ala Asp Val Ile

1

5

10

15

aat gca gca gag aag ctc cag gtg gtg ggc agg gct gtc aca ggc gtg 96
 Asn Ala Ala Glu Lys Leu Gln Val Val Gly Arg Ala Val Thr Gly Val
 20 25 30
 gac aat gtg gat ctg gag cct ccc acg agg aag ggc atc cta gtc atg 144
 Asp Asn Val Asp Leu Glu Pro Pro Thr Arg Lys Gly Ile Leu Val Met
 35 40 45
 aac acc ccc aac ggg aac agc ctc agt gct gcg gag ctc acc tgt ggg 192
 Asn Thr Pro Asn Gly Asn Ser Leu Ser Ala Ala Glu Leu Thr Cys Gly
 50 55 60
 atg atc atg tgc ctg gcc agg cag att ccc cag aca aca gct tgc atg 240
 Met Ile Met Cys Leu Ala Arg Gln Ile Pro Gln Thr Thr Ala Ser Met
 65 70 75 80
 aaa gat ggc aaa tgg gac cgg aag aag ttc atg ggc aca gaa ctg aac 288
 Lys Asp Gly Lys Trp Asp Arg Lys Lys Phe Met Gly Thr Glu Leu Asn
 85 90 95
 ggg aag aca ctg gga att ctt ggc ctc ggc aga atc gga aga gag gtg 336
 Gly Lys Thr Leu Gly Ile Leu Gly Leu Gly Arg Ile Gly Arg Glu Val
 100 105 110
 gcc acc cga atg caa tcc ttt gga atg aag act gta ggc tat gac ccc 384
 Ala Thr Arg Met Gln Ser Phe Gly Met Lys Thr Val Gly Tyr Asp Pro
 115 120 125
 atc atc tct cct gaa gtc gcc gcc tcc ttt ggt gtt cag cag ctg ccg 432
 Ile Ile Ser Pro Glu Val Ala Ala Ser Phe Gly Val Gln Gln Leu Pro
 130 135 140
 ctg gag gag atc tgg cct ctc tgt gac ttt ata act gtc cat acc cca 480
 Leu Glu Glu Ile Trp Pro Leu Cys Asp Phe Ile Thr Val His Thr Pro
 145 150 155 160
 ctc ctg ccc tct acc aca ggc tta ctg aat gac agc acc ttt gct cag 528
 Leu Leu Pro Ser Thr Thr Gly Leu Leu Asn Asp Ser Thr Phe Ala Gln

165	170	175	
tgc aag aaa ggt gtg cga gtg gtg aac tgt gct cga gga ggc att gta	576		
Cys Lys Lys Gly Val Arg Val Val Asn Cys Ala Arg Gly Gly Ile Val			
180	185	190	
gat gaa ggt gcc ctg ctg cgt gcc ctg cag tct ggt cag tgt gct ggg	624		
Asp Glu Gly Ala Leu Leu Arg Ala Leu Gln Ser Gly Gln Cys Ala Gly			
195	200	205	
gct gca ctg gat gtg ttt aca gaa gag cca cca cgg gac cgg gcc tta	672		
Ala Ala Leu Asp Val Phe Thr Glu Glu Pro Pro Arg Asp Arg Ala Leu			
210	215	220	
gtg gac cac gag aat gtc atc agc tgt ccc cac ctg ggt gcc agc acc	720		
Val Asp His Glu Asn Val Ile Ser Cys Pro His Leu Gly Ala Ser Thr			
225	230	235	240
aag gaa gcc cag agc cgc tgt ggg gag gaa atc gca gtc cag ttt gtg	768		
Lys Glu Ala Gln Ser Arg Cys Gly Glu Glu Ile Ala Val Gln Phe Val			
245	250	255	
gac atg gtg aag ggg aaa tct cta aca ggc gtt gtg aac gcc cag gcc	816		
Asp Met Val Lys Gly Lys Ser Leu Thr Gly Val Val Asn Ala Gln Ala			
260	265	270	
ctc acc agt gcc ttc tct cca cac acc aag cct tgg att ggt ctg gca	864		
Leu Thr Ser Ala Phe Ser Pro His Thr Lys Pro Trp Ile Gly Leu Ala			
275	280	285	
gaa gca atg ggc acg ctg atg cac gcc tgg gct ggc tcc cct aaa ggg	912		
Glu Ala Met Gly Thr Leu Met His Ala Trp Ala Gly Ser Pro Lys Gly			
290	295	300	
acc atc cag gtg gtt aca caa gga aca tct ctg aag aat gct ggg acc	960		
Thr Ile Gln Val Val Thr Gln Gly Thr Ser Leu Lys Asn Ala Gly Thr			
305	310	315	320
tgg ctg agc cct gca gtc att gtt gcc ctt ctg aga gaa gca tct aag	1008		

Trp Leu Ser Pro Ala Val Ile Val Ala Leu Leu Arg Glu Ala Ser Lys
 325 330 335
 cag gca gac gtg aac ttg gtg aac gct aag cta ctg gtg aaa gag gct 1056
 Gln Ala Asp Val Asn Leu Val Asn Ala Lys Leu Leu Val Lys Glu Ala
 340 345 350
 ggc ctc aat gtc acc acc tcc cac aac cct ggg gtt cca ggg gag cag 1104
 Gly Leu Asn Val Thr Thr Ser His Asn Pro Gly Val Pro Gly Glu Gln
 355 360 365
 ggt agc ggg gaa tgc ctc ctg act gtg gcc cta gca ggt gcc ccc tac 1152
 Gly Ser Gly Glu Cys Leu Leu Thr Val Ala Leu Ala Gly Ala Pro Tyr
 370 375 380
 caa gcc gtg ggc ttg gtc cag ggc acc aca cca atg ctg cag atg ctc 1200
 Gln Ala Val Gly Leu Val Gln Gly Thr Thr Pro Met Leu Gln Met Leu
 385 390 395 400
 aac gga gct gtc ttc aga cca gag gtg cca cta cgc agg ggc caa ccc 1248
 Asn Gly Ala Val Phe Arg Pro Glu Val Pro Leu Arg Arg Gly Gln Pro
 405 410 415
 ctg ctc gta ttc cgg gct cag ccc tcc gac cct ggg atg ctg ccc act 1296
 Leu Leu Val Phe Arg Ala Gln Pro Ser Asp Pro Gly Met Leu Pro Thr
 420 425 430
 atg att ggc ctc ctg gca gaa gcg ggt gta cag ctg ctg tcc tac caa 1344
 Met Ile Gly Leu Leu Ala Glu Ala Gly Val Gln Leu Leu Ser Tyr Gln
 435 440 445
 acc tcc atg gtg tct gac gga gag ccc tgg cat gtc atg ggc ctg tcc 1392
 Thr Ser Met Val Ser Asp Gly Glu Pro Trp His Val Met Gly Leu Ser
 450 455 460
 tcc ctg ctg ccc agc ctg gaa aca tgg aaa cag cat gta ttg gag gct 1440
 Ser Leu Leu Pro Ser Leu Glu Thr Trp Lys Gln His Val Leu Glu Ala
 465 470 475 480

ttc cag ttc tgc ttc tga ccctgggggtt cagcactctc agccccacag 1488

Phe Gln Phe Cys Phe

485

gctcttctga agaaaccgga tcctgtgacc tatagggaga ggggatcgca gaaccagggc 1548

atctgccctga actaatacct agtaaagaat tcttaactcc a 1589

<210> 150

<211> 485

<212> PRT

<213> Mus musculus

<400> 150

Glu Gly Leu Ile Val Arg Ser Ala Thr Lys Val Thr Ala Asp Val Ile

1 5 10 15

Asn Ala Ala Glu Lys Leu Gln Val Val Gly Arg Ala Val Thr Gly Val

20 25 30

Asp Asn Val Asp Leu Glu Pro Pro Thr Arg Lys Gly Ile Leu Val Met

35 40 45

Asn Thr Pro Asn Gly Asn Ser Leu Ser Ala Ala Glu Leu Thr Cys Gly

50 55 60

Met Ile Met Cys Leu Ala Arg Gln Ile Pro Gln Thr Thr Ala Ser Met

65 70 75 80

Lys Asp Gly Lys Trp Asp Arg Lys Lys Phe Met Gly Thr Glu Leu Asn

85 90 95

Gly Lys Thr Leu Gly Ile Leu Gly Leu Gly Arg Ile Gly Arg Glu Val

100 105 110

Ala Thr Arg Met Gln Ser Phe Gly Met Lys Thr Val Gly Tyr Asp Pro

115 120 125

Ile Ile Ser Pro Glu Val Ala Ala Ser Phe Gly Val Gln Gln Leu Pro

130 135 140
 Leu Glu Glu Ile Trp Pro Leu Cys Asp Phe Ile Thr Val His Thr Pro
 145 150 155 160
 Leu Leu Pro Ser Thr Thr Gly Leu Leu Asn Asp Ser Thr Phe Ala Gln
 165 170 175
 Cys Lys Lys Gly Val Arg Val Val Asn Cys Ala Arg Gly Gly Ile Val
 180 185 190
 Asp Glu Gly Ala Leu Leu Arg Ala Leu Gln Ser Gly Gln Cys Ala Gly
 195 200 205
 Ala Ala Leu Asp Val Phe Thr Glu Glu Pro Pro Arg Asp Arg Ala Leu
 210 215 220
 Val Asp His Glu Asn Val Ile Ser Cys Pro His Leu Gly Ala Ser Thr
 225 230 235 240
 Lys Glu Ala Gln Ser Arg Cys Gly Glu Glu Ile Ala Val Gln Phe Val
 245 250 255
 Asp Met Val Lys Gly Lys Ser Leu Thr Gly Val Val Asn Ala Gln Ala
 260 265 270
 Leu Thr Ser Ala Phe Ser Pro His Thr Lys Pro Trp Ile Gly Leu Ala
 275 280 285
 Glu Ala Met Gly Thr Leu Met His Ala Trp Ala Gly Ser Pro Lys Gly
 290 295 300
 Thr Ile Gln Val Val Thr Gln Gly Thr Ser Leu Lys Asn Ala Gly Thr
 305 310 315 320
 Trp Leu Ser Pro Ala Val Ile Val Ala Leu Leu Arg Glu Ala Ser Lys
 325 330 335
 Gln Ala Asp Val Asn Leu Val Asn Ala Lys Leu Leu Val Lys Glu Ala
 340 345 350
 Gly Leu Asn Val Thr Thr Ser His Asn Pro Gly Val Pro Gly Glu Gln
 355 360 365

Gly Ser Gly Glu Cys Leu Leu Thr Val Ala Leu Ala Gly Ala Pro Tyr
 370 375 380
 Gln Ala Val Gly Leu Val Gln Gly Thr Thr Pro Met Leu Gln Met Leu
 385 390 395 400
 Asn Gly Ala Val Phe Arg Pro Glu Val Pro Leu Arg Arg Gly Gln Pro
 405 410 415
 Leu Leu Val Phe Arg Ala Gln Pro Ser Asp Pro Gly Met Leu Pro Thr
 420 425 430
 Met Ile Gly Leu Leu Ala Glu Ala Gly Val Gln Leu Leu Ser Tyr Gln
 435 440 445
 Thr Ser Met Val Ser Asp Gly Glu Pro Trp His Val Met Gly Leu Ser
 450 455 460
 Ser Leu Leu Pro Ser Leu Glu Thr Trp Lys Gln His Val Leu Glu Ala
 465 470 475 480
 Phe Gln Phe Cys Phe
 485

<210> 151

<211> 535

<212> DNA

<213> Mus musculus

<400> 151

ggtgatgctc caagccctga ggagaagctg catcttatca cccggaacct gcaggaggtt 60
 ctaggggaag agaagctgaa ggagatcctg aaggagcggg aacttaaagt ttactggggc 120
 acggccacca cgggcaagcc acacgtggct tactttgtac ccatgtccaa gatcgctgac 180
 tttttgaagg caggggtgtga ggtaaccatc ctgtttgcag acctccatgc atacctggac 240
 aacatgaaag ccccttgga gcttctagaa cttcgaacca gttactatga gaatgtgac 300
 aaggccatgc tggagagtat tggcgtgcc ttggagaagc tcaagtttat caaaggcacc 360

411/2644

```

ggt aga ctt ggt tcc aca att ttt gtt gct aat ctt gac ttc aaa gtt      288
Gly Arg Leu Gly Ser Thr Ile Phe Val Ala Asn Leu Asp Phe Lys Val
      85              90              95

ggt tgg aag aaa tta aag gaa gtg ttc agc ata gct gga act gtg aag      336
Gly Trp Lys Lys Leu Lys Glu Val Phe Ser Ile Ala Gly Thr Val Lys
      100             105             110

cga gct gat att aaa gaa gac aag gat ggc aag agc aga ggc atg ggc      384
Arg Ala Asp Ile Lys Glu Asp Lys Asp Gly Lys Ser Arg Gly Met Gly
      115             120             125

act gtc act ttt gag cag gca att gaa gca gtc caa gca att tcc atg      432
Thr Val Thr Phe Glu Gln Ala Ile Glu Ala Val Gln Ala Ile Ser Met
      130             135             140

ttc aat ggg cag ttt tta ttt gat aga cct atg cat gtg aaa atg gat      480
Phe Asn Gly Gln Phe Leu Phe Asp Arg Pro Met His Val Lys Met Asp
      145             150             155             160

gac aaa tct gtc cct cat gaa gac tac cgt tca cat gat agt aag aca      528
Asp Lys Ser Val Pro His Glu Asp Tyr Arg Ser His Asp Ser Lys Thr
      165             170             175

tca cag tta cca cgt ggt ctt gga ggc att gga atg gga ctt ggt cca      576
Ser Gln Leu Pro Arg Gly Leu Gly Gly Ile Gly Met Gly Leu Gly Pro
      180             185             190

ggt gga cag cct att agt gcc agc cag cgt aac ata act ggt gta atg      624
Gly Gly Gln Pro Ile Ser Ala Ser Gln Arg Asn Ile Thr Gly Val Met
      195             200             205

gga aat ttg ggt cca agt gga gtt ggg ttt ggt ggt ctg gaa gca atg      672
Gly Asn Leu Gly Pro Ser Gly Val Gly Phe Gly Gly Leu Glu Ala Met
      210             215             220

aat agc atg gca ggc ttt ggt gga gtt ggc cga atg gga gag cta tac      720
Asn Ser Met Ala Gly Phe Gly Gly Val Gly Arg Met Gly Glu Leu Tyr

```


225	230	235	240	
cgt ggt gca atg act agt agc atg gag cga gat ttc gga cgt ggt gat	768			
Arg Gly Ala Met Thr Ser Ser Met Glu Arg Asp Phe Gly Arg Gly Asp				
245	250	255		
att gga tta agt cga ggc ttt ggc gat tcc ttt ggt aga ctt ggc agt	816			
Ile Gly Leu Ser Arg Gly Phe Gly Asp Ser Phe Gly Arg Leu Gly Ser				
260	265	270		
gca atg att gga ggg ttt gca gga aga ata gga gct tct aac atg ggt	864			
Ala Met Ile Gly Gly Phe Ala Gly Arg Ile Gly Ala Ser Asn Met Gly				
275	280	285		
cca gta gga act gga ata agc ggc agc atg agc ggc atg agc act gtg	912			
Pro Val Gly Thr Gly Ile Ser Gly Ser Met Ser Gly Met Ser Thr Val				
290	295	300		
act gga ggc atg ggc atg gga ctg gac cgc atg agc tcc agc ttc gac	960			
Thr Gly Gly Met Gly Met Gly Leu Asp Arg Met Ser Ser Ser Phe Asp				
305	310	315	320	
agg atg ggg cca ggc att gga gcc ata ctg gaa agg agc atc gat gta	1008			
Arg Met Gly Pro Gly Ile Gly Ala Ile Leu Glu Arg Ser Ile Asp Val				
325	330	335		
gac cga ggg ttt tta tca ggt ccc atg gga agc gga atg aga gac aga	1056			
Asp Arg Gly Phe Leu Ser Gly Pro Met Gly Ser Gly Met Arg Asp Arg				
340	345	350		
tta ggc tcc aaa ggc aac cag ata ttt gtt aga aat ctt cct ttt gac	1104			
Leu Gly Ser Lys Gly Asn Gln Ile Phe Val Arg Asn Leu Pro Phe Asp				
355	360	365		
ttg act tgg cag aaa tta aaa gag aaa ttc agc caa ttg ggt cat gta	1152			
Leu Thr Trp Gln Lys Leu Lys Glu Lys Phe Ser Gln Leu Gly His Val				
370	375	380		
atg ttt gca gag ata aag atg gag aat ggc aag tca aaa ggc tgt ggg	1200			

Met Phe Ala Glu Ile Lys Met Glu Asn Gly Lys Ser Lys Gly Cys Gly
 385 390 395 400
 aca gtc agg ttt gaa tct gca gag tca gcg gaa aag gcc tgc agg atc 1248
 Thr Val Arg Phe Glu Ser Ala Glu Ser Ala Glu Lys Ala Cys Arg Ile
 405 410 415
 atg aat ggc atc aag atc agc ggc agg gaa atc gat gtg cgc ttg gac 1296
 Met Asn Gly Ile Lys Ile Ser Gly Arg Glu Ile Asp Val Arg Leu Asp
 420 425 430
 cgc aat gcg taa tttcaagcat ggttgggaacc tttcctcatic tgtttatgac 1348
 Arg Asn Ala
 435
 tctcctagta aaagtcattt ttagtaatgt tgtatgctta caaatgctgt aaaaatgaac 1408
 tttacaact cccaccagct attaacagga tagtgiggaa aatgtactgt gagttttttg 1468
 ttttttgitt ttgtttttt ttttttttt ttttggttct caagtttgag tttctaaaga 1528
 cagcacatct gatcattcag tttcagtga tggacatacc atttttaatg aaataagcca 1588
 tttgtttatt ttcagtagca gagtttgtct gtccagttt tcccgacctt ggtgtaagct 1648
 cacagatact ttgttttctt ttaaaatctt tgctttgtat gtgagttaaa ggaaagaaag 1708
 ggctcagaca aattaggatg gattttgggt tggtttaaat tacittttctc tgcttataaa 1768
 gaatagtaat taagtgttag actctaaagt tgaagatgct tttatttga cctaaatgaa 1828
 gacatgaatt ttcttctttt tgccctctc ccatccatc tttccacata acactattaa 1888
 aaaatatcaa actccacaac ccttattct attatttcca ataattccaa tttcatatag 1948
 aactgataaa gtagcaagtc ctaagtataa cactaggcag accaccccca actttcggtc 2008
 tagtttccag ccattaaaaat gaactgctaa gaacagaaat aaaattgaaa tgttgagaga 2068
 gattgttata tatgtgagtc ccttgctatt cacttctata ggagcagatg cattcgtaaa 2128
 tgcagtcctta ataaaccagg gaagacctag gcatagcata tcaaacacat tggatccac 2188
 gatgtagat atagccatgt ctcctttacc tgcagaagaa tagcatgttg ttaaaatgtg 2248
 cacatcaata ctatatitaa ttaataatct tcataagaaa aacactggat actttttgtt 2308
 ggtagtitt agaaaactgt tattgttaga gcaagagtct tattgaattt gtatttctt 2368
 gggttagtat tttaaagtct taacatttat ttaataattg tctttattta ttaaacatt 2428

tttacc

2434

<210> 153

<211> 435

<212> PRT

<213> Mus musculus

<400> 153

Lys Asp Glu Glu Phe Val Lys Lys Ala Leu Glu Thr Met Asn Lys Tyr
 1 5 10 15
 Asp Leu Ser Gly Arg Pro Leu Asn Ile Lys Glu Asp Pro Asp Gly Glu
 20 25 30
 Asn Ala Arg Arg Ala Leu Gln Arg Thr Gly Thr Ser Phe Gln Gly Ser
 35 40 45
 His Ala Ser Asp Val Gly Ser Gly Leu Val Asn Leu Pro Pro Ser Ile
 50 55 60
 Leu Asn Asn Pro Asn Ile Pro Pro Glu Val Ile Ser Asn Leu Gln Ala
 65 70 75 80
 Gly Arg Leu Gly Ser Thr Ile Phe Val Ala Asn Leu Asp Phe Lys Val
 85 90 95
 Gly Trp Lys Lys Leu Lys Glu Val Phe Ser Ile Ala Gly Thr Val Lys
 100 105 110
 Arg Ala Asp Ile Lys Glu Asp Lys Asp Gly Lys Ser Arg Gly Met Gly
 115 120 125
 Thr Val Thr Phe Glu Gln Ala Ile Glu Ala Val Gln Ala Ile Ser Met
 130 135 140
 Phe Asn Gly Gln Phe Leu Phe Asp Arg Pro Met His Val Lys Met Asp
 145 150 155 160
 Asp Lys Ser Val Pro His Glu Asp Tyr Arg Ser His Asp Ser Lys Thr

	165	170	175
Ser Gln Leu Pro Arg Gly Leu Gly Gly Ile Gly Met Gly Leu Gly Pro			
	180	185	190
Gly Gly Gln Pro Ile Ser Ala Ser Gln Arg Asn Ile Thr Gly Val Met			
	195	200	205
Gly Asn Leu Gly Pro Ser Gly Val Gly Phe Gly Gly Leu Glu Ala Met			
	210	215	220
Asn Ser Met Ala Gly Phe Gly Gly Val Gly Arg Met Gly Glu Leu Tyr			
225	230	235	240
Arg Gly Ala Met Thr Ser Ser Met Glu Arg Asp Phe Gly Arg Gly Asp			
	245	250	255
Ile Gly Leu Ser Arg Gly Phe Gly Asp Ser Phe Gly Arg Leu Gly Ser			
	260	265	270
Ala Met Ile Gly Gly Phe Ala Gly Arg Ile Gly Ala Ser Asn Met Gly			
	275	280	285
Pro Val Gly Thr Gly Ile Ser Gly Ser Met Ser Gly Met Ser Thr Val			
	290	295	300
Thr Gly Gly Met Gly Met Gly Leu Asp Arg Met Ser Ser Ser Phe Asp			
305	310	315	320
Arg Met Gly Pro Gly Ile Gly Ala Ile Leu Glu Arg Ser Ile Asp Val			
	325	330	335
Asp Arg Gly Phe Leu Ser Gly Pro Met Gly Ser Gly Met Arg Asp Arg			
	340	345	350
Leu Gly Ser Lys Gly Asn Gln Ile Phe Val Arg Asn Leu Pro Phe Asp			
	355	360	365
Leu Thr Trp Gln Lys Leu Lys Glu Lys Phe Ser Gln Leu Gly His Val			
	370	375	380
Met Phe Ala Glu Ile Lys Met Glu Asn Gly Lys Ser Lys Gly Cys Gly			
385	390	395	400

Thr Val Arg Phe Glu Ser Ala Glu Ser Ala Glu Lys Ala Cys Arg Ile

405

410

415

Met Asn Gly Ile Lys Ile Ser Gly Arg Glu Ile Asp Val Arg Leu Asp

420

425

430

Arg Asn Ala

435

<210> 154

<211> 566

<212> DNA

<213> Mus musculus

<400> 154

```

aattcggcac gacggggaac tgcngggcgc gacgcgtgtc tctctccctc actctctctg 60
tgtgaaagtg tgtgcgtgcc cgagtgtgcg cgcgcgggtg tgtggactcg gaggtggggg 120
cagccgagtt agtcccaagt cgtcggactc catttgctat tcttttcttt ctctcccaca 180
cccggtgtgt agtggggtgt cgtcttttgc tctcttttca ttcattctcca gacctttaga 240
ggttttttta gggttgggga tagtggggag ggcaggcgag gggaaaggag gaggacatgg 300
agatgaagaa gaagattaac atggagttaga agaacagagc cccggaggag gtgacagagt 360
tagtctctga taattgcttg tgtgtcaatg gggaaatcga aggcctgaat gacaccttta 420
aggaactgga gtttcttagc atggccaacg tggagttagg ttccttggcc cggcttccca 480
gcttgaataa actccggaag ttggaactta gtgacaatat aatttctgga ggcttgggaag 540
tcctggcaga gaaatgtcaa atctta                                     566

```

<210> 155

<211> 1044

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (138).. (749)

<400> 155

```

ttcgggtcgg ggggcggagg gaagagcgga cgggcgggac gccggcgcca gacgcggagg 60
aaaggagctg cgactaccgc ccagaggccg ccgagccagc gacgcctgag ctagtcgaga 120
ccgtcgcgcg cgcccc atg gcg gcc gcc aag gac agt cac gag gac cat 170
      Met Ala Ala Ala Lys Asp Ser His Glu Asp His
              1              5              10
gat act tcc aca gag aat gca gat gag tcc aac cac gac ccc cag ttc 218
Asp Thr Ser Thr Glu Asn Ala Asp Glu Ser Asn His Asp Pro Gln Phe
              15              20              25
gag cca ata gtt tct ctt ccc gag caa gaa att aaa acg ctg gag gaa 266
Glu Pro Ile Val Ser Leu Pro Glu Gln Glu Ile Lys Thr Leu Glu Glu
              30              35              40
gat gaa gag gaa ctt ttt aag atg cgt gca aag ctg ttc cgg ttt gct 314
Asp Glu Glu Glu Leu Phe Lys Met Arg Ala Lys Leu Phe Arg Phe Ala
              45              50              55
tca gag aat gac ctc cca gaa tgg aag gag cga ggc act gga gat gtc 362
Ser Glu Asn Asp Leu Pro Glu Trp Lys Glu Arg Gly Thr Gly Asp Val
              60              65              70              75
aag ctt ctg aag cac aag gag aaa ggg acc atc cgc ctt ctt atg agg 410
Lys Leu Leu Lys His Lys Glu Lys Gly Thr Ile Arg Leu Leu Met Arg
              80              85              90
agg gac aaa acc ttg aag ata tgc gcc aac cac tat att aca cca atg 458
Arg Asp Lys Thr Leu Lys Ile Cys Ala Asn His Tyr Ile Thr Pro Met
              95              100              105
atg gag ctg aag ccg aat gct ggc agt gac cga gcc tgg gtc tgg aat 506

```

```

Met Glu Leu Lys Pro Asn Ala Gly Ser Asp Arg Ala Trp Val Trp Asn
      110              115              120
acc cac acc gac ttt gct gac gag tgc ccc aag cct gag ctg ctc gcc 554
Thr His Thr Asp Phe Ala Asp Glu Cys Pro Lys Pro Glu Leu Leu Ala
      125              130              135
atc cgc ttc cta aat gct gag aat gca caa aag ttc aaa aca aag ttt 602
Ile Arg Phe Leu Asn Ala Glu Asn Ala Gln Lys Phe Lys Thr Lys Phe
      140              145              150              155
gaa gaa tgc agg aaa gaa att gaa gag aga gaa aag aaa gga cca ggc 650
Glu Glu Cys Arg Lys Glu Ile Glu Glu Arg Glu Lys Lys Gly Pro Gly
      160              165              170
aaa aat gat aat gcc gaa aag gtg gcc gag aag ctg gaa gcc ctt tca 698
Lys Asn Asp Asn Ala Glu Lys Val Ala Glu Lys Leu Glu Ala Leu Ser
      175              180              185
gtg agg gag gcc aga gag gag gct gaa gag aag tct gag gag aaa caa 746
Val Arg Glu Ala Arg Glu Glu Ala Glu Glu Lys Ser Glu Glu Lys Gln
      190              195              200
tga atcactctgt ctttttcctt tccttttcctt tttaaaaatt tgccctaccc 799
tttaagggttt gtttttctgt ttgtttttta caagggactt tataaagaac tgaattccaa 859
ttttcagggtt gttttgtttt gttttttttt taactttttt ttacctccaa gttttgacac 919
cattgaacat gacttcagaa atccattccc cagctcatga aaatgtactg tgctaacttt 979
tctttttcca tagtggaaca cattatttta tagtaataaa aaagatcttt gaactaaaaa 1039
aaaaa 1044

```

<210> 156

<211> 203

<212> PRT

<213> Mus musculus

<400> 156

Met Ala Ala Ala Lys Asp Ser His Glu Asp His Asp Thr Ser Thr Glu
 1 5 10 15
 Asn Ala Asp Glu Ser Asn His Asp Pro Gln Phe Glu Pro Ile Val Ser
 20 25 30
 Leu Pro Glu Gln Glu Ile Lys Thr Leu Glu Glu Asp Glu Glu Glu Leu
 35 40 45
 Phe Lys Met Arg Ala Lys Leu Phe Arg Phe Ala Ser Glu Asn Asp Leu
 50 55 60
 Pro Glu Trp Lys Glu Arg Gly Thr Gly Asp Val Lys Leu Leu Lys His
 65 70 75 80
 Lys Glu Lys Gly Thr Ile Arg Leu Leu Met Arg Arg Asp Lys Thr Leu
 85 90 95
 Lys Ile Cys Ala Asn His Tyr Ile Thr Pro Met Met Glu Leu Lys Pro
 100 105 110
 Asn Ala Gly Ser Asp Arg Ala Trp Val Trp Asn Thr His Thr Asp Phe
 115 120 125
 Ala Asp Glu Cys Pro Lys Pro Glu Leu Leu Ala Ile Arg Phe Leu Asn
 130 135 140
 Ala Glu Asn Ala Gln Lys Phe Lys Thr Lys Phe Glu Glu Cys Arg Lys
 145 150 155 160
 Glu Ile Glu Glu Arg Glu Lys Lys Gly Pro Gly Lys Asn Asp Asn Ala
 165 170 175
 Glu Lys Val Ala Glu Lys Leu Glu Ala Leu Ser Val Arg Glu Ala Arg
 180 185 190
 Glu Glu Ala Glu Glu Lys Ser Glu Glu Lys Gln
 195 200

<210> 157

<211> 1091

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (66).. (1010)

<400> 157

```

ggcagcagcc tcgccagcca gccgccagca gcctgcagcc tgcacccgct cagccccgca 60
cagcc atg ttt cag cca gct ggg cac ggc cag gac tgg gcc atg gag ggc 110
      Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly
          1             5             10             15
ccg cgg gat ggc ctc aag aag gag cgc ttg gtg gac gat cgc cac gac 158
Pro Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp
          20             25             30
agc ggc ctg gac tcc atg aag gac gag gag tac gag caa atg gtg aag 206
Ser Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys
          35             40             45
gag ctg cgg gag atc cgc ctg cag ccg cag gag gcg ccg ctg gcc gcc 254
Glu Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala
          50             55             60
gag ccc tgg aag cag cag ctc acg gag gac gga gac tcg ttc ctg cac 302
Glu Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His
          65             70             75
ttg gca atc atc cac gaa gag aag ccg ctg acc atg gaa gtc att ggt 350
Leu Ala Ile Ile His Glu Glu Lys Pro Leu Thr Met Glu Val Ile Gly
          80             85             90             95
cag gtg aag gga gac ctg gcc ttc ctc aac ttc cag aac aac ctg cag 398

```

Gln Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln
 100 105 110
 cag act cca ctc cac ttg gct gtg atc acc aac cag cca gga att gct 446
 Gln Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Gly Ile Ala
 115 120 125
 gag gca ctt ctg aaa gct ggc tgt gat cct gag ctc cga gac ttt cga 494
 Glu Ala Leu Leu Lys Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg
 130 135 140
 gga aat acc cct cta cat ctt gcc tgt gag cag ggc tgc ctg gcc agt 542
 Gly Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser
 145 150 155
 gta gca gtc ttg acg cag acc tgc aca ccc cag cat ctc cac tcc gtc 590
 Val Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val
 160 165 170 175
 ctg cag gcc acc aac tac aat ggc cac acg tgt ctg cac cta gcc tct 638
 Leu Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser
 180 185 190
 act cac ggc tac ctg gcc atc gtg gag cac ttg gtg act ttg ggt gct 686
 Thr His Gly Tyr Leu Ala Ile Val Glu His Leu Val Thr Leu Gly Ala
 195 200 205
 gat gtc aac gct cag gag ccc tgc aat ggc cgg aca gcc ctc cac ctt 734
 Asp Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu
 210 215 220
 gcg gtg gac ctg cag aat cct gac ctg gtt tgc ctc ttg ttg aaa tgt 782
 Ala Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys
 225 230 235
 ggg gct gat gtc aac agg gta acc tac caa ggc tac tcc ccc tac cag 830
 Gly Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln
 240 245 250 255

ctt acc tgg ggc cgc cca agt acc cgg ata cag cag cag ctg ggc cag 878
 Leu Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln
 260 265 270
 ctg acc ctg gaa aat ctc cag atg cta ccc gag agc gag gat gag gag 926
 Leu Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu
 275 280 285
 agc tat gac acg gag tca gaa ttc aca gag gat gag ctg ccc tat gat 974
 Ser Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp
 290 295 300
 gac tgt gtg ttt gga ggc cag cgt ctg aca tta taa gtggaaagt 1020
 Asp Cys Val Phe Gly Gly Gln Arg Leu Thr Leu
 305 310 315
 gcaaaaaaga atgtggactt gtatatattgt acaaataagag ttttattttt ctaaaaaaaaa 1080
 aaaaaaaaaa a 1091

<210> 158

<211> 314

<212> PRT

<213> Mus musculus

<400> 158

Met Phe Gln Pro Ala Gly His Gly Gln Asp Trp Ala Met Glu Gly Pro
 1 5 10 15
 Arg Asp Gly Leu Lys Lys Glu Arg Leu Val Asp Asp Arg His Asp Ser
 20 25 30
 Gly Leu Asp Ser Met Lys Asp Glu Glu Tyr Glu Gln Met Val Lys Glu
 35 40 45
 Leu Arg Glu Ile Arg Leu Gln Pro Gln Glu Ala Pro Leu Ala Ala Glu
 50 55 60

Pro Trp Lys Gln Gln Leu Thr Glu Asp Gly Asp Ser Phe Leu His Leu
 65 70 75 80
 Ala Ile Ile His Glu Glu Lys Pro Leu Thr Met Glu Val Ile Gly Gln
 85 90 95
 Val Lys Gly Asp Leu Ala Phe Leu Asn Phe Gln Asn Asn Leu Gln Gln
 100 105 110
 Thr Pro Leu His Leu Ala Val Ile Thr Asn Gln Pro Gly Ile Ala Glu
 115 120 125
 Ala Leu Leu Lys Ala Gly Cys Asp Pro Glu Leu Arg Asp Phe Arg Gly
 130 135 140
 Asn Thr Pro Leu His Leu Ala Cys Glu Gln Gly Cys Leu Ala Ser Val
 145 150 155 160
 Ala Val Leu Thr Gln Thr Cys Thr Pro Gln His Leu His Ser Val Leu
 165 170 175
 Gln Ala Thr Asn Tyr Asn Gly His Thr Cys Leu His Leu Ala Ser Thr
 180 185 190
 His Gly Tyr Leu Ala Ile Val Glu His Leu Val Thr Leu Gly Ala Asp
 195 200 205
 Val Asn Ala Gln Glu Pro Cys Asn Gly Arg Thr Ala Leu His Leu Ala
 210 215 220
 Val Asp Leu Gln Asn Pro Asp Leu Val Ser Leu Leu Leu Lys Cys Gly
 225 230 235 240
 Ala Asp Val Asn Arg Val Thr Tyr Gln Gly Tyr Ser Pro Tyr Gln Leu
 245 250 255
 Thr Trp Gly Arg Pro Ser Thr Arg Ile Gln Gln Gln Leu Gly Gln Leu
 260 265 270
 Thr Leu Glu Asn Leu Gln Met Leu Pro Glu Ser Glu Asp Glu Glu Ser
 275 280 285
 Tyr Asp Thr Glu Ser Glu Phe Thr Glu Asp Glu Leu Pro Tyr Asp Asp

290 295 300
 Cys Val Phe Gly Gly Gln Arg Leu Thr Leu
 305 310

<210> 159

<211> 888

<212> DNA

<213> Mus musculus

<400> 159

gtcgtcgtca gcttgacaaa agtaagctga agccaggaac cagagttgct ttggatatga 60
 ccacactaac catcatgaga tatctgccaa gagaggtgga tccattgggt tataacatgt 120
 ctacagagga tccctggaaat gtatcittatt ctgagattgg aggccigtca gaacagattc 180
 gggagttaag agaggttaata gaattgcctc ttacaaatcc agaattattc cagcgtgtag 240
 gaataatacc tccaaaaggc tgtttgctct atggaccgcc agcactggga aaacactcct 300
 ggcacgagct gttgccagcc agctggactg caacttccta aaggttgtat ctagttctat 360
 tgtagacaag tacattgggt aaagtgcctg ttgattaga gaaatgttta attatgccag 420
 ggaccaccag ccatgcatcatttttatgga tgaaatagat gctattgggt gccgtcgggt 480
 ttctgaggga acatcagctg acagagagat tcagagaact ttaatggagt tactagnaca 540
 gatggatgga ttgatactc tgcatagagt taaatgatca tggctacaac agaccagatc 600
 actggatcct gcttgctcgc caggaagata gatgaaaatc atacgattcc caatgacagc 660
 agttggttat gaaatcagcg gcctatcaac catgtgaatg attgacaatg tacttagatc 720
 gtittgcgcc tggaagtttc ttccagggtg caatgccgcc agttttgtct gggtttgaac 780
 ctccaaggtc ccggagggcg ccgggacgcg ttaaagggtg gcgaattgaa aatggaagtt 840
 gccgtaggaa tccggaaaaa gcgccctctg tggtcggtgc gccccctc 888

<210> 160

<211> 1276

<212> DNA

<213> Mus musculus

<400> 160

```

gaaccgagcc tggigccgcg cagtcagctc agccccctgt ggcggctccc tcccggictc 60
tcctcctacg agcagcatga aagccttcag gtccggigag tccgttagga aaaacagcct 120
gtcggaccac agcttgggca tcicccggag caaaaccccg gtggacgacc cgatgagtct 180
gctctacaac atgaacgact gctactccaa gctcaaggaa ctggtgccc a gcatccccc 240
gaacaagaag gtgaccaaga tggaaatcct gcagcacgtc atcgattaca tcttggacct 300
gcagatcgcc ctggactcgc atcccactat cgtcagcctg catcaccaga gacctggaca 360
gaaccaggcg tccaggacgc gcttgaccac cctgaacacg gacatcagca tctgtcctt 420
gcaggcatct gaattccctt ctgagcttat gtcgatgat agcaaagtac tctgtggcta 480
aataaatggc atttggggac ttttctttt ctttttactt tctctttttc ttttgcacaa 540
gaagaagtct acaagatctt ttaagacttt tgttatcagc catttcacca ggagaacacg 600
ttgaatggac ctttttaaaa agaaagcgga aggaaaacta aggatgatcg tcttgcccag 660
gtgtcgttct ccggcctigga ctgtgatacc gttatttatg agagactttc agtgcccttt 720
ctacagttagg aaggttttct ttatatacta ttcccacat ggggagcgaa aaggttaaaa 780
aaaagaaaaa aatcacaagg aattgccc aa tgtaagcaga ctttgccctt tcacaaaggt 840
ggagcgtgaa ttccagaagg acccagtatt cggttactta aatgaagtct tcggtcagaa 900
atggcctttt tgacacgagc ctactgaatg ctgtgtatat atttatatat aaatatatat 960
atattgagtg aaccttgtag actctttaat tagagttttc ttgtatagtg gcagaaataa 1020
cctattttctg cattaaaatg taatgacgta cttatgctaa actttttata aaagtttagt 1080
tgtaaaactta acccttttat acaaaataaa tcaagtggtt ttattgaatg ttgattgctt 1140
gctttatttc agacaaccag tgctttgatt ttttttatgc tatgttataa ctgaacccaa 1200
ataaatacca gttcaaatat atgtagactg tattaagatt ataataaaat gtgtctgaca 1260
tcaaaaaaaaa aaaaaa

```

1276

<210> 161

<211> 2934

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (566).. (2011)

<400> 161

```

aaaaaacgga agtagacgcc cactcatatt ttcttcaatg tcaagcaaaa tgaaaatatt 60
tccaggatga tcatcgcggt ctaccggcct ccagtactgc ctagaagctg aagaggaggt 120
ggagtgcccg aggagacaac tgccaccggg tcaccgcgcg gtgagcgcca ctctgggagt 180
gaagcgagac ggagggagaa cacacgtgtt acctgcttta ttctgggact gtttgggtct 240
gtgtcctccc ggggcagctc tccgcccgcg cgcccgcggt cgtggaaggc ctccacagaa 300
cgcacccacc gctcagccgc ccccgctcgc cgccctcagc ccagcttcac agccgagctc 360
gccgcggggc gcaggaagct cttttgctac atgccttgcc agcgccggag cctgcggctc 420
aactgcgctg ctgccggagc gctcagtgcc gcctccgctg cccgctcccc ccgcgcccc 480
ctccgaacct gctggctgcc cgccgcgctg ctgccccctt cccgtgccgc cgccgcgccc 540
gccgcgccc cccgacgctt ggggtg atg ctg gac atg gga gat agg aaa gag 592

```

Met Leu Asp Met Gly Asp Arg Lys Glu

1

5

```

gtg aaa atg att ccc aag tcc tgc ttc agc atc aac agc ctg gtc ccc 640

```

Val Lys Met Ile Pro Lys Ser Ser Phe Ser Ile Asn Ser Leu Val Pro

10

15

20

25

```

gag gcc gtc cag aac gac aac cac cac gcg agc cac ggc cac cac aac 688

```

Glu Ala Val Gln Asn Asp Asn His His Ala Ser His Gly His His Asn

30

35

40

```

agc cac cac ccc cag cat cac cat cat cat cac cac cac cac cac ccg 736

```

Ser His His Pro Gln His His His His His His His His His His Pro

45

50

55

```

ccg ccg ccc gcg ccc cag ccg cct cca ccg ccg ccc cag cag cag cag 784

```

Pro Pro Pro Ala Pro Gln Pro Pro Pro Pro Pro Pro Gln Gln Gln Gln
 60 65 70
 cag cag ccg ccc ccc gcc ccg cag ccc ccg cag gcg cgc ggc gcc cca 832
 Gln Gln Pro Pro Pro Ala Pro Gln Pro Pro Gln Ala Arg Gly Ala Pro
 75 80 85
 gca gcc gac gac gac aag ggt ccc cag ccg ctc ctg ctc ccg ccc tcc 880
 Ala Ala Asp Asp Asp Lys Gly Pro Gln Pro Leu Leu Leu Pro Pro Ser
 90 95 100 105
 acc gcc ctg gac ggg gcc aag gct gac gca ctt gga gcc aaa ggc gag 928
 Thr Ala Leu Asp Gly Ala Lys Ala Asp Ala Leu Gly Ala Lys Gly Glu
 110 115 120
 ccg ggc ggc ggg ccg gcg gag ctg gcg ccc gtc ggg ccg gac gag aag 976
 Pro Gly Gly Gly Pro Ala Glu Leu Ala Pro Val Gly Pro Asp Glu Lys
 125 130 135
 gag aag ggc gcg ggc gcc ggg ggg gag gag aag aaa ggg gcg ggc gag 1024
 Glu Lys Gly Ala Gly Ala Gly Gly Glu Glu Lys Lys Gly Ala Gly Glu
 140 145 150
 ggc ggc aag gac ggg gag ggg ggc aag gag ggc gac aag aag aac ggc 1072
 Gly Gly Lys Asp Gly Glu Gly Gly Lys Glu Gly Asp Lys Lys Asn Gly
 155 160 165
 aag tac gag aag ccg ccg ttc agc tac aac gcg ctc atc atg atg gcc 1120
 Lys Tyr Glu Lys Pro Pro Phe Ser Tyr Asn Ala Leu Ile Met Met Ala
 170 175 180 185
 atc agg cag agt ccc gag aag cgc ctg acg ctc aat ggc atc tat gag 1168
 Ile Arg Gln Ser Pro Glu Lys Arg Leu Thr Leu Asn Gly Ile Tyr Glu
 190 195 200
 ttc atc atg aag aac ttc ccc tac tac cgc gag aac aag cag ggc tgg 1216
 Phe Ile Met Lys Asn Phe Pro Tyr Tyr Arg Glu Asn Lys Gln Gly Trp
 205 210 215

cag aac tcc atc cgc cac aac ctg tcc ctc aac aag tgc ttc gtg aag 1264
 Gln Asn Ser Ile Arg His Asn Leu Ser Leu Asn Lys Cys Phe Val Lys
 220 225 230
 gta ccg cgc cac tac gac gac ccg ggc aag ggc aac tac tgg atg ctc 1312
 Val Pro Arg His Tyr Asp Asp Pro Gly Lys Gly Asn Tyr Trp Met Leu
 235 240 245
 gac ccg tcg agc gac gac gtg ttc atc ggc ggc acg acc ggc aag ctg 1360
 Asp Pro Ser Ser Asp Asp Val Phe Ile Gly Gly Thr Thr Gly Lys Leu
 250 255 260 265
 cgg cgc cgc tcc acc acg tct cgg gcc aag ctg gcc ttt aag cgc ggg 1408
 Arg Arg Arg Ser Thr Thr Ser Arg Ala Lys Leu Ala Phe Lys Arg Gly
 270 275 280
 gcg cgc ctc acc tcc acc ggc ctc acc ttc atg gac cgc gcc ggc tcc 1456
 Ala Arg Leu Thr Ser Thr Gly Leu Thr Phe Met Asp Arg Ala Gly Ser
 285 290 295
 ctc tac tgg ccc atg tcg ccc ttc ctg tcc ctg cac cac ccc cgc gcc 1504
 Leu Tyr Trp Pro Met Ser Pro Phe Leu Ser Leu His His Pro Arg Ala
 300 305 310
 agc agc act ttg agt tac aac ggg acc acg tcg gcc tac ccc agc cac 1552
 Ser Ser Thr Leu Ser Tyr Asn Gly Thr Thr Ser Ala Tyr Pro Ser His
 315 320 325
 ccc atg ccc tac agc tcc gtg ttg act caa aac tcg ctg ggc aac aac 1600
 Pro Met Pro Tyr Ser Ser Val Leu Thr Gln Asn Ser Leu Gly Asn Asn
 330 335 340 345
 cac tcc ttc tcc acc gcc aac ggg ctg agt gtg gac cgg ctg gtc aac 1648
 His Ser Phe Ser Thr Ala Asn Gly Leu Ser Val Asp Arg Leu Val Asn
 350 355 360
 ggg gag atc ccg tac gcc acg cac cac ctc acg gcc gct gcg ctc gcc 1696
 Gly Glu Ile Pro Tyr Ala Thr His His Leu Thr Ala Ala Ala Leu Ala

365	370	375	
gcc tgc gtg ccc tgc ggc ctg tgc gtg ccc tgc tcc ggg acc tac tcc			1744
Ala Ser Val Pro Cys Gly Leu Ser Val Pro Cys Ser Gly Thr Tyr Ser			
380	385	390	
ctc aac ccc tgc tcc gtc aac ctg ctc gcg ggc cag acc agt tac ttt			1792
Leu Asn Pro Cys Ser Val Asn Leu Leu Ala Gly Gln Thr Ser Tyr Phe			
395	400	405	
ttc ccc cac gtc ccg cac ccg tca atg act tgc cag acc agc acg tcc			1840
Phe Pro His Val Pro His Pro Ser Met Thr Ser Gln Thr Ser Thr Ser			
410	415	420	425
atg agc gcc cgg gcc gcg tcc tcc tct acg tgc ccg cag gcc ccc tgc			1888
Met Ser Ala Arg Ala Ala Ser Ser Ser Thr Ser Pro Gln Ala Pro Ser			
430	435	440	
acc ctg ccc tgt gag tct tta aga ccc tct ttg cca agt ttt acg aca			1936
Thr Leu Pro Cys Glu Ser Leu Arg Pro Ser Leu Pro Ser Phe Thr Thr			
445	450	455	
gga ctg tcc ggg gga ctg tct gat tat ttc aca cat caa aat cag ggg			1984
Gly Leu Ser Gly Gly Leu Ser Asp Tyr Phe Thr His Gln Asn Gln Gly			
460	465	470	
tct tct tcc aac cct tta ata cat taa catccggggg accagactgt			2031
Ser Ser Ser Asn Pro Leu Ile His			
475	480		
aagtgaacgt tttacacaca ttgcatgtt aaatgataat taaaaaata agtccaggga			2091
ttttttatta agccccccct cccatttct gtacgtttgt tcagtcctta gggtcgttta			2151
ctattctaac acggtgtgga gtgtcagcga ggtgcaatgt gggagaatac attgtagaat			2211
ataaggtttg gacgtcaaat tatagtagaa tgtgtatcta aatagtgact gctttgcat			2271
ttcattcaaa cctgacaagt ctatctcaac aggcgtccag atttccatgt gtgcagtatt			2331
ataagttatc atggagctat ctgggtggacg caggccttga gaacaacctt aattatgaag			2391
agagttttta aatgtttaa tgaattttgt atttaagaat ttgtagtaaa ggtgcccaag			2451

gaattatatt ggccatttat tgttttgtcc ttttctttaa agaactgttt ctttcctttt 2511
 gtttactttt agaccaaaga ttggattcta gcaaatgcac ttggtatact aagtattaaa 2571
 acaagtaaac aaacaaacga aaaaggaagg ttgtttagtt ggcaacactg cccattcaat 2631
 tgaatccgaa aggacaaaat taaggattgc cttcagtttg tgttgtgtat atttcgatgt 2691
 atgtggtcac taacagggtca cttttatttt ttctaaatgt agtgaaatgt taataacctat 2751
 tgtacttata ggtaaacctt gcaaataatgt aacctgtgtt gcgcaaatgc cgcatacaatt 2811
 tgagtgattg ttaatgttgt cttaaaaattt cttgattgtg atactgtggt catatgcccg 2871
 tgtttgtcac ttacaaaaat gtttactatg aacacacaga aataaaaaat aggctaaatt 2931
 cat 2934

<210> 162

<211> 481

<212> PRT

<213> Mus musculus

<400> 162

Met	Leu	Asp	Met	Gly	Asp	Arg	Lys	Glu	Val	Lys	Met	Ile	Pro	Lys	Ser
1				5				10					15		
Ser	Phe	Ser	Ile	Asn	Ser	Leu	Val	Pro	Glu	Ala	Val	Gln	Asn	Asp	Asn
				20				25					30		
His	His	Ala	Ser	His	Gly	His	His	Asn	Ser	His	His	Pro	Gln	His	His
				35				40					45		
His	His	His	His	His	His	His	His	Pro	Pro	Pro	Pro	Ala	Pro	Gln	Pro
				50				55				60			
Pro	Pro	Pro	Pro	Pro	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Pro	Pro	Pro	Ala
				65				70				75			80
Gln	Pro	Pro	Gln	Ala	Arg	Gly	Ala	Pro	Ala	Ala	Asp	Asp	Asp	Lys	Gly
				85				90						95	
Pro	Gln	Pro	Leu	Leu	Leu	Pro	Pro	Ser	Thr	Ala	Leu	Asp	Gly	Ala	Lys

100	105	110
Ala Asp Ala Leu Gly Ala Lys Gly Glu Pro Gly Gly Gly Pro Ala Glu		
115	120	125
Leu Ala Pro Val Gly Pro Asp Glu Lys Glu Lys Gly Ala Gly Ala Gly		
130	135	140
Gly Glu Glu Lys Lys Gly Ala Gly Glu Gly Gly Lys Asp Gly Glu Gly		
145	150	155
Gly Lys Glu Gly Asp Lys Lys Asn Gly Lys Tyr Glu Lys Pro Pro Phe		
165	170	175
Ser Tyr Asn Ala Leu Ile Met Met Ala Ile Arg Gln Ser Pro Glu Lys		
180	185	190
Arg Leu Thr Leu Asn Gly Ile Tyr Glu Phe Ile Met Lys Asn Phe Pro		
195	200	205
Tyr Tyr Arg Glu Asn Lys Gln Gly Trp Gln Asn Ser Ile Arg His Asn		
210	215	220
Leu Ser Leu Asn Lys Cys Phe Val Lys Val Pro Arg His Tyr Asp Asp		
225	230	235
Pro Gly Lys Gly Asn Tyr Trp Met Leu Asp Pro Ser Ser Asp Asp Val		
245	250	255
Phe Ile Gly Gly Thr Thr Gly Lys Leu Arg Arg Arg Ser Thr Thr Ser		
260	265	270
Arg Ala Lys Leu Ala Phe Lys Arg Gly Ala Arg Leu Thr Ser Thr Gly		
275	280	285
Leu Thr Phe Met Asp Arg Ala Gly Ser Leu Tyr Trp Pro Met Ser Pro		
290	295	300
Phe Leu Ser Leu His His Pro Arg Ala Ser Ser Thr Leu Ser Tyr Asn		
305	310	315
Gly Thr Thr Ser Ala Tyr Pro Ser His Pro Met Pro Tyr Ser Ser Val		
325	330	335

Leu Thr Gln Asn Ser Leu Gly Asn Asn His Ser Phe Ser Thr Ala Asn
 340 345 350
 Gly Leu Ser Val Asp Arg Leu Val Asn Gly Glu Ile Pro Tyr Ala Thr
 355 360 365
 His His Leu Thr Ala Ala Ala Leu Ala Ala Ser Val Pro Cys Gly Leu
 370 375 380
 Ser Val Pro Cys Ser Gly Thr Tyr Ser Leu Asn Pro Cys Ser Val Asn
 385 390 395 400
 Leu Leu Ala Gly Gln Thr Ser Tyr Phe Phe Pro His Val Pro His Pro
 405 410 415
 Ser Met Thr Ser Gln Thr Ser Thr Ser Met Ser Ala Arg Ala Ala Ser
 420 425 430
 Ser Ser Thr Ser Pro Gln Ala Pro Ser Thr Leu Pro Cys Glu Ser Leu
 435 440 445
 Arg Pro Ser Leu Pro Ser Phe Thr Thr Gly Leu Ser Gly Gly Leu Ser
 450 455 460
 Asp Tyr Phe Thr His Gln Asn Gln Gly Ser Ser Ser Asn Pro Leu Ile
 465 470 475 480
 His

<210> 163

<211> 1748

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (260).. (1537)

<400> 163

gaaaagtctc gttccaagtt tggcgagagg gagagagagg agagcggctc agacctcgct 60
 acccgccagc ggggaggagg cagaagagga gatcgcggcg tctgggggga gaaccagac 120
 ggccagaccg aactcaggct tttccgagcg aggactgcgt gacgtgcctg ggagaggcaa 180
 ggagcgccctg ccgggctgct cttgactagc gagagagaag tccgaggcgg ccaagggggg 240
 cgaaacgacc cgacgcaag atg gcg agt aaa gag atg ttt gaa gat act gtg 292

Met Ala Ser Lys Glu Met Phe Glu Asp Thr Val

1

5

10

gag gag cgt gtc atc aac gaa gag tat aaa atc tgg aag aag aat aca 340
 Glu Glu Arg Val Ile Asn Glu Glu Tyr Lys Ile Trp Lys Lys Asn Thr

15

20

25

ccg ttt ctg tat gac ctg gtt atg acc cat gct ctt cag tgg ccc agt 388
 Pro Phe Leu Tyr Asp Leu Val Met Thr His Ala Leu Gln Trp Pro Ser

30

35

40

ctt acc gtt cag tgg ctt cct gaa gtg act aaa cca gaa gga aag gat 436
 Leu Thr Val Gln Trp Leu Pro Glu Val Thr Lys Pro Glu Gly Lys Asp

45

50

55

tat gcc ctt cat tgg cta gtg ctg ggc act cat aca tct gat gag cag 484
 Tyr Ala Leu His Trp Leu Val Leu Gly Thr His Thr Ser Asp Glu Gln

60

65

70

75

aac cat ctg gtg gtt gct cga gtt cat att ccc aat gat gat gca cag 532
 Asn His Leu Val Val Ala Arg Val His Ile Pro Asn Asp Asp Ala Gln

80

85

90

ttt gat gct tcc cac tgt gac agt gac aag gga gaa ttc ggt ggc ttt 580
 Phe Asp Ala Ser His Cys Asp Ser Asp Lys Gly Glu Phe Gly Gly Phe

95

100

105

ggt tct gta aca ggg aaa att gaa tgt gaa att aaa att aac cat gaa 628
 Gly Ser Val Thr Gly Lys Ile Glu Cys Glu Ile Lys Ile Asn His Glu

110

115

120

gga gaa gtg aat cgt gct cgt tat atg cca cag aat cct cac atc att 676
 Gly Glu Val Asn Arg Ala Arg Tyr Met Pro Gln Asn Pro His Ile Ile
 125 130 135
 gcc aca aaa aca cca tct tct gat gtt ttg gtt ttt gac tat aca aaa 724
 Ala Thr Lys Thr Pro Ser Ser Asp Val Leu Val Phe Asp Tyr Thr Lys
 140 145 150 155
 cac cct gca aaa cca gat cca agt gga gaa tgt aat cct gat ctt aga 772
 His Pro Ala Lys Pro Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg
 160 165 170
 tta aga ggt cac caa aag gaa ggc tat ggt ctt tcc tgg aat tct aat 820
 Leu Arg Gly His Gln Lys Glu Gly Tyr Gly Leu Ser Trp Asn Ser Asn
 175 180 185
 ctg agt ggg cat ctc ctg agt gca tct gat gac cat act gtc tgc ctg 868
 Leu Ser Gly His Leu Leu Ser Ala Ser Asp Asp His Thr Val Cys Leu
 190 195 200
 tgg gat ata aat gca gga cca aag gaa ggc aaa att gtg gat gct aaa 916
 Trp Asp Ile Asn Ala Gly Pro Lys Glu Gly Lys Ile Val Asp Ala Lys
 205 210 215
 gca atc ttt act ggc cac tca gct gtt gta gag gat gtg gcc tgg cat 964
 Ala Ile Phe Thr Gly His Ser Ala Val Val Glu Asp Val Ala Trp His
 220 225 230 235
 ctg ctg cat gag tcc ttg ttt gga tct gtt gct gat gat cag aaa ctt 1012
 Leu Leu His Glu Ser Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu
 240 245 250
 atg ata tgg gac acc aga tcc aat acc act tct aag ccg agc cat ttg 1060
 Met Ile Trp Asp Thr Arg Ser Asn Thr Thr Ser Lys Pro Ser His Leu
 255 260 265
 gtg gat gca cac acc gct gag gtc aac tgc ctc tca ttc aat ccc tac 1108
 Val Asp Ala His Thr Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr

270	275	280	
agc gag ttc att ctg gca act ggc tct gca gat aag act gta gct tta			1156
Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu			
285	290	295	
tgg gac ctg cgt aat ctg aaa cta aaa ctc cac acc ttt gaa tcg cat			1204
Trp Asp Leu Arg Asn Leu Lys Leu Lys Leu His Thr Phe Glu Ser His			
300	305	310	315
aag gat gaa att ttc cag gtc cac tgg tct cca cat aat gaa act att			1252
Lys Asp Glu Ile Phe Gln Val His Trp Ser Pro His Asn Glu Thr Ile			
320	325	330	
ctg gcc tca agt ggt act gat cgc cgc ctg aat gtg tgg gat tta agt			1300
Leu Ala Ser Ser Gly Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser			
335	340	345	
aaa att gga gaa gaa caa tca gca gaa gat gca gaa gat ggg cct cca			1348
Lys Ile Gly Glu Glu Gln Ser Ala Glu Asp Ala Glu Asp Gly Pro Pro			
350	355	360	
gag ctc ctg ttt att cat gga ggg cac act gcc aag att tct gac ttc			1396
Glu Leu Leu Phe Ile His Gly Gly His Thr Ala Lys Ile Ser Asp Phe			
365	370	375	
agc tgg aat ccc aat gaa cct tgg gtc att tgc tct gtg tct gaa gat			1444
Ser Trp Asn Pro Asn Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp			
380	385	390	395
aac atc atg cag ata tgg cag atg gct gaa aat att tac aat gat gaa			1492
Asn Ile Met Gln Ile Trp Gln Met Ala Glu Asn Ile Tyr Asn Asp Glu			
400	405	410	
gag tca gat gtc acg gca tcg gaa ctg gag ggg caa gga tct taa			1537
Glu Ser Asp Val Thr Ala Ser Glu Leu Glu Gly Gln Gly Ser			
415	420	425	
acccaaagta tgagttgttt ttatigaatg tattgctaca tgaatgcttg atttgtcaag			1597

cgccaaaag gcattgtata gtaggaaatg taagtgggac ggcttctggc attctttacc 1657
 ctctgattct agcactttca agtgagctgt tgcgtactgt atcatattgt agctattagg 1717
 ggataaaaag gaatgttgct taagaacgga c 1748

<210> 164

<211> 425

<212> PRT

<213> Mus musculus

<400> 164

Met	Ala	Ser	Lys	Glu	Met	Phe	Glu	Asp	Thr	Val	Glu	Glu	Arg	Val	Ile
1				5					10					15	
Asn	Glu	Glu	Tyr	Lys	Ile	Trp	Lys	Lys	Asn	Thr	Pro	Phe	Leu	Tyr	Asp
				20					25					30	
Leu	Val	Met	Thr	His	Ala	Leu	Gln	Trp	Pro	Ser	Leu	Thr	Val	Gln	Trp
				35					40					45	
Leu	Pro	Glu	Val	Thr	Lys	Pro	Glu	Gly	Lys	Asp	Tyr	Ala	Leu	His	Trp
				50					55					60	
Leu	Val	Leu	Gly	Thr	His	Thr	Ser	Asp	Glu	Gln	Asn	His	Leu	Val	Val
				65					70					75	
Ala	Arg	Val	His	Ile	Pro	Asn	Asp	Asp	Ala	Gln	Phe	Asp	Ala	Ser	His
				85					90					95	
Cys	Asp	Ser	Asp	Lys	Gly	Glu	Phe	Gly	Gly	Phe	Gly	Ser	Val	Thr	Gly
				100					105					110	
Lys	Ile	Glu	Cys	Glu	Ile	Lys	Ile	Asn	His	Glu	Gly	Glu	Val	Asn	Arg
				115					120					125	
Ala	Arg	Tyr	Met	Pro	Gln	Asn	Pro	His	Ile	Ile	Ala	Thr	Lys	Thr	Pro
				130					135					140	
Ser	Ser	Asp	Val	Leu	Val	Phe	Asp	Tyr	Thr	Lys	His	Pro	Ala	Lys	Pro

145	150	155	160
Asp Pro Ser Gly Glu Cys Asn Pro Asp Leu Arg Leu Arg Gly His Gln			
165	170	175	
Lys Glu Gly Tyr Gly Leu Ser Trp Asn Ser Asn Leu Ser Gly His Leu			
180	185	190	
Leu Ser Ala Ser Asp Asp His Thr Val Cys Leu Trp Asp Ile Asn Ala			
195	200	205	
Gly Pro Lys Glu Gly Lys Ile Val Asp Ala Lys Ala Ile Phe Thr Gly			
210	215	220	
His Ser Ala Val Val Glu Asp Val Ala Trp His Leu Leu His Glu Ser			
225	230	235	240
Leu Phe Gly Ser Val Ala Asp Asp Gln Lys Leu Met Ile Trp Asp Thr			
245	250	255	
Arg Ser Asn Thr Thr Ser Lys Pro Ser His Leu Val Asp Ala His Thr			
260	265	270	
Ala Glu Val Asn Cys Leu Ser Phe Asn Pro Tyr Ser Glu Phe Ile Leu			
275	280	285	
Ala Thr Gly Ser Ala Asp Lys Thr Val Ala Leu Trp Asp Leu Arg Asn			
290	295	300	
Leu Lys Leu Lys Leu His Thr Phe Glu Ser His Lys Asp Glu Ile Phe			
305	310	315	320
Gln Val His Trp Ser Pro His Asn Glu Thr Ile Leu Ala Ser Ser Gly			
325	330	335	
Thr Asp Arg Arg Leu Asn Val Trp Asp Leu Ser Lys Ile Gly Glu Glu			
340	345	350	
Gln Ser Ala Glu Asp Ala Glu Asp Gly Pro Pro Glu Leu Leu Phe Ile			
355	360	365	
His Gly Gly His Thr Ala Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn			
370	375	380	

Glu Pro Trp Val Ile Cys Ser Val Ser Glu Asp Asn Ile Met Gln Ile
 385 390 395 400
 Trp Gln Met Ala Glu Asn Ile Tyr Asn Asp Glu Glu Ser Asp Val Thr
 405 410 415
 Ala Ser Glu Leu Glu Gly Gln Gly Ser
 420 425

<210> 165

<211> 1594

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (85).. (1506)

<400> 165

ggcggcagca gcagcagcag ccccggtctgc gggtcgagac ggcggcgagg cgccccctcc 60
 cccgtgccgg ggcgcggcga aggg atg tgg ggc ttt gcg gga gga agg ctt 111
 Met Trp Gly Phe Ala Gly Gly Arg Leu
 1 5
 ttc ggc atc ttc tcg gcc ccg gtg ctg gtg gcg gtg gtt tgc tgc gct 159
 Phe Gly Ile Phe Ser Ala Pro Val Leu Val Ala Val Val Cys Cys Ala
 10 15 20 25
 cag agc gta aac gac ccc ggg aac atg tcc ttt gtg aag gag acg gtc 207
 Gln Ser Val Asn Asp Pro Gly Asn Met Ser Phe Val Lys Glu Thr Val
 30 35 40
 gac aag ctg ttg aaa ggc tac gac att cgc ctg aga ccc gac ttc ggg 255
 Asp Lys Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp Phe Gly

45	50	55	
ggt ccc cca gtc tgc gtg ggg atg aac atc gac atc gcc agc atc gac			303
Gly Pro Pro Val Cys Val Gly Met Asn Ile Asp Ile Ala Ser Ile Asp			
60	65	70	
atg gtt tct gaa gtc aac atg gat tat acc tta act atg tat ttc caa			351
Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr Phe Gln			
75	80	85	
caa tac tgg aga gat aaa agg ctc gcc tat tct ggg atc cct ctc aac			399
Gln Tyr Trp Arg Asp Lys Arg Leu Ala Tyr Ser Gly Ile Pro Leu Asn			
90	95	100	105
ctc acg ctt gac aat cga gtg gct gac cag ctc tgg gtg ccc gac aca			447
Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro Asp Thr			
110	115	120	
tat ttc tta aat gac aaa aag tca ttt gtc cac gga gtg aca gtg aaa			495
Tyr Phe Leu Asn Asp Lys Lys Ser Phe Val His Gly Val Thr Val Lys			
125	130	135	
aac cgc atg atc cgc ctc cac cct gat ggg aca gtg ctg tat ggg ctc			543
Asn Arg Met Ile Arg Leu His Pro Asp Gly Thr Val Leu Tyr Gly Leu			
140	145	150	
agg atc act acg aca gca gcg tgc atg atg gac ctc aga aga tac cca			591
Arg Ile Thr Thr Thr Ala Ala Cys Met Met Asp Leu Arg Arg Tyr Pro			
155	160	165	
ctg gat gag caa aac tgc act ttg gaa att gaa agc tat ggc tac act			639
Leu Asp Glu Gln Asn Cys Thr Leu Glu Ile Glu Ser Tyr Gly Tyr Thr			
170	175	180	185
acg gat gac att gaa ttt tac tgg cgt ggc ggg gac aag gct gtc act			687
Thr Asp Asp Ile Glu Phe Tyr Trp Arg Gly Gly Asp Lys Ala Val Thr			
190	195	200	
ggc gtg gaa agg atc gag ctc cca cag ttc tcc att gta gag cac cgt			735

Gly Val Glu Arg Ile Glu Leu Pro Gln Phe Ser Ile Val Glu His Arg
 205 210 215
 ctg gtc tcc agg aat gtt gtc ttc gcc aca ggt gcc tat cct cga ctt 783
 Leu Val Ser Arg Asn Val Val Phe Ala Thr Gly Ala Tyr Pro Arg Leu
 220 225 230
 tca ttg agt ttt cgg ttg aag aga aat atc ggg tac ttc att ctg cag 831
 Ser Leu Ser Phe Arg Leu Lys Arg Asn Ile Gly Tyr Phe Ile Leu Gln
 235 240 245
 acg tat atg ccc tca atc ctg atc aca atc ctc tgg tgg gtg tcc ttc 879
 Thr Tyr Met Pro Ser Ile Leu Ile Thr Ile Leu Ser Trp Val Ser Phe
 250 255 260 265
 tgg atc aat tat gat gca tct gct gct cga gtt gcc ctt ggg att acc 927
 Trp Ile Asn Tyr Asp Ala Ser Ala Ala Arg Val Ala Leu Gly Ile Thr
 270 275 280
 acc gtg ctc acc atg aca acc atc aac act cac ctt cgg gag act cta 975
 Thr Val Leu Thr Met Thr Thr Ile Asn Thr His Leu Arg Glu Thr Leu
 285 290 295
 ccc aaa att ccc tat gtc aaa gcc atc gac atg tac ctg atg ggc tgc 1023
 Pro Lys Ile Pro Tyr Val Lys Ala Ile Asp Met Tyr Leu Met Gly Cys
 300 305 310
 ttt gtc ttt gta ttc ctg gca ctt ctg gag tat gcc ttt gtc aac tac 1071
 Phe Val Phe Val Phe Leu Ala Leu Leu Glu Tyr Ala Phe Val Asn Tyr
 315 320 325
 att ttc ttt gga aga ggt ccc caa agg cag aag aag ctt gcg gag aag 1119
 Ile Phe Phe Gly Arg Gly Pro Gln Arg Gln Lys Lys Leu Ala Glu Lys
 330 335 340 345
 aca gcc aag gcc aag aat gat cgt tct aag agt gaa ata aac cgg gtg 1167
 Thr Ala Lys Ala Lys Asn Asp Arg Ser Lys Ser Glu Ile Asn Arg Val
 350 355 360

gat gct cac ggg aat atc cta tta gca ccg atg gat gtt cac aat gaa 1215
Asp Ala His Gly Asn Ile Leu Leu Ala Pro Met Asp Val His Asn Glu
365 370 375
atg aat gag gtt gca ggc agc gtt ggt gac acc agg aat tca gca ata 1263
Met Asn Glu Val Ala Gly Ser Val Gly Asp Thr Arg Asn Ser Ala Ile
380 385 390
tcc ttt gac aac tca gga atc cag tat agg aaa cag agc atg ccc aag 1311
Ser Phe Asp Asn Ser Gly Ile Gln Tyr Arg Lys Gln Ser Met Pro Lys
395 400 405
gaa ggg cat ggg cgg tac atg gga gac aga agc atc ccg cac aag aag 1359
Glu Gly His Gly Arg Tyr Met Gly Asp Arg Ser Ile Pro His Lys Lys
410 415 420 425
acc cac cta cgg agg agg tct tca cag ctc aaa atc aaa atc cct gat 1407
Thr His Leu Arg Arg Arg Ser Ser Gln Leu Lys Ile Lys Ile Pro Asp
430 435 440
cta acc gat gtg aat gcc ata gac aga tgg tcc cgc atc gtg ttt cca 1455
Leu Thr Asp Val Asn Ala Ile Asp Arg Trp Ser Arg Ile Val Phe Pro
445 450 455
ttc acc ttt tct ctc ttc aat tta gtt tac tgg ctg tac tat gtt aac 1503
Phe Thr Phe Ser Leu Phe Asn Leu Val Tyr Trp Leu Tyr Tyr Val Asn
460 465 470
tga gtgactgtac ttgatttttc aaagacttca tttaacactg agtgaaatat 1556
taccctgcct gtcaagtttt tataccagta cacataca 1594

<210> 166

<211> 473

<212> PRT

<213> Mus musculus

<400> 166

```

Met Trp Gly Phe Ala Gly Gly Arg Leu Phe Gly Ile Phe Ser Ala Pro
  1           5           10           15
Val Leu Val Ala Val Val Cys Cys Ala Gln Ser Val Asn Asp Pro Gly
          20           25           30
Asn Met Ser Phe Val Lys Glu Thr Val Asp Lys Leu Leu Lys Gly Tyr
          35           40           45
Asp Ile Arg Leu Arg Pro Asp Phe Gly Gly Pro Pro Val Cys Val Gly
          50           55           60
Met Asn Ile Asp Ile Ala Ser Ile Asp Met Val Ser Glu Val Asn Met
          65           70           75           80
Asp Tyr Thr Leu Thr Met Tyr Phe Gln Gln Tyr Trp Arg Asp Lys Arg
          85           90           95
Leu Ala Tyr Ser Gly Ile Pro Leu Asn Leu Thr Leu Asp Asn Arg Val
          100          105          110
Ala Asp Gln Leu Trp Val Pro Asp Thr Tyr Phe Leu Asn Asp Lys Lys
          115          120          125
Ser Phe Val His Gly Val Thr Val Lys Asn Arg Met Ile Arg Leu His
          130          135          140
Pro Asp Gly Thr Val Leu Tyr Gly Leu Arg Ile Thr Thr Thr Ala Ala
          145          150          155          160
Cys Met Met Asp Leu Arg Arg Tyr Pro Leu Asp Glu Gln Asn Cys Thr
          165          170          175
Leu Glu Ile Glu Ser Tyr Gly Tyr Thr Thr Asp Asp Ile Glu Phe Tyr
          180          185          190
Trp Arg Gly Gly Asp Lys Ala Val Thr Gly Val Glu Arg Ile Glu Leu
          195          200          205
Pro Gln Phe Ser Ile Val Glu His Arg Leu Val Ser Arg Asn Val Val
          210          215          220

```

Phe Ala Thr Gly Ala Tyr Pro Arg Leu Ser Leu Ser Phe Arg Leu Lys
 225 230 235 240
 Arg Asn Ile Gly Tyr Phe Ile Leu Gln Thr Tyr Met Pro Ser Ile Leu
 245 250 255
 Ile Thr Ile Leu Ser Trp Val Ser Phe Trp Ile Asn Tyr Asp Ala Ser
 260 265 270
 Ala Ala Arg Val Ala Leu Gly Ile Thr Thr Val Leu Thr Met Thr Thr
 275 280 285
 Ile Asn Thr His Leu Arg Glu Thr Leu Pro Lys Ile Pro Tyr Val Lys
 290 295 300
 Ala Ile Asp Met Tyr Leu Met Gly Cys Phe Val Phe Val Phe Leu Ala
 305 310 315 320
 Leu Leu Glu Tyr Ala Phe Val Asn Tyr Ile Phe Phe Gly Arg Gly Pro
 325 330 335
 Gln Arg Gln Lys Lys Leu Ala Glu Lys Thr Ala Lys Ala Lys Asn Asp
 340 345 350
 Arg Ser Lys Ser Glu Ile Asn Arg Val Asp Ala His Gly Asn Ile Leu
 355 360 365
 Leu Ala Pro Met Asp Val His Asn Glu Met Asn Glu Val Ala Gly Ser
 370 375 380
 Val Gly Asp Thr Arg Asn Ser Ala Ile Ser Phe Asp Asn Ser Gly Ile
 385 390 395 400
 Gln Tyr Arg Lys Gln Ser Met Pro Lys Glu Gly His Gly Arg Tyr Met
 405 410 415
 Gly Asp Arg Ser Ile Pro His Lys Lys Thr His Leu Arg Arg Arg Ser
 420 425 430
 Ser Gln Leu Lys Ile Lys Ile Pro Asp Leu Thr Asp Val Asn Ala Ile
 435 440 445
 Asp Arg Trp Ser Arg Ile Val Phe Pro Phe Thr Phe Ser Leu Phe Asn

450 455 460
 Leu Val Tyr Trp Leu Tyr Tyr Val Asn
 465 470

<210> 167

<211> 3597

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (95).. (2491)

<400> 167

ctccgcaagc cgaggtccgc cgacaccgac ccgagaccct ccgagaggcg gaacgcgcgg 60
 agcccgcccg cgtgtcggcg gacgctgcga aaag atg aat ttg caa ctg gtt tcc 115

Met Asn Leu Gln Leu Val Ser

1

5

tgg att gga ttg atc agt ttg att tgt tct gta ttt ggc caa aca gat 163
 Trp Ile Gly Leu Ile Ser Leu Ile Cys Ser Val Phe Gly Gln Thr Asp

10

15

20

aaa aat aga tgt tta aaa gca aat gcc aaa tct tgc gga gaa tgt ata 211
 Lys Asn Arg Cys Leu Lys Ala Asn Ala Lys Ser Cys Gly Glu Cys Ile

25

30

35

caa gca ggg cca aat tgt ggg tgg tgt aca aat acg aca ttt ttg caa 259
 Gln Ala Gly Pro Asn Cys Gly Trp Cys Thr Asn Thr Thr Phe Leu Gln

40

45

50

55

gaa gga atg cct act tct gca cga tgt gat gat tta gaa gct ttg aaa 307
 Glu Gly Met Pro Thr Ser Ala Arg Cys Asp Asp Leu Glu Ala Leu Lys

60	65	70	
aag aag ggt tgc cag cca agt gac ata gag aat ccc aga ggc tct caa			355
Lys Lys Gly Cys Gln Pro Ser Asp Ile Glu Asn Pro Arg Gly Ser Gln			
75	80	85	
act ata aag aaa aat aaa aat gtc acc aat cgc agc aaa ggg atg gca			403
Thr Ile Lys Lys Asn Lys Asn Val Thr Asn Arg Ser Lys Gly Met Ala			
90	95	100	
gag aag ctc cgg cca gaa gac att act cag atc caa cca caa cag ctg			451
Glu Lys Leu Arg Pro Glu Asp Ile Thr Gln Ile Gln Pro Gln Gln Leu			
105	110	115	
ctt cta aaa ttg aga tca gga gaa cca cag aag ttt aca tta aaa ttc			499
Leu Leu Lys Leu Arg Ser Gly Glu Pro Gln Lys Phe Thr Leu Lys Phe			
120	125	130	135
aag agg gct gaa gat tac cct att gat ctc tac tac ctt atg gat ctc			547
Lys Arg Ala Glu Asp Tyr Pro Ile Asp Leu Tyr Tyr Leu Met Asp Leu			
140	145	150	
tcc tac tct atg aaa gat gat ctg gag aat gtg aaa agt ctt gga acg			595
Ser Tyr Ser Met Lys Asp Asp Leu Glu Asn Val Lys Ser Leu Gly Thr			
155	160	165	
gat ttg atg aat gaa atg agg agg att act tca gac ttc cgc att ggc			643
Asp Leu Met Asn Glu Met Arg Arg Ile Thr Ser Asp Phe Arg Ile Gly			
170	175	180	
ttt ggc tca ttt gtg gag aaa act gtg atg ccg tat att agc aca acc			691
Phe Gly Ser Phe Val Glu Lys Thr Val Met Pro Tyr Ile Ser Thr Thr			
185	190	195	
cca gca aag cta aga aat cct tgt aca agt gaa caa aac tgc acc agc			739
Pro Ala Lys Leu Arg Asn Pro Cys Thr Ser Glu Gln Asn Cys Thr Ser			
200	205	210	215
cca ttt agc tac aaa aat gtg ctt agt ctt act gac aga gga gag ttt			787

Pro Phe Ser Tyr Lys Asn Val Leu Ser Leu Thr Asp Arg Gly Glu Phe
 220 225 230
 ttc aat gaa ctt gtt ggt cag caa cgc ata tct gga aac ttg gat tct 835
 Phe Asn Glu Leu Val Gly Gln Gln Arg Ile Ser Gly Asn Leu Asp Ser
 235 240 245
 cca gaa ggt ggc ttt gat gca atc atg cag gtt gcg gtt tgt gga tcg 883
 Pro Glu Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser
 250 255 260
 ctg att ggc tgg agg aat gta aca cga ctg ctg gtg ttt tcc acg gat 931
 Leu Ile Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp
 265 270 275
 gct ggg ttt cac ttt gct gga gat ggg aaa ctt ggt ggt att gtt tta 979
 Ala Gly Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu
 280 285 290 295
 ccc aat gat gga caa tgt cac ctg gaa aat aat gta tat aca atg agc 1027
 Pro Asn Asp Gly Gln Cys His Leu Glu Asn Asn Val Tyr Thr Met Ser
 300 305 310
 cat tac tat gat tat cct tca att gct cac ctt gtt cag aaa cta agt 1075
 His Tyr Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser
 315 320 325
 gaa aat aat att cag acg att ttt gca gtt act gaa gag ttc caa cct 1123
 Glu Asn Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro
 330 335 340
 gtt tac aag gaa ttg aag aat ttg att cct aag tca gca gtg ggc aca 1171
 Val Tyr Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala Val Gly Thr
 345 350 355
 ctg tct gga aac tct agt aat gtg atc cag cta atc atc gat gcc tac 1219
 Leu Ser Gly Asn Ser Ser Asn Val Ile Gln Leu Ile Ile Asp Ala Tyr
 360 365 370 375

aac tct ctt tct tca gaa gtc att ctg gaa aat agc aaa ttg cca gac	1267
Asn Ser Leu Ser Ser Glu Val Ile Leu Glu Asn Ser Lys Leu Pro Asp	
380 385 390	
gga gta aca ata aat tac aaa tcc tat tgc aag aat ggg gtg aat ggg	1315
Gly Val Thr Ile Asn Tyr Lys Ser Tyr Cys Lys Asn Gly Val Asn Gly	
395 400 405	
aca gga gaa aat gga cga aag tgt tcc aac att tct att gga gat gag	1363
Thr Gly Glu Asn Gly Arg Lys Cys Ser Asn Ile Ser Ile Gly Asp Glu	
410 415 420	
gtt caa ttt gaa att agc ata act gct aat aaa tgt cca aat aag gag	1411
Val Gln Phe Glu Ile Ser Ile Thr Ala Asn Lys Cys Pro Asn Lys Glu	
425 430 435	
tct gaa acc att aaa att aaa cct ctg ggc ttc act gaa gaa gta gag	1459
Ser Glu Thr Ile Lys Ile Lys Pro Leu Gly Phe Thr Glu Glu Val Glu	
440 445 450 455	
gtc gtt ctt cag ttc atc tgt aag tgc aat tgt caa agc cat ggc atc	1507
Val Val Leu Gln Phe Ile Cys Lys Cys Asn Cys Gln Ser His Gly Ile	
460 465 470	
cca gcc agt ccc aag tgc cat gag gga aat ggg aca ttt gag tgt gga	1555
Pro Ala Ser Pro Lys Cys His Glu Gly Asn Gly Thr Phe Glu Cys Gly	
475 480 485	
gcc tgc agg tgc aat gag ggg cgt gtt ggg agg cac tgt gaa tgt agc	1603
Ala Cys Arg Cys Asn Glu Gly Arg Val Gly Arg His Cys Glu Cys Ser	
490 495 500	
aca gat gaa gtg aac agt gaa gac atg gac gct tac tgc agg aaa gag	1651
Thr Asp Glu Val Asn Ser Glu Asp Met Asp Ala Tyr Cys Arg Lys Glu	
505 510 515	
aac agt tcg gaa atc tgc agt aac aat gga gaa tgt gtc tgt gga cag	1699
Asn Ser Ser Glu Ile Cys Ser Asn Asn Gly Glu Cys Val Cys Gly Gln	

520	525	530	535	
tgt gtg tgt agg aag aga gat aat aca aat gaa att tac tct gga aaa				1747
Cys Val Cys Arg Lys Arg Asp Asn Thr Asn Glu Ile Tyr Ser Gly Lys				
540	545	550		
ttc tgc gag tgt gat aac ttc aac tgt gat agg tct aat ggc tta att				1795
Phe Cys Glu Cys Asp Asn Phe Asn Cys Asp Arg Ser Asn Gly Leu Ile				
555	560	565		
tgt gga ggc aat ggc gtg tgc agg tgt cgt gtt tgt gaa tgc tat ccc				1843
Cys Gly Gly Asn Gly Val Cys Arg Cys Arg Val Cys Glu Cys Tyr Pro				
570	575	580		
aat tac act ggc agt gca tgt gac tgt tct ttg gac act ggt cca tgt				1891
Asn Tyr Thr Gly Ser Ala Cys Asp Cys Ser Leu Asp Thr Gly Pro Cys				
585	590	595		
cta gcg tca aat ggt cag atc tgc aat ggc cgg ggt att tgt gaa tgt				1939
Leu Ala Ser Asn Gly Gln Ile Cys Asn Gly Arg Gly Ile Cys Glu Cys				
600	605	610	615	
ggt gct tgt aag tgc aca gat ccc aag ttt caa ggg cca act tgt gag				1987
Gly Ala Cys Lys Cys Thr Asp Pro Lys Phe Gln Gly Pro Thr Cys Glu				
620	625	630		
aca tgt cag acc tgc ctt ggc gtc tgt gca gag cat aaa gaa tgt gtt				2035
Thr Cys Gln Thr Cys Leu Gly Val Cys Ala Glu His Lys Glu Cys Val				
635	640	645		
cag tgc aga gcc ttc aat aaa gga gaa aag aaa gac acg tgt gca cag				2083
Gln Cys Arg Ala Phe Asn Lys Gly Glu Lys Lys Asp Thr Cys Ala Gln				
650	655	660		
gag tgc tcc cac ttc aat ctc acc aaa gta gaa agc agg gag aag ttg				2131
Glu Cys Ser His Phe Asn Leu Thr Lys Val Glu Ser Arg Glu Lys Leu				
665	670	675		
ccc cag ccg gtg cag gtc gat cct gtg acc cat tgc aag gag aag gac				2179

Pro Gln Pro Val Gln Val Asp Pro Val Thr His Cys Lys Glu Lys Asp
 680 685 690 695
 att gat gac tgc tgg ttc tat ttc acc tat tca gtg aat ggc aac aat 2227
 Ile Asp Asp Cys Trp Phe Tyr Phe Thr Tyr Ser Val Asn Gly Asn Asn
 700 705 710
 gaa gct atc gtg cat gtt gtg gag act cca gac tgt cct act ggt ccc 2275
 Glu Ala Ile Val His Val Val Glu Thr Pro Asp Cys Pro Thr Gly Pro
 715 720 725
 gac atc atc cca att gta gca ggc gtg gtt gct gga att gtt ctt att 2323
 Asp Ile Ile Pro Ile Val Ala Gly Val Val Ala Gly Ile Val Leu Ile
 730 735 740
 ggc ctt gcc ttg ctg ctg att tgg aaa ctt tta atg ata att cat gac 2371
 Gly Leu Ala Leu Leu Leu Ile Trp Lys Leu Leu Met Ile Ile His Asp
 745 750 755
 aga agg gaa ttt gct aaa ttt gaa aag gag aaa atg aat gcc aag tgg 2419
 Arg Arg Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala Lys Trp
 760 765 770 775
 gac acg ggt gaa aat cct att tac aag agt gcc gtg aca act gtg gtc 2467
 Asp Thr Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr Val Val
 780 785 790
 aat ccg aag tat gag gga aaa tga atcctactca ggcggatttt gcaacaccaa 2521
 Asn Pro Lys Tyr Glu Gly Lys
 795
 gctcacagca gcagcatcct agtcacagta gggtagtttt ggggctctgt ggccagggtt 2581
 ttattcacat gcaggtttgg aaaatgtaca atatgtataa tttttaattt tttattattt 2641
 tgaaaataat gttataatcc atgccaggga ctgacagaag acttgagaaa gcatctttat 2701
 ccttgtcagc tgaggtcaca gtgtgccttt ttaacccttc ctctctggacc attggaatca 2761
 agctctcact agattgaatg acactgctag tgccaatgca gggcagagct gagcagcgtc 2821
 gcagcatctg aaccatgact gattttcagc ttacagggt ggccagggtt ggttatacag 2881

aatcaaagaa cagtccttgc tggtaggcttt gtcttttggt tagcctgctg gctgcctctg 2941
 ggaattccca gtagatgatg tggaagacaa gagtgttgac agtttccaat taaaataaaa 3001
 ttgacacagi tgatgttcaa gtccattgga aaaattctga gaggtgggaa ggaaatctta 3061
 gctttaaaac cigtgtgcca ttgtgagttt ctgatccctg taactccgac gccittttctt 3121
 tataaatcca accttgata aaagtactgg gaacttctct gctaaaaagt ccttgactta 3181
 gcactattca cataaaggcc ataatttttag tagcattgct gagtggggac cttttgggtt 3241
 gagcttattt tacctttttt ttttttcttt aattcctggt gctcctttat caccttctct 3301
 aatcttttaa tgtgtctggt tgcaatatgg gggtagact ttttatcatt accttttctt 3361
 ttccttggct gtacatttac ctttttcaca aatactgtaa gctgtcctgc tgcttgcagg 3421
 actacagggc ctggcagggc cccccagcaa caattcacc acagtgcacc tgcacatgcc 3481
 tttctacat gcttgctctg tctcgaacta gtcacaatct tgttttaagt gccitttcat 3541
 ttgacagtg ctattaactg aagttattta ttaaaataaa aaggcctaaa tacatt 3597

<210> 168

<211> 798

<212> PRT

<213> Mus musculus

<400> 168

Met Asn Leu Gln Leu Val Ser Trp Ile Gly Leu Ile Ser Leu Ile Cys

1 5 10 15

Ser Val Phe Gly Gln Thr Asp Lys Asn Arg Cys Leu Lys Ala Asn Ala

20 25 30

Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys

35 40 45

Thr Asn Thr Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys

50 55 60

Asp Asp Leu Glu Ala Leu Lys Lys Lys Gly Cys Gln Pro Ser Asp Ile

65 70 75 80

Glu Asn Pro Arg Gly Ser Gln Thr Ile Lys Lys Asn Lys Asn Val Thr
 85 90 95
 Asn Arg Ser Lys Gly Met Ala Glu Lys Leu Arg Pro Glu Asp Ile Thr
 100 105 110
 Gln Ile Gln Pro Gln Gln Leu Leu Leu Lys Leu Arg Ser Gly Glu Pro
 115 120 125
 Gln Lys Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp
 130 135 140
 Leu Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Lys Asp Asp Leu Glu
 145 150 155 160
 Asn Val Lys Ser Leu Gly Thr Asp Leu Met Asn Glu Met Arg Arg Ile
 165 170 175
 Thr Ser Asp Phe Arg Ile Gly Phe Gly Ser Phe Val Glu Lys Thr Val
 180 185 190
 Met Pro Tyr Ile Ser Thr Thr Pro Ala Lys Leu Arg Asn Pro Cys Thr
 195 200 205
 Ser Glu Gln Asn Cys Thr Ser Pro Phe Ser Tyr Lys Asn Val Leu Ser
 210 215 220
 Leu Thr Asp Arg Gly Glu Phe Phe Asn Glu Leu Val Gly Gln Gln Arg
 225 230 235 240
 Ile Ser Gly Asn Leu Asp Ser Pro Glu Gly Gly Phe Asp Ala Ile Met
 245 250 255
 Gln Val Ala Val Cys Gly Ser Leu Ile Gly Trp Arg Asn Val Thr Arg
 260 265 270
 Leu Leu Val Phe Ser Thr Asp Ala Gly Phe His Phe Ala Gly Asp Gly
 275 280 285
 Lys Leu Gly Gly Ile Val Leu Pro Asn Asp Gly Gln Cys His Leu Glu
 290 295 300
 Asn Asn Val Tyr Thr Met Ser His Tyr Tyr Asp Tyr Pro Ser Ile Ala

305	310	315	320
His Leu Val Gln Lys Leu Ser Glu Asn Asn Ile Gln Thr Ile Phe Ala			
325	330	335	
Val Thr Glu Glu Phe Gln Pro Val Tyr Lys Glu Leu Lys Asn Leu Ile			
340	345	350	
Pro Lys Ser Ala Val Gly Thr Leu Ser Gly Asn Ser Ser Asn Val Ile			
355	360	365	
Gln Leu Ile Ile Asp Ala Tyr Asn Ser Leu Ser Ser Glu Val Ile Leu			
370	375	380	
Glu Asn Ser Lys Leu Pro Asp Gly Val Thr Ile Asn Tyr Lys Ser Tyr			
385	390	395	400
Cys Lys Asn Gly Val Asn Gly Thr Gly Glu Asn Gly Arg Lys Cys Ser			
405	410	415	
Asn Ile Ser Ile Gly Asp Glu Val Gln Phe Glu Ile Ser Ile Thr Ala			
420	425	430	
Asn Lys Cys Pro Asn Lys Glu Ser Glu Thr Ile Lys Ile Lys Pro Leu			
435	440	445	
Gly Phe Thr Glu Glu Val Glu Val Val Leu Gln Phe Ile Cys Lys Cys			
450	455	460	
Asn Cys Gln Ser His Gly Ile Pro Ala Ser Pro Lys Cys His Glu Gly			
465	470	475	480
Asn Gly Thr Phe Glu Cys Gly Ala Cys Arg Cys Asn Glu Gly Arg Val			
485	490	495	
Gly Arg His Cys Glu Cys Ser Thr Asp Glu Val Asn Ser Glu Asp Met			
500	505	510	
Asp Ala Tyr Cys Arg Lys Glu Asn Ser Ser Glu Ile Cys Ser Asn Asn			
515	520	525	
Gly Glu Cys Val Cys Gly Gln Cys Val Cys Arg Lys Arg Asp Asn Thr			
530	535	540	

Asn Glu Ile Tyr Ser Gly Lys Phe Cys Glu Cys Asp Asn Phe Asn Cys
 545 550 555 560
 Asp Arg Ser Asn Gly Leu Ile Cys Gly Gly Asn Gly Val Cys Arg Cys
 565 570 575
 Arg Val Cys Glu Cys Tyr Pro Asn Tyr Thr Gly Ser Ala Cys Asp Cys
 580 585 590
 Ser Leu Asp Thr Gly Pro Cys Leu Ala Ser Asn Gly Gln Ile Cys Asn
 595 600 605
 Gly Arg Gly Ile Cys Glu Cys Gly Ala Cys Lys Cys Thr Asp Pro Lys
 610 615 620
 Phe Gln Gly Pro Thr Cys Glu Thr Cys Gln Thr Cys Leu Gly Val Cys
 625 630 635 640
 Ala Glu His Lys Glu Cys Val Gln Cys Arg Ala Phe Asn Lys Gly Glu
 645 650 655
 Lys Lys Asp Thr Cys Ala Gln Glu Cys Ser His Phe Asn Leu Thr Lys
 660 665 670
 Val Glu Ser Arg Glu Lys Leu Pro Gln Pro Val Gln Val Asp Pro Val
 675 680 685
 Thr His Cys Lys Glu Lys Asp Ile Asp Asp Cys Trp Phe Tyr Phe Thr
 690 695 700
 Tyr Ser Val Asn Gly Asn Asn Glu Ala Ile Val His Val Val Glu Thr
 705 710 715 720
 Pro Asp Cys Pro Thr Gly Pro Asp Ile Ile Pro Ile Val Ala Gly Val
 725 730 735
 Val Ala Gly Ile Val Leu Ile Gly Leu Ala Leu Leu Leu Ile Trp Lys
 740 745 750
 Leu Leu Met Ile Ile His Asp Arg Arg Glu Phe Ala Lys Phe Glu Lys
 755 760 765
 Glu Lys Met Asn Ala Lys Trp Asp Thr Gly Glu Asn Pro Ile Tyr Lys

770 775 780
 Ser Ala Val Thr Thr Val Val Asn Pro Lys Tyr Glu Gly Lys
 785 790 795

<210> 169

<211> 2063

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (73).. (648)

<400> 169

ccctccggcg gagaagctga ggacaagatc taatttgaaa tattaaaagt tggatacaaaa 60
 actgtttccg aa atg cag aca att aag tgt gtt gtt gtt ggt gat ggt gct 111

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala

1 5 10

gtt ggt aaa aca tgt ctc ctg ata tcc tac aca aca aac aaa ttc cca 159
 Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro

15 20 25

tcg gaa tat gta cca act gtt ttt gac aac tat gca gtc aca gtt atg 207
 Ser Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met

30 35 40 45

att ggt gga gag cca tac act ctt gga ctt ttt gat act gca ggg caa 255
 Ile Gly Gly Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln

50 55 60

gag gat tat gac aga cta cga ccg cta agt tat cca cag aca gat gtt 303
 Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val

65	70	75	
ttt cta gta tgt ttc tca gtg gtc tct cca tcc tca ttt gaa aat gtg	351		
Phe Leu Val Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val			
80	85	90	
aaa gaa aag tgg gtg cct gag ata act cac cac tgt cca aag act cct	399		
Lys Glu Lys Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro			
95	100	105	
ttc ttg ctt gtt ggg acc caa att gat ctc aga gat gac ccc tct act	447		
Phe Leu Leu Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr			
110	115	120	125
att gag aaa ctt gcc aag aac aaa cag aag cct att act cca gag act	495		
Ile Glu Lys Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr			
130	135	140	
gct gaa aag ctg gcg cgg gat ctg aag gct gtc aag tat gtg gag tgc	543		
Ala Glu Lys Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys			
145	150	155	
tcc gcc ctc aca cag aaa ggc cta aag aat gtg ttt gat gaa gca ata	591		
Ser Ala Leu Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile			
160	165	170	
ttg gct gcc ctg gag cct cca gaa ccg aag aag agc cgc agg tgt gtg	639		
Leu Ala Ala Leu Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val			
175	180	185	
ctg cta tga acgcatctcc agagcccttt ctgcacagct ggtgttgtcg	688		
Leu Leu			
190			
tcatactaaa agcaatgttt aaatcaaact aaagattaaa aattaaaatt tgtttctgca	748		
ataatgacaa acgccctgca cctacccaca tgcactcatg tgagacaagg cccattagta	808		
tggccctcc ttgcccttcc agtaatagtt aattttgaat aattatgtat tgtctgaaaa	868		
gcaatgagtg ctagtitttg ttttctttgt ttaaaaaaaaa aaacaaaaat cccacaaaac	928		

gtttgttggt tttttgttta aaagcaagca tgcttgtatt gactgtaata gactaattca 988
 gattgtcaaa gctgctccct ggttccattt tggagagtaa tctggggcat ctctgtgtct 1048
 tctgttttgt ttgttttgtt ttttctcaa ccctctctc cttttgggt gtgtatgggg 1108
 ttgtttctta gacttgtatt ttaaaatttg ttaaccatag gacagcctgt ggggaggagg 1168
 acagagtatt tccacattcc actccctagg tctagtttag caaacgtgc cccacctggt 1228
 gctcttagga aggagtatag aaacgcctcg attaacaacg tattccttct tgaaagttgc 1288
 ctttctctc cacctctgag tgggtccagt ctgtgatga actcatgaag gtgggtggac 1348
 gctgtctgc ccctcttct aggatgcact ctatagtga ctgtgacttt caagggtatt 1408
 tgtttgcat ttctgtattt agggaggga ataatttcta acttctttca ttgataaatg 1468
 aaaagtattg cacctttgaa atacacaaa tggattgagt tcctaattaa aaaaagttct 1528
 ttggccctg tcagtcattt tcttacctg ttagcacaga ttcacaactc actgtgtagt 1588
 gticctagat tcagctgaag acctggtacc tagggttcct aacgggatgg tgtaggaaa 1648
 cacatcatgg ctgatgattg ccatctcctt tcaggatg aggtcacagg cctgcttcct 1708
 taagaagcta tgagcatggg gtggggagca tacttttaac caacatgggg accagtcagg 1768
 gctatccct ttttcttcc atgcctatga ggaaccttg aacaactggc tgaagctttc 1828
 gcaagaaaaa tggcgagagc ctcatgattc ttataagtg ttaatagaga cttatcaga 1888
 ttattttgtt tgcaggttcc agtttttaa aaatgttttag ataatctcct tccccagtcc 1948
 tgatcttgtg gattcgttag tgccgaacca atgccttctt gtgtctcaac tctttgtata 2008
 tgaattcttt tcagatgtat taaacaaaca aaacccttca aaaaaaaaaa aaaaa 2063

<210> 170

<211> 191

<212> PRT

<213> Mus musculus

<400> 170

Met Gln Thr Ile Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys

1

5

10

15

Thr Cys Leu Leu Ile Ser Tyr Thr Thr Asn Lys Phe Pro Ser Glu Tyr

20	25	30
Val Pro Thr Val Phe Asp Asn Tyr Ala Val Thr Val Met Ile Gly Gly		
35	40	45
Glu Pro Tyr Thr Leu Gly Leu Phe Asp Thr Ala Gly Gln Glu Asp Tyr		
50	55	60
Asp Arg Leu Arg Pro Leu Ser Tyr Pro Gln Thr Asp Val Phe Leu Val		
65	70	75
Cys Phe Ser Val Val Ser Pro Ser Ser Phe Glu Asn Val Lys Glu Lys		
85	90	95
Trp Val Pro Glu Ile Thr His His Cys Pro Lys Thr Pro Phe Leu Leu		
100	105	110
Val Gly Thr Gln Ile Asp Leu Arg Asp Asp Pro Ser Thr Ile Glu Lys		
115	120	125
Leu Ala Lys Asn Lys Gln Lys Pro Ile Thr Pro Glu Thr Ala Glu Lys		
130	135	140
Leu Ala Arg Asp Leu Lys Ala Val Lys Tyr Val Glu Cys Ser Ala Leu		
145	150	155
Thr Gln Lys Gly Leu Lys Asn Val Phe Asp Glu Ala Ile Leu Ala Ala		
165	170	175
Leu Glu Pro Pro Glu Pro Lys Lys Ser Arg Arg Cys Val Leu Leu		
180	185	190

<210> 171

<211> 5425

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (324).. (2423)

<400> 171

agagctggag gcggccggac cgggccagac agatttcctg ctctcctgta gggctgaggg 60
 ctgccggctg cgggctacgg gctgcgggct acaggctacg ggctacggac tgcgggctgc 120
 gagagaagtc accggcgggc caggtacctc actgcctacg cgcgtcccca cgaccctccc 180
 tcgcgccggc ggggacagcg gacgccccgg agcggagcgc gtcgggctgg cgcccgaggag 240
 atgcggagtc gccgcggcgg agcgatcggg gctacagcac cggtccttgg gagactatag 300
 ccctcatttc cccttggigc acc atg gag ccc ttc tgt cca ctc ctg ctg gca 353

Met Glu Pro Phe Cys Pro Leu Leu Leu Ala

1 5 10

agt ttt agc ttg tgc ctc gcc aga gct ggc cag ggc aac gac acc acc 401
 Ser Phe Ser Leu Ser Leu Ala Arg Ala Gly Gln Gly Asn Asp Thr Thr

15 20 25

cca aca gag agc aac tgg acc agc aca act gca ggc cct ccg gac cct 449
 Pro Thr Glu Ser Asn Trp Thr Ser Thr Thr Ala Gly Pro Pro Asp Pro

30 35 40

ggc gca tcc cag ccg ctg ctc acc tgg ctg ctg ctg ccc ctg ctc ctc 497
 Gly Ala Ser Gln Pro Leu Leu Thr Trp Leu Leu Leu Pro Leu Leu Leu

45 50 55

ctc ctg ttc ctg ctt gca gcc tac ttc ttc agg ttc cgg aag cag agg 545
 Leu Leu Phe Leu Leu Ala Ala Tyr Phe Phe Arg Phe Arg Lys Gln Arg

60 65 70

aag gcc gtg gtc agc agc aac gac aag aaa atg cct aac ggc atc tta 593
 Lys Ala Val Val Ser Ser Asn Asp Lys Lys Met Pro Asn Gly Ile Leu

75 80 85 90

gaa gag caa gag cag cag aga gtg atg ctg ctg agc aga tct cca tca 641
 Glu Glu Gln Glu Gln Gln Arg Val Met Leu Leu Ser Arg Ser Pro Ser

95 100 105

```

ggc ccc aag aag ttc ttc ccc atc ccc gtg gag cac ctg gag gag gag      689
Gly Pro Lys Lys Phe Phe Pro Ile Pro Val Glu His Leu Glu Glu Glu
      110              115              120
atc cgg gtg aga tct gcg gat gac tgc aag cga ttc cga gag gag ttc      737
Ile Arg Val Arg Ser Ala Asp Asp Cys Lys Arg Phe Arg Glu Glu Phe
      125              130              135
aat tca ttg cca tct gga cac ata caa gga acc ttt gaa cta gca aat      785
Asn Ser Leu Pro Ser Gly His Ile Gln Gly Thr Phe Glu Leu Ala Asn
      140              145              150
aaa gaa gaa aac aga gaa aaa aac aga tac ccc aac att ctg ccc aat      833
Lys Glu Glu Asn Arg Glu Lys Asn Arg Tyr Pro Asn Ile Leu Pro Asn
155              160              165              170
gat cat tgc aga gtg att ttg agc caa gtg gat gga atc ccc tgc tct      881
Asp His Cys Arg Val Ile Leu Ser Gln Val Asp Gly Ile Pro Cys Ser
      175              180              185
gac tac att aat gct tcc tac atc gat ggc tac aaa gaa aag aac aaa      929
Asp Tyr Ile Asn Ala Ser Tyr Ile Asp Gly Tyr Lys Glu Lys Asn Lys
      190              195              200
ttc ata gca gct caa ggc cct aag cag gag aca gtg aat gac ttc tgg      977
Phe Ile Ala Ala Gln Gly Pro Lys Gln Glu Thr Val Asn Asp Phe Trp
      205              210              215
aga atg gtc tgg gag caa agg tca gcc acc atc gtc atg ttg acg aac      1025
Arg Met Val Trp Glu Gln Arg Ser Ala Thr Ile Val Met Leu Thr Asn
      220              225              230
ctg aag gag agg aag gag gag aag tgc tac cag tac tgg cca gac cag      1073
Leu Lys Glu Arg Lys Glu Glu Lys Cys Tyr Gln Tyr Trp Pro Asp Gln
235              240              245              250
ggc tgt tgg acc tac ggc aac atc cgg gtg tgt gta gag gac tgc gtg      1121
Gly Cys Trp Thr Tyr Gly Asn Ile Arg Val Cys Val Glu Asp Cys Val

```


255	260	265	
gtc ctg gtg gat tac acg atc cga aag ttc tgc atc cat ccg caa ctc			1169
Val Leu Val Asp Tyr Thr Ile Arg Lys Phe Cys Ile His Pro Gln Leu			
270	275	280	
cca gac agc tgc aaa gcc ccg cgg ctg gtc tca cag ctg cac ttc acc			1217
Pro Asp Ser Cys Lys Ala Pro Arg Leu Val Ser Gln Leu His Phe Thr			
285	290	295	
agc tgg cct gac ttc ggg gtg ccg ttt acc ccc atc ggg atg ctc aag			1265
Ser Trp Pro Asp Phe Gly Val Pro Phe Thr Pro Ile Gly Met Leu Lys			
300	305	310	
ttc ctg aag aaa gtg aag aca ctc aac ccc tca cat gct ggg ccc att			1313
Phe Leu Lys Lys Val Lys Thr Leu Asn Pro Ser His Ala Gly Pro Ile			
315	320	325	330
gtg gtt cac tgt agc gcg ggc gtg ggt cgg act ggc acc ttc att gtg			1361
Val Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Thr Phe Ile Val			
335	340	345	
atc gat gcc atg atg gac atg ata cac tcg gag cag aag gtt gac gtc			1409
Ile Asp Ala Met Met Asp Met Ile His Ser Glu Gln Lys Val Asp Val			
350	355	360	
ttt gag ttt gtg tct aga atc cgc aat cag cgc cct cag atg gtc cag			1457
Phe Glu Phe Val Ser Arg Ile Arg Asn Gln Arg Pro Gln Met Val Gln			
365	370	375	
acg gat gtt cag tat aca ttc atc tac caa gcc tta ctg gaa tac tac			1505
Thr Asp Val Gln Tyr Thr Phe Ile Tyr Gln Ala Leu Leu Glu Tyr Tyr			
380	385	390	
ctc tat ggg gac aca gag ctg gat gtg tcc tcc ctg gag agg cac ctg			1553
Leu Tyr Gly Asp Thr Glu Leu Asp Val Ser Ser Leu Glu Arg His Leu			
395	400	405	410
cag acg ctc cat agc aca gcc acc cat ttt gac aag atc ggg ctg gag			1601

Gln Thr Leu His Ser Thr Ala Thr His Phe Asp Lys Ile Gly Leu Glu
 415 420 425
 gaa gag ttc agg aag ctg acc aac gtg cga atc atg aag gag aac atg 1649
 Glu Glu Phe Arg Lys Leu Thr Asn Val Arg Ile Met Lys Glu Asn Met
 430 435 440
 agg acg ggc aac ctg cct gcc aac atg aag aag gcc cgc gtc atc cag 1697
 Arg Thr Gly Asn Leu Pro Ala Asn Met Lys Lys Ala Arg Val Ile Gln
 445 450 455
 atc att cca tat gac ttc aat cgg gtc atc ctg tcc atg aaa aga ggg 1745
 Ile Ile Pro Tyr Asp Phe Asn Arg Val Ile Leu Ser Met Lys Arg Gly
 460 465 470
 caa gag ttc aca gac tat atc aac gca tcc ttc ata gat ggc tac agg 1793
 Gln Glu Phe Thr Asp Tyr Ile Asn Ala Ser Phe Ile Asp Gly Tyr Arg
 475 480 485 490
 cag aag gac tac ttc atg gcc aca cag ggg cct ctg gct cac aca ggt 1841
 Gln Lys Asp Tyr Phe Met Ala Thr Gln Gly Pro Leu Ala His Thr Gly
 495 500 505
 gag gac ttc tgg agg atg gta tgg gag tgg aag tct cac aca atc gtc 1889
 Glu Asp Phe Trp Arg Met Val Trp Glu Trp Lys Ser His Thr Ile Val
 510 515 520
 atg ctg acg gag gtg cag gag cgg gaa cag gat aaa tgc tac cag tat 1937
 Met Leu Thr Glu Val Gln Glu Arg Glu Gln Asp Lys Cys Tyr Gln Tyr
 525 530 535
 tgg cca acg gag ggc tcg gtg act cat gga gat ata act ata gag ata 1985
 Trp Pro Thr Glu Gly Ser Val Thr His Gly Asp Ile Thr Ile Glu Ile
 540 545 550
 aag agc gac acc ctg tct gaa gca atc agc gta cga gac ttt ctg gtt 2033
 Lys Ser Asp Thr Leu Ser Glu Ala Ile Ser Val Arg Asp Phe Leu Val
 555 560 565 570

acc ttc aaa cag ccc ctg gcc cgc cag gaa gag cag gtc cgc atg gtg 2081
 Thr Phe Lys Gln Pro Leu Ala Arg Gln Glu Glu Gln Val Arg Met Val
 575 580 585
 aga caa ttc cat ttc cat ggc tgg cct gag gtt ggc atc ccc gct gaa 2129
 Arg Gln Phe His Phe His Gly Trp Pro Glu Val Gly Ile Pro Ala Glu
 590 595 600
 ggc aaa ggc atc att gac ctg att gca gca gtg cag aag cag cag cag 2177
 Gly Lys Gly Ile Ile Asp Leu Ile Ala Ala Val Gln Lys Gln Gln Gln
 605 610 615
 cag acg ggc aac cac ccc atc acc gtg cac tgc agc gcg gga gca ggg 2225
 Gln Thr Gly Asn His Pro Ile Thr Val His Cys Ser Ala Gly Ala Gly
 620 625 630
 cgg aca ggt aca ttc ata gca ctc agt aac att ttg gaa cga gtg aaa 2273
 Arg Thr Gly Thr Phe Ile Ala Leu Ser Asn Ile Leu Glu Arg Val Lys
 635 640 645 650
 gcc gag gga ctc cta gac gtg ttt caa gct gtg aag agc tta aga ctt 2321
 Ala Glu Gly Leu Leu Asp Val Phe Gln Ala Val Lys Ser Leu Arg Leu
 655 660 665
 cag aga cca cac atg gtg cag acc ctg gag caa tat gaa ttc tgc tac 2369
 Gln Arg Pro His Met Val Gln Thr Leu Glu Gln Tyr Glu Phe Cys Tyr
 670 675 680
 aaa gtg gta caa gat ttt atc gat ata ttt tct gat tat gct aat ttc 2417
 Lys Val Val Gln Asp Phe Ile Asp Ile Phe Ser Asp Tyr Ala Asn Phe
 685 690 695
 aaa tga agattcctgc cttaaaatat tttttaattt aatggtcagt atattttgta 2473
 Lys
 700
 aaaaaaaaaa aagagatcat gttaatttat ttcctagtgg atattaatat ccttcctaata 2533
 tcctttgtat atattttggtt atgttctaaa ggctacctgc tgtaagggtta ttaaattgta 2593

aatgcccttt ttaaaaattg gaataacatg ttaaggtcaa atactatctg gaaagatata 2653
tatttctgct aacaccagtc agtatcttag ttctattaga ttcatgttat gtgggtgtccc 2713
acatcagggtg tcacatgggtg tcacacatca tgcactgtga aatgtagttc ttaacatgtc 2773
aaatgtgttt gtgagaagac actaaccctt gaaacccctt gtggagaaac cagtagagga 2833
ctccgagtca gagcacattt actctcccca ccaactgtcg caccagggc atcggaatgt 2893
ggcaaacagt gtgcatgggg gctttggtag agtcctgggt ctccagccatg tgggtccatcc 2953
ttgcatttga aagatcagag tggaagcaga caccggcagtg catcactgca ctgctagcac 3013
gtgggaggct ggggcataag gatttgggtc aggtcaggcc aggccagctt gggctacagt 3073
gagactctgt aacacaacaa acaacaacaa cccagagggt ttgaaacc aaatccaggt 3133
ctcagatgta caagggttag atgggtgtga ctttctatg agttttaaaa ggcattcatg 3193
agaggctgtg tagtgccact gtaggcttga taaagagatg tgttatacca ggccatctat 3253
tctcacaggc ctccagtacc ctccaaacta gccatctgag ctgtgttctt ggaaccactt 3313
gctgcctgcc tgtgtgctg gctcagaatc cactcaagct cattcccaac ggcccgccca 3373
ctgacacagc tgcctgtact gaccctaatt gggcctacag gctcaaccac aggtgcacac 3433
acacacacac acacacacac acacggtaga atggccacaa actgttgac tgtcaatttg 3493
ctgatactca accacagctg cagcacacac acacacacac acacacacac acacacacac 3553
acacacacac acacacggta gaatggccac aaactgttgc actgtcaatt tgcctgatagc 3613
catttcagga tgcagattt tctttgtaaa aagttaagat ggittgtlaag aaaggaattc 3673
ttaaaaatct agatttgtac agtttttttc ttaaattgtc cactcttgg tgtttaattt 3733
ttaaaaatga gaggggggga agatccta atcaacttacc ttggaggaa aggtgtctga 3793
gacctctgag ttcagggtgc agtgacaggc gcactgcctg agagggtagg ttaggaggag 3853
ggagaggagg aggaggaatg tagaaacatt gacttcaata aaaattatct tcctatggca 3913
tttagatacc tagcaaatga gcacaatgtt aaaaaaaaaa aaaaaaagac atctggtcta 3973
actcattgta ggctttgaac acagtttggg aacttttttt ttaaactttt taaaagagaa 4033
atgaaaatac aaaggcctta tctccatgga ggactgatca tgctgccta ttgcacagtt 4093
tgttcttgtt cgtgtacaag ggacaacccc agggctctgc actgcttcat acaggtgaac 4153
gggtcaccac gcttatctca agccccgcag ctctgagtgt cccatccaga ggcacaagct 4213
ggcactcagc atgcaggatg aaagcagaca gtggccactg tcaccaccac caccagctgc 4273
aggcagggtt ggctgcctgt gctttgtggg agctccctt ctctgagcag ccttgagca 4333

caggcagaag atggaagatg gaggagcttt ccctggccag tggctcatt tgtctccatc 4393
 ttagacccaa gctcaacgcc ttgctgtaac tgaagcggga cagagggcag taagcccact 4453
 agaattaagg tgacctcaca tgggtcccaa gccaaagttc ggccacgcac cttaggcacc 4513
 caacttagtt aciggtcctt agaatcccag gcctctcttg tatcaagaaa tgccttaggg 4573
 tagatctttt caggatgtct agaaaagiat tctaattgagt gtttttcctc accttgggga 4633
 tgccccaggt tctcctgcag gcagagaccc tgcctgtttc taaacagctt gtctcattcc 4693
 agagaaaaac agaagccacg ctctctgtggg cacagttggg gcagcacttg tactttggag 4753
 gggccaatcc ctctagtctc ttgactaatg ccatagcaaa attcagcctc cgtaagacac 4813
 agagcctctg tgtacaaggg gtctcctagg gggaggaggg cggctcagc atcttctctg 4873
 tgiacctggc atgtcccttt cttcttccct caaagaagct ccggtgttta tgacaccgac 4933
 aaccttctta gtctctgtt gcatgcggtt gtgctcaacg ccaaacagtc atcagagctg 4993
 agcgttctga tcaggigcgt ctcttggta ctgtgtgact tgccttactc tctctccatg 5053
 ggctggatga acgaggaatg cacacctgtg tttccaagg tagttttatg tgtttttaaa 5113
 acctttttaa atgagcctga tacctgtgtt tcagcatttg gccacgttgt tggtttttgt 5173
 ttttcatgta tatttactga tatatttttg ttgttaacca agtcatgttt aatttatgtg 5233
 caattcttta taatatgtgt atgtgttatg gtccaactc tcatatatta ttccttgatc 5293
 acatttatcg ttgtatcttg ctctgttatg ccagtgtatg tcgtgaatt cttagacat 5353
 gtgaactgca agattgaaaa catccggatt cgagaataaa tctctgacta ccagcctgta 5413
 aaaaaaaaaa aa 5425

<210> 172

<211> 699

<212> PRT

<213> Mus musculus

<400> 172

Met Glu Pro Phe Cys Pro Leu Leu Leu Ala Ser Phe Ser Leu Ser Leu

1

5

10

15

Ala Arg Ala Gly Gln Gly Asn Asp Thr Thr Pro Thr Glu Ser Asn Trp

466/2644

Asn Ile Arg Val Cys Val Glu Asp Cys Val Val Leu Val Asp Tyr Thr
 260 265 270
 Ile Arg Lys Phe Cys Ile His Pro Gln Leu Pro Asp Ser Cys Lys Ala
 275 280 285
 Pro Arg Leu Val Ser Gln Leu His Phe Thr Ser Trp Pro Asp Phe Gly
 290 295 300
 Val Pro Phe Thr Pro Ile Gly Met Leu Lys Phe Leu Lys Lys Val Lys
 305 310 315 320
 Thr Leu Asn Pro Ser His Ala Gly Pro Ile Val Val His Cys Ser Ala
 325 330 335
 Gly Val Gly Arg Thr Gly Thr Phe Ile Val Ile Asp Ala Met Met Asp
 340 345 350
 Met Ile His Ser Glu Gln Lys Val Asp Val Phe Glu Phe Val Ser Arg
 355 360 365
 Ile Arg Asn Gln Arg Pro Gln Met Val Gln Thr Asp Val Gln Tyr Thr
 370 375 380
 Phe Ile Tyr Gln Ala Leu Leu Glu Tyr Tyr Leu Tyr Gly Asp Thr Glu
 385 390 395 400
 Leu Asp Val Ser Ser Leu Glu Arg His Leu Gln Thr Leu His Ser Thr
 405 410 415
 Ala Thr His Phe Asp Lys Ile Gly Leu Glu Glu Glu Phe Arg Lys Leu
 420 425 430
 Thr Asn Val Arg Ile Met Lys Glu Asn Met Arg Thr Gly Asn Leu Pro
 435 440 445
 Ala Asn Met Lys Lys Ala Arg Val Ile Gln Ile Ile Pro Tyr Asp Phe
 450 455 460
 Asn Arg Val Ile Leu Ser Met Lys Arg Gly Gln Glu Phe Thr Asp Tyr
 465 470 475 480
 Ile Asn Ala Ser Phe Ile Asp Gly Tyr Arg Gln Lys Asp Tyr Phe Met

	485	490	495
Ala Thr Gln Gly Pro Leu Ala His Thr Gly Glu Asp Phe Trp Arg Met			
	500	505	510
Val Trp Glu Trp Lys Ser His Thr Ile Val Met Leu Thr Glu Val Gln			
	515	520	525
Glu Arg Glu Gln Asp Lys Cys Tyr Gln Tyr Trp Pro Thr Glu Gly Ser			
	530	535	540
Val Thr His Gly Asp Ile Thr Ile Glu Ile Lys Ser Asp Thr Leu Ser			
545	550	555	560
Glu Ala Ile Ser Val Arg Asp Phe Leu Val Thr Phe Lys Gln Pro Leu			
	565	570	575
Ala Arg Gln Glu Glu Gln Val Arg Met Val Arg Gln Phe His Phe His			
	580	585	590
Gly Trp Pro Glu Val Gly Ile Pro Ala Glu Gly Lys Gly Ile Ile Asp			
	595	600	605
Leu Ile Ala Ala Val Gln Lys Gln Gln Gln Gln Thr Gly Asn His Pro			
	610	615	620
Ile Thr Val His Cys Ser Ala Gly Ala Gly Arg Thr Gly Thr Phe Ile			
625	630	635	640
Ala Leu Ser Asn Ile Leu Glu Arg Val Lys Ala Glu Gly Leu Leu Asp			
	645	650	655
Val Phe Gln Ala Val Lys Ser Leu Arg Leu Gln Arg Pro His Met Val			
	660	665	670
Gln Thr Leu Glu Gln Tyr Glu Phe Cys Tyr Lys Val Val Gln Asp Phe			
	675	680	685
Ile Asp Ile Phe Ser Asp Tyr Ala Asn Phe Lys			
	690	695	

<210> 173

<211> 215

<212> DNA

<213> Mus musculus

<400> 173

ttagacgagg caagcaggag gtgatgcgat gcttggatga atgggtagcc agatgaggtg 60
 gtggtcagag agccagactt agaagctcct cagactatgc cgaaggagcc acctggcacc 120
 caggcatcat cgcaccacat gccactcttg ttgttgatgt gtgagcttct agaacgtggg 180
 aattacactg agtatgcgct cctcctcttg agctc 215

<210> 174

<211> 952

<212> DNA

<213> Mus musculus

<400> 174

cgcggtaagc agcggcgctcc gcgggctagt agccaacatg cagctctttg tccgcgcccc 60
 ggaactacac accctcgagg tgaccggcca ggagacggtc gccagatca aagatcatgt 120
 ggcctccctg gaaggcattg cccccgaaga tcaagtcgtg ctcttggcag gctcgccgct 180
 ggaggatgag gccaccctag gccagtgttg cgtagaggcc ctgaccactc tggaagtagc 240
 aggccgcatg ctgggaggta aagttcacgg ttccctggct cgggctggaa aagttagagg 300
 tcagactccc aaggtggcca aacaggaaaa gaagaagaag aagacaggcc gggccaagag 360
 gcgaatcgag tacaaccggc gctttgtcaa tgttgtgcca ctttttgaa gaagaagggc 420
 ccaatgccaa ttcctaagtc gtattgccac catgccatgc taataaagcc actgtgtcca 480
 gaaaaaggag aaaaangagg tagggagggg gaganggaga gggagagaaa gaaattaaaa 540
 acttgggcgc gaggtttatt cctttgggtg gggttatitt cgttgccatg gcggcggtta 600
 taaatgctgg cttggaacc ccggggttac aaatttagtc gntttgagaa tccccctttg 660
 gcagttggtg ataggaagac ccggacggtt ggcgttccaa aaattcccgt tgaatgcgaa 720
 tgcgccccct tttggcgatt agcgggggnt ttgtgttagg gagctgttag atgtgaacct 780

gcgggccc ttt cgtctccttt ttcagatcgg ggggcgtgag gtgccgcctg ggagatgtaa 840
 gagggcgtgt tttggccgca aaatgggtgt gcgccgcccg agatgtcttt ctggcgggta 900
 tttcaccaca ttttgttttg gnaatacaaa aattgagcgg ggtgttcgct ga 952

<210> 175

<211> 479

<212> DNA

<213> Mus musculus

<400> 175

aattcggcac cccgctctca tctcacgcac gatgatgaag aacatcttgg gccatgcatt 60
 ctatcagctc gccgtggtct ttacactctt atttgcctga gaaaagt ttt ttgatatcga 120
 cagcgggagg aatgcgcctc tgcacgctcc cccgtcagaa cattacacca tegtgttcaa 180
 tacctttgtg ctgatgcagc tcttcaatga aataaacgcc cggaaaattc acggggaaaag 240
 aaatgtgttt gaaggaatct tcaataacgc catcttctgc accattgtcc tgggcacctt 300
 tgttggtgcag ataataattg tgcagtttgg cgggaagcct ttcagctgct cagaactttc 360
 aatagagcaa tggctgttgt cgatatctct gggaatgggg accttactct ggggccagct 420
 tatttcaacc cattccaacc agccgcttaa agtttccaaa aggtagcttg gtcatggaa 479

<210> 176

<211> 550

<212> DNA

<213> Mus musculus

<400> 176

cgggatcaag gatctcgtca tgattctgaa caggataatt cagacaacaa taccatcttc 60
 gtgcaaggcc taggcgagaa tgttacaatt gaatctgttg ctgattactt caagcagatt 120
 ggaattatta agacaaacaa gaaaactgga cagcctatga ttaatttgta cacagacagg 180
 gaaactggca agttgaaggg tgaggcaaca gtttcatttg atgaccacc ttctgctaaa 240

gcagctatcg actggtttga tggtaaagaa ttctctggga atcctattaa agtttcattt 300
gctacccgcc gagctgactt caatcggggt ggtggaaatg gtcgcggagg ccgagggcga 360
ggaggaccca tgggccgtgg aggciatgga ggaggtagga gtggtggtagg tggccgggga 420
ggattcccag tggaggtagt ggaggtaggag gacagcaacg agctggagac tggaagtgtc 480
ctaattccac atgtgagaac gigaacttct ctggagaaa tgaatgcaac cagtgtgaagg 540
cacctaagcc 550

<210> 177

<211> 492

<212> DNA

<213> Mus musculus

<400> 177

caaagcggaa ggctacaagt ggcacttcaa tgagaccgtg cttactgtgt ggtcagcgcc 60
taattactgc taccgctgtg gcaatgtggc agccatctta gaactggatg agcacctcca 120
gaaagatttc atcatcttcg aggctgcacc ccaagagaca cgtggcatcc cctccaaaaa 180
gccagtggcc gactatttcc tgtgactcct tggccccagc cctctggcc ctgggaccac 240
tgtgactgcc ctctgcccag tcggaggctg ggtctgaggg gctgcctggc ttgtcttgcc 300
ccagggtgcg gacttgctct ggagaggtag agcctggct cctggcttcc tctcctttct 360
cccacttgat ccatgaagtt ttcagtcatt tttttttct tttttcctt tttttcctt 420
cttttttctt ttgtttttg tttttagata aaacatttg agaaaaaaag aaaaaaatc 480
taataaaaga ag 492

<210> 178

<211> 456

<212> DNA

<213> Mus musculus

<400> 178

ctctcttgca ctcttcatgg cgaagaagaa gacaccccca aagaggaggc ggaacgcac 60
 gggggggagt tcaaaggga ccagtcggcc agggactccc agtgcagaag cagcaagcac 120
 ctcttctacc ctgcgggctg cagccagcaa gctggagcag gggaagcgga cgagtgcagac 180
 tccagcagcc aagcgcttc ggaatggacac gggccccag agcctgtctg ggaagtcac 240
 acccagcagc ggtgatgtcc aggtgacaga ggacgctgtg cccgctacct gacccgcaag 300
 cccatgacca caaaggacct gctgaagaag ttccagacca agaagacagg gctgagcagc 360
 gagcagacag taaatgtgt ggcgcagatc ctcaagcgcc tcaacctga gcgcaagatg 420
 attggtgata agatgcactt ctccctcaaa gagtga 456

<210> 179

<211> 2283

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (362).. (1321)

<400> 179

gtgtttgcaa aaaggga aaa gtactttgct gcctctttaa gactagggt gggagaaaaga 60
 agaggagaga gaaagaaagg agagaagttt ggagcccgag gcttaagcct ttccaaaaaac 120
 taatcacaac aatcgcgcg gcccaggag gagagtctcc ctgttttttc atcccaattg 180
 cacttcgccc gtctcgagct ccgcttcccc ccaactattc tccgccagat ctccgcgag 240
 ggccgtgcac gccgaggccc ccgcccgcgg cccctgcac ccggcccccg agcgcgggccc 300
 ccacagtccc ggccggggccg agggttggcg gccgcccggc ggccggccgc ccagcgccc 360
 c atg tat aac atg atg gag acg gag ctg aag ccg ccg ggc ccg cag caa 409

Met Tyr Asn Met Met Glu Thr Glu Leu Lys Pro Pro Gly Pro Gln Gln

1

5

10

15

gct tgc ggg ggc ggc ggc gga gga ggc aac gcc acg gcg gcg gcg acc 457

Ala Ser Gly Gly Gly Gly Gly Gly Gly Gly Asn Ala Thr Ala Ala Ala Thr	
20 25 30	
ggc ggc aac cag aag aac agc ccg gac cgc gtc aag agg ccc atg aac	505
Gly Gly Asn Gln Lys Asn Ser Pro Asp Arg Val Lys Arg Pro Met Asn	
35 40 45	
gcc ttc atg gta tgg tcc cgg ggg cag cgg cgt aag atg gcc cag gag	553
Ala Phe Met Val Trp Ser Arg Gly Gln Arg Arg Lys Met Ala Gln Glu	
50 55 60	
aac ccc aag atg cac aac tcg gag atc agc aag cgc ctg ggc gcg gag	601
Asn Pro Lys Met His Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu	
65 70 75 80	
tgg aaa ctt ttg tcc gag acc gag aag cgg ccg ttc atc gac gag gcc	649
Trp Lys Leu Leu Ser Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala	
85 90 95	
aag cgg ctg cgc gct ctg cac atg aag gag cac ccg gat tat aaa tac	697
Lys Arg Leu Arg Ala Leu His Met Lys Glu His Pro Asp Tyr Lys Tyr	
100 105 110	
cgg ccg cgg cgg aaa acc aag acg ctc atg aag aag gat aag tac acg	745
Arg Pro Arg Arg Lys Thr Lys Thr Leu Met Lys Lys Asp Lys Tyr Thr	
115 120 125	
ctt ccc gga ggc ttg ctg gcc ccc ggc ggg aac agc atg gcg agc ggg	793
Leu Pro Gly Gly Leu Leu Ala Pro Gly Gly Asn Ser Met Ala Ser Gly	
130 135 140	
gtt ggg gtg ggc gcc ggc ctg ggt ggc ggg ctg aac cag cgc atg gac	841
Val Gly Val Gly Ala Gly Leu Gly Gly Gly Leu Asn Gln Arg Met Asp	
145 150 155 160	
agc tac gcg cac atg aac ggc tgg agc aac ggc agc tac agc atg atg	889
Ser Tyr Ala His Met Asn Gly Trp Ser Asn Gly Ser Tyr Ser Met Met	
165 170 175	

cag gag cag ctg ggc tac ccg cag cac ccg ggc ctc aac gct cac ggc 937
 Gln Glu Gln Leu Gly Tyr Pro Gln His Pro Gly Leu Asn Ala His Gly
 180 185 190
 gcg gca cag atg caa ccg atg cac cgc tac gtc gtc agc gcc ctg cag 985
 Ala Ala Gln Met Gln Pro Met His Arg Tyr Val Val Ser Ala Leu Gln
 195 200 205
 tac aac tcc atg acc agc tcg cag acc tac atg aac ggc tcg ccc acc 1033
 Tyr Asn Ser Met Thr Ser Ser Gln Thr Tyr Met Asn Gly Ser Pro Thr
 210 215 220
 tac agc atg tcc tac tcg cag cag ggc acc ccc ggt atg gcg ctg ggc 1081
 Tyr Ser Met Ser Tyr Ser Gln Gln Gly Thr Pro Gly Met Ala Leu Gly
 225 230 235 240
 tcc atg ggc tct gtg gtc aag tcc gag gcc agc tcc agc ccc ccc gtg 1129
 Ser Met Gly Ser Val Val Lys Ser Glu Ala Ser Ser Ser Pro Pro Val
 245 250 255
 gtt acc tct tcc tcc cac tcc agg gcg ccc tgc cag gcc ggg gac ctc 1177
 Val Thr Ser Ser Ser His Ser Arg Ala Pro Cys Gln Ala Gly Asp Leu
 260 265 270
 cgg gac atg atc agc atg tac ctc ccc ggc gcc gag gtg ccg gag ccc 1225
 Arg Asp Met Ile Ser Met Tyr Leu Pro Gly Ala Glu Val Pro Glu Pro
 275 280 285
 gct gcg ccc agt aga ctg cac atg gcc cag cac tac cag agc ggc ccg 1273
 Ala Ala Pro Ser Arg Leu His Met Ala Gln His Tyr Gln Ser Gly Pro
 290 295 300
 gtg ccc ggc acg gcc aaa tac ggc aca ctg ccc ctg tcg cac atg tga 1321
 Val Pro Gly Thr Ala Lys Tyr Gly Thr Leu Pro Leu Ser His Met
 305 310 315 320
 gggctggact gcgaactgga gaaggggaga gattttcaaa gagatacaag agaattggga 1381
 ggggtgcaaa aagaggagag taggaaaaat ctgataatgc ycaaaaggaa aaaaaccacc 1441

aatcccatcc aaattaacgc tttttcggtg atgccgacta gaaaactttt atgagagatc 1501
tggaggaaaa aaactacgca aaactttttt ttaaagttct agtggtacgt taggcgcttc 1561
gcaggagatt cgcaaaagtc tttaccagta atatttagag ctagactccg ggcgatgaaa 1621
aaaaagtttt aatatitgca agcaactttt gtacagtatt tategagata aacatggcaa 1681
tcaaagtgtc attgtttata agctgagaat ttgccaatat ttttcgagga aagggaacaa 1741
gctgggaaaa gattctgcag ttaaatttag gaccgttaca aacaaggaag gagtttattc 1801
ggatttgaac attttagttt taaaattgta caaaaggaaa acatgagagc aagtactggc 1861
aagaccgttt tcgtggtcctt gtttaaggca aacgttctag attgtagtaa atttttaact 1921
tactgttaaa ggcaaaaaaa aaatgcccat gcaggttgat atcgttggta attataata 1981
gcttttgttc aatcctaccc tttcattttg ttcacataaa aaatatggaa ttactgtgtt 2041
tgaaatattt tcttatggtt tgaatatatt ctgtaaattg tgatatitaa aggtttttcc 2101
ccccitttat tttccgtagt tgtattttta aagattcggc tctcttattg gaatcaggct 2161
ggcgagaatc catgtatata ttgtaactaa taccatcctt ataacagcta cattttcggc 2221
ttaagttttt actccattat gcacagtttg agataaataa atttttgaaa tatggacact 2281
ga 2283

<210> 180

<211> 319

<212> PRT

<213> Mus musculus

<400> 180

Met	Tyr	Asn	Met	Met	Glu	Thr	Glu	Leu	Lys	Pro	Pro	Gly	Pro	Gln	Gln
1				5					10					15	
Ala	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Asn	Ala	Thr	Ala	Ala	Ala	Thr
			20						25					30	
Gly	Gly	Asn	Gln	Lys	Asn	Ser	Pro	Asp	Arg	Val	Lys	Arg	Pro	Met	Asn
			35						40					45	
Ala	Phe	Met	Val	Trp	Ser	Arg	Gly	Gln	Arg	Arg	Lys	Met	Ala	Gln	Glu

50	55	60
Asn Pro Lys Met His Asn Ser Glu Ile Ser Lys Arg Leu Gly Ala Glu		
65	70	75
Trp Lys Leu Leu Ser Glu Thr Glu Lys Arg Pro Phe Ile Asp Glu Ala		
85	90	95
Lys Arg Leu Arg Ala Leu His Met Lys Glu His Pro Asp Tyr Lys Tyr		
100	105	110
Arg Pro Arg Arg Lys Thr Lys Thr Leu Met Lys Lys Asp Lys Tyr Thr		
115	120	125
Leu Pro Gly Gly Leu Leu Ala Pro Gly Gly Asn Ser Met Ala Ser Gly		
130	135	140
Val Gly Val Gly Ala Gly Leu Gly Gly Gly Leu Asn Gln Arg Met Asp		
145	150	155
Ser Tyr Ala His Met Asn Gly Trp Ser Asn Gly Ser Tyr Ser Met Met		
165	170	175
Gln Glu Gln Leu Gly Tyr Pro Gln His Pro Gly Leu Asn Ala His Gly		
180	185	190
Ala Ala Gln Met Gln Pro Met His Arg Tyr Val Val Ser Ala Leu Gln		
195	200	205
Tyr Asn Ser Met Thr Ser Ser Gln Thr Tyr Met Asn Gly Ser Pro Thr		
210	215	220
Tyr Ser Met Ser Tyr Ser Gln Gln Gly Thr Pro Gly Met Ala Leu Gly		
225	230	235
Ser Met Gly Ser Val Val Lys Ser Glu Ala Ser Ser Ser Pro Pro Val		
245	250	255
Val Thr Ser Ser Ser His Ser Arg Ala Pro Cys Gln Ala Gly Asp Leu		
260	265	270
Arg Asp Met Ile Ser Met Tyr Leu Pro Gly Ala Glu Val Pro Glu Pro		
275	280	285

Ala Ala Pro Ser Arg Leu His Met Ala Gln His Tyr Gln Ser Gly Pro

290

295

300

Val Pro Gly Thr Ala Lys Tyr Gly Thr Leu Pro Leu Ser His Met

305

310

315

<210> 181

<211> 1387

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (118).. (1266)

<400> 181

cccggggcccg gccgcccgtcg cgggaccccg tgcccggccg ccgtcgccac cgccgccccg 60

gccgaccgag ggaccggccc gccgcggct gctccggacc tagaggatca agtcata 117

atg gga gca ttt tta gac aag cca aag atg gag aag cat aat gcc cag 165

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

1

5

10

15

ggg cag ggg aat ggg tta cga tac ggc cta agc agc atg caa ggt tgg 213

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20

25

30

cga gtt gaa atg gag gac gca cac acg gct gtg atc ggt ttg cca agt 261

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35

40

45

gga ctt gag aca tgg tca ttc ttt gct gta tat gat ggg cat gct ggt 309

Gly Leu Glu Thr Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50

55

60

478/2644

210	215	220	
gaa agg tct gaa gaa gat gac cag ttc atc atc ctt gca tgc gat ggc 837			
Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly			
225	230	235	240
atc tgg gac gtc atg ggg aac gaa gag ctc tgt gac ttt gtg aga tcc 885			
Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser			
245	250	255	
aga ctt gaa gtc act gat gac ctt gag aaa gtt tgc aat gaa gta gtc 933			
Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val			
260	265	270	
gac acc tgc ttg tat aag gga agt cga gac aac atg agt gtg att ttg 981			
Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu			
275	280	285	
atc tgt ttt cca agt gca ccc aaa gtc tcg gca gag gcg gtg aag aag 1029			
Ile Cys Phe Pro Ser Ala Pro Lys Val Ser Ala Glu Ala Val Lys Lys			
290	295	300	
gag gcg gag ctg gac aag tac ctg gag agc aga gta gaa gaa atc ata 1077			
Glu Ala Glu Leu Asp Lys Tyr Leu Glu Ser Arg Val Glu Glu Ile Ile			
305	310	315	320
aag aag cag gtg gaa ggc gtc cct gac tta gtc cac gtg atg cgc acg 1125			
Lys Lys Gln Val Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr			
325	330	335	
tta gcc agt gag aac atc ccc agc ctc cca cca ggg ggt gaa ttg gca 1173			
Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala			
340	345	350	
agc aag cgg aat gta att gaa gcc gtt tac aat aga ctg aac cct tac 1221			
Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr			
355	360	365	
aaa aat gac gac act gat tct gcg tca acc gat gat atg tgg taa 1266			

Lys Asn Asp Asp Thr Asp Ser Ala Ser Thr Asp Asp Met Trp

370

375

380

agccgc tcac ccagccgtgg actcaccttc gcctgcaaag gggaagccag ctcaccccttg 1326

ccgagcccttt accatccatc accgacttca caggagggtc tgacacgggt gaggactgca 1386

g

1387

<210> 182

<211> 382

<212> PRT

<213> Mus musculus

<400> 182

Met Gly Ala Phe Leu Asp Lys Pro Lys Met Glu Lys His Asn Ala Gln

1

5

10

15

Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu Ser Ser Met Gln Gly Trp

20

25

30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35

40

45

Gly Leu Glu Thr Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50

55

60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65

70

75

80

Asn Asn Gln Asp Phe Arg Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85

90

95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100

105

110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115

120

125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys

130	135	140
Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe		
145	150	155
Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln		
	165	170
Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala		
	180	185
Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys		
	195	200
Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile		
	210	215
Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly		
225	230	235
Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser		
	245	250
Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val		
	260	265
Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu		
	275	280
Ile Cys Phe Pro Ser Ala Pro Lys Val Ser Ala Glu Ala Val Lys Lys		
	290	295
Glu Ala Glu Leu Asp Lys Tyr Leu Glu Ser Arg Val Glu Glu Ile Ile		
305	310	315
Lys Lys Gln Val Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr		
	325	330
Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala		
	340	345
Ser Lys Arg Asn Val Ile Glu Ala Val Tyr Asn Arg Leu Asn Pro Tyr		
	355	360
		365

Lys Asn Asp Asp Thr Asp Ser Ala Ser Thr Asp Asp Met Trp

370

375

380

<210> 183

<211> 1454

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (282).. (1385)

<400> 183

ttacaaaagc ttttctttgc ttcacgtagt tcctggtttc ttcaaacaatg aactcacagg 60
cagaaatcgc caactcagca attaagagcc tticctgtgg aagctcttgc atgaggtagt 120
agaagccttt attctcttct ccaagtaagg cattagctgg caatcggaca tcttcaaaga 180
atagttgtgc tgigtctga gctttcattc ccatcttatg cagcttccgg gccttgataa 240
atcctttcat tccgttttcc accaaaaaga gactgtttgc c atg gag gcg aac ggg 296

Met Glu Ala Asn Gly

1

5

ttc gga ctc cag aat ttc ccg gag ctg aag aat gac acg ttc ctg aga 344

Phe Gly Leu Gln Asn Phe Pro Glu Leu Lys Asn Asp Thr Phe Leu Arg

10

15

20

gca gcc tgg gga gag gaa aca gac tat act ccc gtt tgg tgc atg aga 392

Ala Ala Trp Gly Glu Glu Thr Asp Tyr Thr Pro Val Trp Cys Met Arg

25

30

35

cag gca ggc cgc tac tta cca gag itt agg gaa acc agg gct gcc cag 440

Gln Ala Gly Arg Tyr Leu Pro Glu Phe Arg Glu Thr Arg Ala Ala Gln

40

45

50

gac ttc ttc agc acc tgc cga tct ccc gag gct tgc tgt gaa ctg act 488
 Asp Phe Phe Ser Thr Cys Arg Ser Pro Glu Ala Cys Cys Glu Leu Thr
 55 60 65
 cta cag cca cta cga agg ttt cct ctg gat gct gcc ata att ttc tct 536
 Leu Gln Pro Leu Arg Arg Phe Pro Leu Asp Ala Ala Ile Ile Phe Ser
 70 75 80 85
 gac atc ctt gtt gta ccc cag gca ttg ggc ata gag gtg acc atg gta 584
 Asp Ile Leu Val Val Pro Gln Ala Leu Gly Ile Glu Val Thr Met Val
 90 95 100
 cct ggc aaa gga ccc agc ttt cca gag cca tta aga gaa gag cgg gac 632
 Pro Gly Lys Gly Pro Ser Phe Pro Glu Pro Leu Arg Glu Glu Arg Asp
 105 110 115
 tta gag cgt cta cgg gat cca gca gca gcg gct tca gag tta ggc tat 680
 Leu Glu Arg Leu Arg Asp Pro Ala Ala Ala Ala Ser Glu Leu Gly Tyr
 120 125 130
 gtg ttc caa gcc atc acc ctt act cga caa cgg ctg gcc gga cgt gtg 728
 Val Phe Gln Ala Ile Thr Leu Thr Arg Gln Arg Leu Ala Gly Arg Val
 135 140 145
 cca cta att ggc ttt gct ggt gct ccg tgg acc cta atg aca tac atg 776
 Pro Leu Ile Gly Phe Ala Gly Ala Pro Trp Thr Leu Met Thr Tyr Met
 150 155 160 165
 gtt gaa ggc ggc agt tca agc acc atg gct cag gcc aaa cga tgg ctc 824
 Val Glu Gly Gly Ser Ser Ser Thr Met Ala Gln Ala Lys Arg Trp Leu
 170 175 180
 tac caa agg cca cag gcc agt cac aag ctg ctt ggc ata ctc act gat 872
 Tyr Gln Arg Pro Gln Ala Ser His Lys Leu Leu Gly Ile Leu Thr Asp
 185 190 195
 gtt ctg gtc cca tac cta ata gga caa gtg gct gct ggt gct cag gca 920
 Val Leu Val Pro Tyr Leu Ile Gly Gln Val Ala Ala Gly Ala Gln Ala

200	205	210	
ttg cag ctc ttt gag tcc cac gca gga cat ctt ggc acc gag ctc ttc			968
Leu Gln Leu Phe Glu Ser His Ala Gly His Leu Gly Thr Glu Leu Phe			
215	220	225	
agc aag ttt gca ctg ccc tac att cgt gat gtg gcc aag cga gtg aag			1016
Ser Lys Phe Ala Leu Pro Tyr Ile Arg Asp Val Ala Lys Arg Val Lys			
230	235	240	245
gct ggg ttg cag aag gca ggc ctg gca cca gtg ccc atg atc atc ttt			1064
Ala Gly Leu Gln Lys Ala Gly Leu Ala Pro Val Pro Met Ile Ile Phe			
250	255	260	
gct aag gat gga cat ttt gcc ctg gaa gag ctg gcc cag gct ggc tat			1112
Ala Lys Asp Gly His Phe Ala Leu Glu Glu Leu Ala Gln Ala Gly Tyr			
265	270	275	
gag gta gtt gga ctt gac tgg aca gtg gct cca aag aaa gcc cgg gaa			1160
Glu Val Val Gly Leu Asp Trp Thr Val Ala Pro Lys Lys Ala Arg Glu			
280	285	290	
cgt gtc ggg aag gca gtg acc ctg cag ggg aac ctg gat ccc tgt gcc			1208
Arg Val Gly Lys Ala Val Thr Leu Gln Gly Asn Leu Asp Pro Cys Ala			
295	300	305	
ttg tat gca tct gag gaa gag atc ggt cgg ctg gtg cag caa atg ctg			1256
Leu Tyr Ala Ser Glu Glu Glu Ile Gly Arg Leu Val Gln Gln Met Leu			
310	315	320	325
gat gac ttt ggg cct caa cgc tca att gcc aac cta ggg cat ggg ctt			1304
Asp Asp Phe Gly Pro Gln Arg Ser Ile Ala Asn Leu Gly His Gly Leu			
330	335	340	
tac cct gac atg gac cca gaa cgt gta gga gcc ttt gtg gat gct gta			1352
Tyr Pro Asp Met Asp Pro Glu Arg Val Gly Ala Phe Val Asp Ala Val			
345	350	355	
cac aaa cat tca cgc ctg ctt cga cag aat tga gtacatgcct ttctgctcaa			1405

His Lys His Ser Arg Leu Leu Arg Gln Asn

360

365

gtgccaccaa cagagattgt ttccaggaga ataaaacttc cagagttgg

1454

<210> 184

<211> 367

<212> PRT

<213> Mus musculus

<400> 184

Met Glu Ala Asn Gly Phe Gly Leu Gln Asn Phe Pro Glu Leu Lys Asn

1

5

10

15

Asp Thr Phe Leu Arg Ala Ala Trp Gly Glu Glu Thr Asp Tyr Thr Pro

20

25

30

Val Trp Cys Met Arg Gln Ala Gly Arg Tyr Leu Pro Glu Phe Arg Glu

35

40

45

Thr Arg Ala Ala Gln Asp Phe Phe Ser Thr Cys Arg Ser Pro Glu Ala

50

55

60

Cys Cys Glu Leu Thr Leu Gln Pro Leu Arg Arg Phe Pro Leu Asp Ala

65

70

75

80

Ala Ile Ile Phe Ser Asp Ile Leu Val Val Pro Gln Ala Leu Gly Ile

85

90

95

Glu Val Thr Met Val Pro Gly Lys Gly Pro Ser Phe Pro Glu Pro Leu

100

105

110

Arg Glu Glu Arg Asp Leu Glu Arg Leu Arg Asp Pro Ala Ala Ala Ala

115

120

125

Ser Glu Leu Gly Tyr Val Phe Gln Ala Ile Thr Leu Thr Arg Gln Arg

130

135

140

Leu Ala Gly Arg Val Pro Leu Ile Gly Phe Ala Gly Ala Pro Trp Thr

145	150	155	160
Leu Met Thr Tyr Met Val Glu Gly Gly Ser Ser Ser Thr Met Ala Gln			
	165	170	175
Ala Lys Arg Trp Leu Tyr Gln Arg Pro Gln Ala Ser His Lys Leu Leu			
	180	185	190
Gly Ile Leu Thr Asp Val Leu Val Pro Tyr Leu Ile Gly Gln Val Ala			
	195	200	205
Ala Gly Ala Gln Ala Leu Gln Leu Phe Glu Ser His Ala Gly His Leu			
	210	215	220
Gly Thr Glu Leu Phe Ser Lys Phe Ala Leu Pro Tyr Ile Arg Asp Val			
	225	230	235
Ala Lys Arg Val Lys Ala Gly Leu Gln Lys Ala Gly Leu Ala Pro Val			
	245	250	255
Pro Met Ile Ile Phe Ala Lys Asp Gly His Phe Ala Leu Glu Glu Leu			
	260	265	270
Ala Gln Ala Gly Tyr Glu Val Val Gly Leu Asp Trp Thr Val Ala Pro			
	275	280	285
Lys Lys Ala Arg Glu Arg Val Gly Lys Ala Val Thr Leu Gln Gly Asn			
	290	295	300
Leu Asp Pro Cys Ala Leu Tyr Ala Ser Glu Glu Glu Ile Gly Arg Leu			
	305	310	315
Val Gln Gln Met Leu Asp Asp Phe Gly Pro Gln Arg Ser Ile Ala Asn			
	325	330	335
Leu Gly His Gly Leu Tyr Pro Asp Met Asp Pro Glu Arg Val Gly Ala			
	340	345	350
Phe Val Asp Ala Val His Lys His Ser Arg Leu Leu Arg Gln Asn			
	355	360	365

<210> 185

<211> 1958

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (204).. (1532)

<400> 185

cagcgggigg cgtgcgcca agtccccac tggcgcgcaa acttaactta ctgttaaggc 60
 gcgggtagag gcaaccgggc tagtigit ttagaggctt ggctggggta gctgacttaa 120
 gtgtcctgtc ttactcccc agttgggtc cagactgaaa acagcagagc ggctaccaga 180
 ctctcacagg agcaagctgt aac atg caa tcg ccc gca agc cgg tgc gga cgc 233

Met Gln Ser Pro Ala Ser Arg Cys Gly Arg

1

5

10

gcc ttg gtg gcg ctg ctg ctg gcc tgt ggc ttc ttg ggg gta tgg gga 281
 Ala Leu Val Ala Leu Leu Leu Ala Cys Gly Phe Leu Gly Val Trp Gly

15

20

25

gag aaa aga gga ttc cca cct gcc caa gcc acg ctg tca ctt ctc ggg 329
 Glu Lys Arg Gly Phe Pro Pro Ala Gln Ala Thr Leu Ser Leu Leu Gly

30

35

40

act aaa gag gta atg acg cca ccc act aag acc tcc tgg acc aga ggt 377
 Thr Lys Glu Val Met Thr Pro Pro Thr Lys Thr Ser Trp Thr Arg Gly

45

50

55

tcc aac tcc agt ctg atg cgt tcc tcc gca cct gcg gag gtg acc aaa 425
 Ser Asn Ser Ser Leu Met Arg Ser Ser Ala Pro Ala Glu Val Thr Lys

60

65

70

gga ggg agg ggg gct gga gtc ccg cca aga tcc ttc cct cct ccg tgc 473
 Gly Gly Arg Gly Ala Gly Val Pro Pro Arg Ser Phe Pro Pro Pro Cys

75	80	85	90	
caa cga aat att gag atc agc aag act ttt aaa tac atc aac acg att	521			
Gln Arg Asn Ile Glu Ile Ser Lys Thr Phe Lys Tyr Ile Asn Thr Ile				
95	100	105		
gtg tcg tgc ctc gtg ttc gtg cta ggc atc atc ggg aac tcc acg ctg	569			
Val Ser Cys Leu Val Phe Val Leu Gly Ile Ile Gly Asn Ser Thr Leu				
110	115	120		
cta aga atc atc tac aag aac aag tgc atg cgc aat ggt ccc aat atc	617			
Leu Arg Ile Ile Tyr Lys Asn Lys Cys Met Arg Asn Gly Pro Asn Ile				
125	130	135		
ttg atc gcc agt ctg gct ctg gga gac cta ctg cac atc atc ata gac	665			
Leu Ile Ala Ser Leu Ala Leu Gly Asp Leu Leu His Ile Ile Ile Asp				
140	145	150		
ata ccc att aac acc tac aag ttg ctc gca gag gac tgg cca ttt gga	713			
Ile Pro Ile Asn Thr Tyr Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly				
155	160	165	170	
gct gag atg tgt aag ctg gtg ccc ttc ata cag aag gct tct gtg gga	761			
Ala Glu Met Cys Lys Leu Val Pro Phe Ile Gln Lys Ala Ser Val Gly				
175	180	185		
atc aca gtg ctg agt ctt tgt gct cta agt att gac aga tat cga gct	809			
Ile Thr Val Leu Ser Leu Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala				
190	195	200		
gtt gct tct tgg agt cga att aaa gga att ggg gtt cca aaa tgg aca	857			
Val Ala Ser Trp Ser Arg Ile Lys Gly Ile Gly Val Pro Lys Trp Thr				
205	210	215		
gca gta gaa att gtt tta att tgg gtg gtc tct gtg gtt ctg gct gtc	905			
Ala Val Glu Ile Val Leu Ile Trp Val Val Ser Val Val Leu Ala Val				
220	225	230		
ccc gaa gcc ata ggt ttt gat atg att acg tcg gac tac aaa gga aag	953			

Pro Glu Ala Ile Gly Phe Asp Met Ile Thr Ser Asp Tyr Lys Gly Lys
 235 240 245 250
 ccc cta agg gtc tgc atg ctt aat ccc ttt cag aaa aca gcc ttc atg 1001
 Pro Leu Arg Val Cys Met Leu Asn Pro Phe Gln Lys Thr Ala Phe Met
 255 260 265
 cag ttt tac aag aca gcc aaa gat tgg tgg ctg ttc agt ttc tac ttc 1049
 Gln Phe Tyr Lys Thr Ala Lys Asp Trp Trp Leu Phe Ser Phe Tyr Phe
 270 275 280
 tgc ttg ccg cta gcc atc act gca gtc ttt tat acc ctg atg acc tgc 1097
 Cys Leu Pro Leu Ala Ile Thr Ala Val Phe Tyr Thr Leu Met Thr Cys
 285 290 295
 gaa atg ctc agg aag aag agc ggt atg cag att gct ttg aat gat cac 1145
 Glu Met Leu Arg Lys Lys Ser Gly Met Gln Ile Ala Leu Asn Asp His
 300 305 310
 tta aag cag aga cga gaa gtg gcc aag aca gtc ttc tgc ctg gtc ctc 1193
 Leu Lys Gln Arg Arg Glu Val Ala Lys Thr Val Phe Cys Leu Val Leu
 315 320 325 330
 gtg ttt gct ctc tgt tgg ctt ccc ctt cac ctc agc cgg atc ctg aag 1241
 Val Phe Ala Leu Cys Trp Leu Pro Leu His Leu Ser Arg Ile Leu Lys
 335 340 345
 ctc acc ctg tat gac cag agc aat cca cac agg tgt gag ctt ctg agc 1289
 Leu Thr Leu Tyr Asp Gln Ser Asn Pro His Arg Cys Glu Leu Leu Ser
 350 355 360
 ttt ttg ttg gtt ttg gac tac att ggt atc aac atg gct tct ttg aac 1337
 Phe Leu Leu Val Leu Asp Tyr Ile Gly Ile Asn Met Ala Ser Leu Asn
 365 370 375
 tcc tgc atc aat cca atc gct ctg tat ttg gtg agc aaa aga ttc aaa 1385
 Ser Cys Ile Asn Pro Ile Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys
 380 385 390

aac tgc ttt aag tca tgt ttg tgc tgc tgg tgc caa acg ttt gag gaa 1433
 Asn Cys Phe Lys Ser Cys Leu Cys Cys Trp Cys Gln Thr Phe Glu Glu
 395 400 405 410
 aag cag tcc ttg gag gag aag cag tcc tgc ctg aag ttc aaa gcc aac 1481
 Lys Gln Ser Leu Glu Glu Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn
 415 420 425
 gat cac gga tat gac aac ttc cgg tcc agc aat aaa tac agc tcg tct 1529
 Asp His Gly Tyr Asp Asn Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser
 430 435 440
 tga aggcaagaac actcgccgaa tctcactgtc ctcatgttg acagatacca 1582
 ttaaaacaaa atgaaaccgt tgccaaatca aaatggaaaa aaccatgcta gcagaaaggt 1642
 gtgcgcgcgt gtgagagga ttatitttaa ctgttctgac gctcaacacc ggatatattc 1702
 acgggctgitt tacaacctaa gaaagctgtg ggaaggaatg aagccctcct ccgtggggaa 1762
 gcacttagat tcttagtcag cacttcagca gagctcttaa aagccccctag tgcgttcaca 1822
 tgccacttac gtttaaaaaa acgagaacit cactgaagtt ctgttcagga gtttattatc 1882
 cagtcctatg aatctggatt caagaaagca tgacatigca aaacaattct taaaaaaaaa 1942
 agcgcccgca gaattc 1958

<210> 186

<211> 442

<212> PRT

<213> Mus musculus

<400> 186

Met Gln Ser Pro Ala Ser Arg Cys Gly Arg Ala Leu Val Ala Leu Leu
 1 5 10 15
 Leu Ala Cys Gly Phe Leu Gly Val Trp Gly Glu Lys Arg Gly Phe Pro
 20 25 30
 Pro Ala Gln Ala Thr Leu Ser Leu Leu Gly Thr Lys Glu Val Met Thr

35	40	45
Pro Pro Thr Lys Thr Ser Trp Thr Arg Gly Ser Asn Ser Ser Leu Met		
50	55	60
Arg Ser Ser Ala Pro Ala Glu Val Thr Lys Gly Gly Arg Gly Ala Gly		
65	70	75
Val Pro Pro Arg Ser Phe Pro Pro Pro Cys Gln Arg Asn Ile Glu Ile		
85	90	95
Ser Lys Thr Phe Lys Tyr Ile Asn Thr Ile Val Ser Cys Leu Val Phe		
100	105	110
Val Leu Gly Ile Ile Gly Asn Ser Thr Leu Leu Arg Ile Ile Tyr Lys		
115	120	125
Asn Lys Cys Met Arg Asn Gly Pro Asn Ile Leu Ile Ala Ser Leu Ala		
130	135	140
Leu Gly Asp Leu Leu His Ile Ile Ile Asp Ile Pro Ile Asn Thr Tyr		
145	150	155
Lys Leu Leu Ala Glu Asp Trp Pro Phe Gly Ala Glu Met Cys Lys Leu		
165	170	175
Val Pro Phe Ile Gln Lys Ala Ser Val Gly Ile Thr Val Leu Ser Leu		
180	185	190
Cys Ala Leu Ser Ile Asp Arg Tyr Arg Ala Val Ala Ser Trp Ser Arg		
195	200	205
Ile Lys Gly Ile Gly Val Pro Lys Trp Thr Ala Val Glu Ile Val Leu		
210	215	220
Ile Trp Val Val Ser Val Val Leu Ala Val Pro Glu Ala Ile Gly Phe		
225	230	235
Asp Met Ile Thr Ser Asp Tyr Lys Gly Lys Pro Leu Arg Val Cys Met		
245	250	255
Leu Asn Pro Phe Gln Lys Thr Ala Phe Met Gln Phe Tyr Lys Thr Ala		
260	265	270

Lys Asp Trp Trp Leu Phe Ser Phe Tyr Phe Cys Leu Pro Leu Ala Ile
 275 280 285
 Thr Ala Val Phe Tyr Thr Leu Met Thr Cys Glu Met Leu Arg Lys Lys
 290 295 300
 Ser Gly Met Gln Ile Ala Leu Asn Asp His Leu Lys Gln Arg Arg Glu
 305 310 315 320
 Val Ala Lys Thr Val Phe Cys Leu Val Leu Val Phe Ala Leu Cys Trp
 325 330 335
 Leu Pro Leu His Leu Ser Arg Ile Leu Lys Leu Thr Leu Tyr Asp Gln
 340 345 350
 Ser Asn Pro His Arg Cys Glu Leu Leu Ser Phe Leu Leu Val Leu Asp
 355 360 365
 Tyr Ile Gly Ile Asn Met Ala Ser Leu Asn Ser Cys Ile Asn Pro Ile
 370 375 380
 Ala Leu Tyr Leu Val Ser Lys Arg Phe Lys Asn Cys Phe Lys Ser Cys
 385 390 395 400
 Leu Cys Cys Trp Cys Gln Thr Phe Glu Glu Lys Gln Ser Leu Glu Glu
 405 410 415
 Lys Gln Ser Cys Leu Lys Phe Lys Ala Asn Asp His Gly Tyr Asp Asn
 420 425 430
 Phe Arg Ser Ser Asn Lys Tyr Ser Ser Ser
 435 440

<210> 187

<211> 1114

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (9).. (1040)

<400> 187

```

ctgcgagc atg gct gca gcc gcc cct ggt cct gtg gag ttg ggc ttc gcc 50
      Met Ala Ala Ala Ala Pro Gly Pro Val Glu Leu Gly Phe Ala
              1              5              10

gag gag gca ccg gcc tgg agg ctg cgc agc gag cag ttt ccc agc aaa 98
Glu Glu Ala Pro Ala Trp Arg Leu Arg Ser Glu Gln Phe Pro Ser Lys
      15              20              25              30

gtg ggc ggg cgg ccc gcg tgg ttg ggc ttg gcg gag ctg ccg ggg ccc 146
Val Gly Gly Arg Pro Ala Trp Leu Gly Leu Ala Glu Leu Pro Gly Pro
              35              40              45

ggg gcg ctg gcg tgt gcg cgc tgc ggc cgc ccg ctc gcc ttc ctg ctg 194
Gly Ala Leu Ala Cys Ala Arg Cys Gly Arg Pro Leu Ala Phe Leu Leu
              50              55              60

cag gtg tac gca ccg ctg ccg ggc cgg gac gac gcc ttc cac cgc agc 242
Gln Val Tyr Ala Pro Leu Pro Gly Arg Asp Asp Ala Phe His Arg Ser
              65              70              75

ctc ttt ctc ttc tgc tgt cgc gag ccg ctg tgt tgc gcc ggc ctg cga 290
Leu Phe Leu Phe Cys Cys Arg Glu Pro Leu Cys Cys Ala Gly Leu Arg
              80              85              90

gtt ttt cgt aat cag cta cca agg aac aac gca ttc tac tcc tat gag 338
Val Phe Arg Asn Gln Leu Pro Arg Asn Asn Ala Phe Tyr Ser Tyr Glu
      95              100              105              110

ccc cct tct gaa aca gaa gct ttg ggt acg gaa tgt gtg tgc ctc cag 386
Pro Pro Ser Glu Thr Glu Ala Leu Gly Thr Glu Cys Val Cys Leu Gln
              115              120              125

ctc aag tct gga gcc cat ctc tgt cgg gtt tgt ggt tgc ttg gcc cct 434

```

Leu Lys Ser Gly Ala His Leu Cys Arg Val Cys Gly Cys Leu Ala Pro
 130 135 140
 atg aca tgc tct agg tgc aaa cag gca cat tac tgc agc aag gag cat 482
 Met Thr Cys Ser Arg Cys Lys Gln Ala His Tyr Cys Ser Lys Glu His
 145 150 155
 cag aca tta gac tgg cgg ctg gga cac aag cag gct tgt aca cag tca 530
 Gln Thr Leu Asp Trp Arg Leu Gly His Lys Gln Ala Cys Thr Gln Ser
 160 165 170
 gac aaa ata gac cat atg gtt cca gac cac aac ttc ctg ttt cca gaa 578
 Asp Lys Ile Asp His Met Val Pro Asp His Asn Phe Leu Phe Pro Glu
 175 180 185 190
 ttt gaa att gta aca gaa aca gaa gat gaa att ttg cct gag gtt gtg 626
 Phe Glu Ile Val Thr Glu Thr Glu Asp Glu Ile Leu Pro Glu Val Val
 195 200 205
 gaa atg gag gat tat tct gaa gtt aca gga agc atg ggg gga att cct 674
 Glu Met Glu Asp Tyr Ser Glu Val Thr Gly Ser Met Gly Gly Ile Pro
 210 215 220
 gag gaa gaa cta gat tcc atg gca aag cac gaa tcc aag gaa gat cac 722
 Glu Glu Glu Leu Asp Ser Met Ala Lys His Glu Ser Lys Glu Asp His
 225 230 235
 ata ttc caa aag ttt aaa tct aaa ata ccc ctt gaa cca gag cag att 770
 Ile Phe Gln Lys Phe Lys Ser Lys Ile Pro Leu Glu Pro Glu Gln Ile
 240 245 250
 ctc agg tat gga aga ggg att aaa ccc atc tgg att tct ggt gaa aat 818
 Leu Arg Tyr Gly Arg Gly Ile Lys Pro Ile Trp Ile Ser Gly Glu Asn
 255 260 265 270
 att cct caa gaa aaa gat att cca gat tgc ccg tgt ggt gcc aag aga 866
 Ile Pro Gln Glu Lys Asp Ile Pro Asp Cys Pro Cys Gly Ala Lys Arg
 275 280 285

ata ttt gaa ttc cag gtc atg cct cag ctg ttg aac cac ctg aag gca 914
 Ile Phe Glu Phe Gln Val Met Pro Gln Leu Leu Asn His Leu Lys Ala
 290 295 300
 gac aga ctc ggc aga agc atc gac tgg ggt gtc ttg gct gtc ttc acc 962
 Asp Arg Leu Gly Arg Ser Ile Asp Trp Gly Val Leu Ala Val Phe Thr
 305 310 315
 tgt gct gag agc tgt agc ctg ggt agc ggc tac aca gaa gaa ttt gtg 1010
 Cys Ala Glu Ser Cys Ser Leu Gly Ser Gly Tyr Thr Glu Glu Phe Val
 320 325 330
 tgg aag cag gat gtg aca gat aca cct taa aaggggttaa attcttgcaa 1060
 Trp Lys Gln Asp Val Thr Asp Thr Pro
 335 340
 aagatatataa ataaaaactt aaataaaaaac taaaaacccc tgacgtagct cgag 1114

<210> 188

<211> 343

<212> PRT

<213> Mus musculus

<400> 188

Met Ala Ala Ala Ala Pro Gly Pro Val Glu Leu Gly Phe Ala Glu Glu
 1 5 10 15
 Ala Pro Ala Trp Arg Leu Arg Ser Glu Gln Phe Pro Ser Lys Val Gly
 20 25 30
 Gly Arg Pro Ala Trp Leu Gly Leu Ala Glu Leu Pro Gly Pro Gly Ala
 35 40 45
 Leu Ala Cys Ala Arg Cys Gly Arg Pro Leu Ala Phe Leu Leu Gln Val
 50 55 60
 Tyr Ala Pro Leu Pro Gly Arg Asp Asp Ala Phe His Arg Ser Leu Phe

65	70	75	80
Leu Phe Cys Cys Arg Glu Pro Leu Cys Cys Ala Gly Leu Arg Val Phe			
	85	90	95
Arg Asn Gln Leu Pro Arg Asn Asn Ala Phe Tyr Ser Tyr Glu Pro Pro			
	100	105	110
Ser Glu Thr Glu Ala Leu Gly Thr Glu Cys Val Cys Leu Gln Leu Lys			
	115	120	125
Ser Gly Ala His Leu Cys Arg Val Cys Gly Cys Leu Ala Pro Met Thr			
	130	135	140
Cys Ser Arg Cys Lys Gln Ala His Tyr Cys Ser Lys Glu His Gln Thr			
145	150	155	160
Leu Asp Trp Arg Leu Gly His Lys Gln Ala Cys Thr Gln Ser Asp Lys			
	165	170	175
Ile Asp His Met Val Pro Asp His Asn Phe Leu Phe Pro Glu Phe Glu			
	180	185	190
Ile Val Thr Glu Thr Glu Asp Glu Ile Leu Pro Glu Val Val Glu Met			
	195	200	205
Glu Asp Tyr Ser Glu Val Thr Gly Ser Met Gly Gly Ile Pro Glu Glu			
	210	215	220
Glu Leu Asp Ser Met Ala Lys His Glu Ser Lys Glu Asp His Ile Phe			
225	230	235	240
Gln Lys Phe Lys Ser Lys Ile Pro Leu Glu Pro Glu Gln Ile Leu Arg			
	245	250	255
Tyr Gly Arg Gly Ile Lys Pro Ile Trp Ile Ser Gly Glu Asn Ile Pro			
	260	265	270
Gln Glu Lys Asp Ile Pro Asp Cys Pro Cys Gly Ala Lys Arg Ile Phe			
	275	280	285
Glu Phe Gln Val Met Pro Gln Leu Leu Asn His Leu Lys Ala Asp Arg			
	290	295	300

Leu Gly Arg Ser Ile Asp Trp Gly Val Leu Ala Val Phe Thr Cys Ala
 305 310 315 320
 Glu Ser Cys Ser Leu Gly Ser Gly Tyr Thr Glu Glu Phe Val Trp Lys
 325 330 335
 Gln Asp Val Thr Asp Thr Pro
 340

<210> 189

<211> 866

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (165).. (743)

<400> 189

ggcacagctg gacctgggtg gggttctctg tggttccatg ctttctggac tctgcctgc 60
 tggctggagc tgctgacagg cctgacatct tctgcaacct ccagcatcag gacaaagaaa 120
 gccgcctcaa accttccaaa tcacttccctc tiggcccagg aaca atg gct gcc atg 176
 Met Ala Ala Met

1

tca gaa gac tct tgc gtc aac ttc aag gaa atg atg ttt att gac aac 224
 Ser Glu Asp Ser Cys Val Asn Phe Lys Glu Met Met Phe Ile Asp Asn
 5 10 15 20
 acg ctt tac ttt ata cct gaa gaa aat gga gac ctg gaa tca gac aac 272
 Thr Leu Tyr Phe Ile Pro Glu Glu Asn Gly Asp Leu Glu Ser Asp Asn
 25 30 35
 ttt ggc cga ctt cac tgt aca acc gca gta ata cgg aat ata aat gac 320

Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn Asp
 40 45 50
 caa gtt ctc ttc gtt gac aaa aga cag cct gtg ttc gag gat atg act 368
 Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met Thr
 55 60 65
 gat att gat caa agt gcc agt gaa ccc cag acc aga ctg ata ata tac 416
 Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile Tyr
 70 75 80
 atg tac aaa gac agt gaa gta aga gga ctg gct gtg acc ctc tct gtg 464
 Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser Val
 85 90 95 100
 aag gat agt aaa atg tct acc ctc tcc tgt aag aac aag atc att tcc 512
 Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile Ser
 105 110 115
 ttt gag gaa atg gat cca cct gaa aat att gat gat ata caa agt gat 560
 Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser Asp
 120 125 130
 ctc ata ttc ttt cag aaa cgt gtt cca gga cac aac aag atg gag ttt 608
 Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu Phe
 135 140 145
 gaa tct tca ctg tat gaa gga cac ttt ctt gct tgc caa aag gaa gat 656
 Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu Asp
 150 155 160
 gat gct ttc aaa ctc att ctg aaa aaa aag gat gaa aat ggg gat aaa 704
 Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp Lys
 165 170 175 180
 tct gta atg ttc act ctc act aac tta cat caa agt tag gtggggaggg 753
 Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 185 190

tttgtgttcc agaaagatga ttagcacaca tgcgccttgt gatgacctcg cctgtatttc 813
cataacagaa tacccgaggc tgcatgattt atagagtaaa cacgtttatt tgt 866

<210> 190

<211> 192

<212> PRT

<213> Mus musculus

<400> 190

Met	Ala	Ala	Met	Ser	Glu	Asp	Ser	Cys	Val	Asn	Phe	Lys	Glu	Met	Met
1				5						10				15	
Phe	Ile	Asp	Asn	Thr	Leu	Tyr	Phe	Ile	Pro	Glu	Glu	Asn	Gly	Asp	Leu
			20					25					30		
Glu	Ser	Asp	Asn	Phe	Gly	Arg	Leu	His	Cys	Thr	Thr	Ala	Val	Ile	Arg
		35					40					45			
Asn	Ile	Asn	Asp	Gln	Val	Leu	Phe	Val	Asp	Lys	Arg	Gln	Pro	Val	Phe
	50					55					60				
Glu	Asp	Met	Thr	Asp	Ile	Asp	Gln	Ser	Ala	Ser	Glu	Pro	Gln	Thr	Arg
	65				70					75				80	
Leu	Ile	Ile	Tyr	Met	Tyr	Lys	Asp	Ser	Glu	Val	Arg	Gly	Leu	Ala	Val
			85						90					95	
Thr	Leu	Ser	Val	Lys	Asp	Ser	Lys	Met	Ser	Thr	Leu	Ser	Cys	Lys	Asn
			100					105					110		
Lys	Ile	Ile	Ser	Phe	Glu	Glu	Met	Asp	Pro	Pro	Glu	Asn	Ile	Asp	Asp
		115						120					125		
Ile	Gln	Ser	Asp	Leu	Ile	Phe	Phe	Gln	Lys	Arg	Val	Pro	Gly	His	Asn
	130					135					140				
Lys	Met	Glu	Phe	Glu	Ser	Ser	Leu	Tyr	Glu	Gly	His	Phe	Leu	Ala	Cys
145					150					155				160	

Gln Lys Glu Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu
 165 170 175
 Asn Gly Asp Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
 180 185 190

<210> 191

<211> 3929

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (571).. (2475)

<400> 191

ttttttttgt acgttggaaa ataactttat ttgttctagg gcattggcca gagtccccctt 60
 agaacttctg aaactgcttc ttggtgccag cagccttggg gaccttgagc acattgaatc 120
 gcacagtctt gctcagggtc ctgcactctc caactgtgac aatgtctccg atctgtacat 180
 ccctgaaaca gggggacagg tgcacagaca tgttcttgtg acgcttctca aagcgattgt 240
 actttcggat gtaatggaga tagtcccggc ggatgacaat ggtcctctgc atcttcatct 300
 tcgtcacgac accagacagg atccgacctc ggatggagac gttaccagtg aaggggcatt 360
 tcttgtctat gtaggtaccc tcaatagcct cttaggcgt ctgaagcct agaccgatat 420
 tcttgiagta ccgagggagt ttttccttgc cggtttctcc cagcagaacc cgcttcttgt 480
 ttigaaagat cgtaggctgc ttttggttaag cagctccgt ctgaatgtcc gccatcttcc 540
 ttcttatttc atagcaaata agaaaaatgt atg ttc tac gca cat ttt gtc ctc 594

Met Phe Tyr Ala His Phe Val Leu

1

5

agt aaa cga ggg cct ctg gcc aaa atc tgg ctg gcg gcc cat tgg gac 642
 Ser Lys Arg Gly Pro Leu Ala Lys Ile Trp Leu Ala Ala His Trp Asp

10	15	20	
aag aag cta acc aaa gcc cat gta ttt gag tgc aac tta gag agc agt	690		
Lys Lys Leu Thr Lys Ala His Val Phe Glu Cys Asn Leu Glu Ser Ser			
25	30	35	40
gtg gag agc atc atc tca cca aag gtg aag atg gcg ctg cgg acg tca	738		
Val Glu Ser Ile Ile Ser Pro Lys Val Lys Met Ala Leu Arg Thr Ser			
45	50	55	
gga cac ctt ctc ctg gga gta gtc cgc atc tat cac agg aaa gcc aaa	786		
Gly His Leu Leu Leu Gly Val Val Arg Ile Tyr His Arg Lys Ala Lys			
60	65	70	
tac ctc ctc gca gac tgt aat gaa gca ttt att aaa ata aag atg gcg	834		
Tyr Leu Leu Ala Asp Cys Asn Glu Ala Phe Ile Lys Ile Lys Met Ala			
75	80	85	
ttt cgg cca ggt gtt gtc gat cta cct gag gaa aat cgg gaa gca gct	882		
Phe Arg Pro Gly Val Val Asp Leu Pro Glu Glu Asn Arg Glu Ala Ala			
90	95	100	
tat aat gcc att act tta cct gag gaa ttc cac gat ttt gat cag cca	930		
Tyr Asn Ala Ile Thr Leu Pro Glu Glu Phe His Asp Phe Asp Gln Pro			
105	110	115	120
ctg cca gat tta gat gat att gac gtc gcc cag cag ttc agc ctg aac	978		
Leu Pro Asp Leu Asp Asp Ile Asp Val Ala Gln Gln Phe Ser Leu Asn			
125	130	135	
caa agc aga gta gaa gag ata acc atg aga gaa gaa gtc gga aac atc	1026		
Gln Ser Arg Val Glu Glu Ile Thr Met Arg Glu Glu Val Gly Asn Ile			
140	145	150	
agt atc cta cag gaa aat gac ttt ggt gac ttc gga atg gat gac cgt	1074		
Ser Ile Leu Gln Glu Asn Asp Phe Gly Asp Phe Gly Met Asp Asp Arg			
155	160	165	
gaa ata atg aga gaa ggc agt gct ttc gag gat gac gac atg tta gtg	1122		

Glu Ile Met Arg Glu Gly Ser Ala Phe Glu Asp Asp Asp Met Leu Val
 170 175 180
 agc acc agc gct tcc aac ctt ctc ctc gag cca gag cag agc acc agc 1170
 Ser Thr Ser Ala Ser Asn Leu Leu Leu Glu Pro Glu Gln Ser Thr Ser
 185 190 195 200
 aac ctg aat gaa aag atg aat cac tta gag tac gaa gac cag tac aaa 1218
 Asn Leu Asn Glu Lys Met Asn His Leu Glu Tyr Glu Asp Gln Tyr Lys
 205 210 215
 gat gac aat ttt gga gaa gga aat gat ggc ggt ata tta gat gac aaa 1266
 Asp Asp Asn Phe Gly Glu Gly Asn Asp Gly Gly Ile Leu Asp Asp Lys
 220 225 230
 ctt ata agt aat aat gat ggt ggc atc ttt gac gat ccc cct gcc ttg 1314
 Leu Ile Ser Asn Asn Asp Gly Gly Ile Phe Asp Asp Pro Pro Ala Leu
 235 240 245
 tct gag gca ggg gtc atg ttg cca gag caa cct gca cat gat gac atg 1362
 Ser Glu Ala Gly Val Met Leu Pro Glu Gln Pro Ala His Asp Asp Met
 250 255 260
 gat gaa gat gac aat ggc tca ctg ggt ggg ccg gat agt ccc gac tct 1410
 Asp Glu Asp Asp Asn Gly Ser Leu Gly Gly Pro Asp Ser Pro Asp Ser
 265 270 275 280
 gtg gat cct gtc gaa ccg atg cca act atg act gat cag aca act ctc 1458
 Val Asp Pro Val Glu Pro Met Pro Thr Met Thr Asp Gln Thr Thr Leu
 285 290 295
 gtc cca aac gag gaa gaa gct ttt gcg ttg gag ccc att gat ata act 1506
 Val Pro Asn Glu Glu Glu Ala Phe Ala Leu Glu Pro Ile Asp Ile Thr
 300 305 310
 gtc aaa gag aca aaa gcc aag agg aag agg aag ctg att gtt gac agt 1554
 Val Lys Glu Thr Lys Ala Lys Arg Lys Arg Lys Leu Ile Val Asp Ser
 315 320 325

gtc aaa gaa ttg gat agt aag acc att aga gcc cag ctt agc gat tat 1602
 Val Lys Glu Leu Asp Ser Lys Thr Ile Arg Ala Gln Leu Ser Asp Tyr
 330 335 340
 tct gat att gtt acg act ctg gac ctg gct ccg cca acc aag aag ctt 1650
 Ser Asp Ile Val Thr Thr Leu Asp Leu Ala Pro Pro Thr Lys Lys Leu
 345 350 355 360
 atg atg tgg aaa gag aca gga gga gtg gaa aag ctc ttc tcc tta cca 1698
 Met Met Trp Lys Glu Thr Gly Gly Val Glu Lys Leu Phe Ser Leu Pro
 365 370 375
 gca cag ccc ctg tgg aat aac cgg cta ctg aag ctc ttc aca cgc tgc 1746
 Ala Gln Pro Leu Trp Asn Asn Arg Leu Leu Lys Leu Phe Thr Arg Cys
 380 385 390
 ctt acc cca ctt gta cca gaa gac ctt agg aag aga agg aaa ggg gga 1794
 Leu Thr Pro Leu Val Pro Glu Asp Leu Arg Lys Arg Arg Lys Gly Gly
 395 400 405
 gag gca gat aat ctg gat gag ttc ctc aaa gag ttt gag aat cca gag 1842
 Glu Ala Asp Asn Leu Asp Glu Phe Leu Lys Glu Phe Glu Asn Pro Glu
 410 415 420
 gtt ccc aga gag gag cag cag cca cag cag cag cag cca cag ccg cag 1890
 Val Pro Arg Glu Glu Gln Gln Pro Gln Gln Gln Gln Pro Gln Pro Gln
 425 430 435 440
 cga gat gtc atc gat gag ccc att ata gaa gag cca agc cgc ctc cag 1938
 Arg Asp Val Ile Asp Glu Pro Ile Ile Glu Glu Pro Ser Arg Leu Gln
 445 450 455
 gac tca gtg atg gag gcc agc aga aca acc ata gaa gaa tca gcc atg 1986
 Asp Ser Val Met Glu Ala Ser Arg Thr Thr Ile Glu Glu Ser Ala Met
 460 465 470
 ccc cca cca ccc cct caa gga gtt aag cgg aaa gcc ggg caa ata gac 2034
 Pro Pro Pro Pro Pro Gln Gly Val Lys Arg Lys Ala Gly Gln Ile Asp

475	480	485	
cca gag cct tcg ata cct cct cag cag gta gag caa atg gaa ata cca			2082
Pro Glu Pro Ser Ile Pro Pro Gln Gln Val Glu Gln Met Glu Ile Pro			
490	495	500	
cca gta gaa ctt ccc cca gag gag cct cca aat atc tgt cag ctg atc			2130
Pro Val Glu Leu Pro Pro Glu Glu Pro Pro Asn Ile Cys Gln Leu Ile			
505	510	515	520
ccg gag tta gag ctc cta ccg gag aag gag aag gaa aaa gag aag gag			2178
Pro Glu Leu Glu Leu Leu Pro Glu Lys Glu Lys Glu Lys Glu Lys Glu			
	525	530	535
aag gaa gag gag gag gag gag gat gaa gat gct tca ggg ggt gat cag			2226
Lys Glu Glu Glu Glu Glu Glu Asp Glu Asp Ala Ser Gly Gly Asp Gln			
	540	545	550
gat caa gag gaa agg aga tgg aac aaa cgc act cag cag atg ctt cat			2274
Asp Gln Glu Glu Arg Arg Trp Asn Lys Arg Thr Gln Gln Met Leu His			
	555	560	565
ggt ctt cag cga gct ctt gct aaa act gga gca gag tct atc agt ttg			2322
Gly Leu Gln Arg Ala Leu Ala Lys Thr Gly Ala Glu Ser Ile Ser Leu			
570	575	580	
ctt gag ctg tgt cga aac aca aac cga aag cag gca gca gca aag ttc			2370
Leu Glu Leu Cys Arg Asn Thr Asn Arg Lys Gln Ala Ala Ala Lys Phe			
585	590	595	600
tac agc ttt ttg gtt ctt aag aag cag caa gcc atc gag ctc aca cag			2418
Tyr Ser Phe Leu Val Leu Lys Lys Gln Gln Ala Ile Glu Leu Thr Gln			
	605	610	615
gaa gag ccg tac agt gac atc att gca acc cct gga cca cgg ttc cat			2466
Glu Glu Pro Tyr Ser Asp Ile Ile Ala Thr Pro Gly Pro Arg Phe His			
	620	625	630
att atc tga tgagctagat gtgttcgagc tagtgataac tcactagtag			2515

Ile Ile

635

atacaaattg ccccgigtg cagggcacca aaacccttta agaaagtitt tagatttctg 2575
 ttigtacaaa aatcittgcc ttttctttct tctttttccc cccagtgttt ctaattttgt 2635
 caaccatatt ttttaaggga actgcttatt tgggttgggt ttgtattcct ggagaaaaca 2695
 gtagcccaag aaccagaag actitttaaca gttcagaaca gatgtgtgca atattggigc 2755
 atgtaagaat atggagtaac agtcaaaagg caccattttt aatgttagtt ticcattact 2815
 atgttgaaag gaaaacctgc ctaggaaatg cctgacactt taagaactgt ggtttgagtc 2875
 ccttgacagg aagagaaaaa tgtcttccca tcagtgaac caccggctctg gtttaaccact 2935
 gtagtaggga tagtgtgtga agcatcgtgc ttgtcttctt gatcatgttt aaagtaaate 2995
 acactgagca agaatttgtg aggttgtgct gacigatctt cggctataatg tctgaaatca 3055
 ttccgtgagt cttaggacct ctgatgcag caccgcagct cagaacgac agacgtctac 3115
 cgtggcgiga ctctcaggg gctgcagac actctcagag gttttggatg ttgtcttgaa 3175
 taatgagac atggaagcag acattcccct gcctctgaag ggcagaccaa tgagagacta 3235
 cccagattg acttccctta agcaaacagt gctgtaaaaa ctaatggctt ctctgatatt 3295
 attataaatg ttagtactca tctttttcca aggctgcaca ctctgtatt gcaacttatt 3355
 ttttaataact ttgcaactat aatcctgtat cagtttccca taatttaagt ggagaaaaac 3415
 atcctaataa aggttttatt attaacagac cagatgcacc agaattatgt gactatataa 3475
 tatcaaaaga tgttcacttg taggacaaaa ttatgttgaa aagttctagc ttaagtgttg 3535
 gcacttttag gggggggaaa tcagtittta aactaagact tccatgtcga cgtataccca 3595
 gtaatttaaa attatgtgaa atatttttaa tatttttaaat ttgtgaactc gtaatactac 3655
 tttaatgatt cagtttctcg agaatggtaa ttgtataaaa ttgctcttgc agttttcttt 3715
 tcaatacgac gtgcctgtaa ccatggatgt cccctttgta aaaagacact gtagataatt 3775
 gaatgtttga ttatagaaag gtcgttagtt tcttgttaaa cattttgta gtccagtttt 3835
 tgtcgcttat tgggtttaat attgttcttg aaaatagtcg atgctatgtt atgtataact 3895
 tttctaataa aagtgtgtt tcaagctgta aaaa 3929

<210> 192

<211> 634

<212> PRT

<213> Mus musculus

<400> 192

```

Met Phe Tyr Ala His Phe Val Leu Ser Lys Arg Gly Pro Leu Ala Lys
  1             5             10             15
Ile Trp Leu Ala Ala His Trp Asp Lys Lys Leu Thr Lys Ala His Val
          20             25             30
Phe Glu Cys Asn Leu Glu Ser Ser Val Glu Ser Ile Ile Ser Pro Lys
          35             40             45
Val Lys Met Ala Leu Arg Thr Ser Gly His Leu Leu Leu Gly Val Val
          50             55             60
Arg Ile Tyr His Arg Lys Ala Lys Tyr Leu Leu Ala Asp Cys Asn Glu
          65             70             75             80
Ala Phe Ile Lys Ile Lys Met Ala Phe Arg Pro Gly Val Val Asp Leu
          85             90             95
Pro Glu Glu Asn Arg Glu Ala Ala Tyr Asn Ala Ile Thr Leu Pro Glu
          100            105            110
Glu Phe His Asp Phe Asp Gln Pro Leu Pro Asp Leu Asp Asp Ile Asp
          115            120            125
Val Ala Gln Gln Phe Ser Leu Asn Gln Ser Arg Val Glu Glu Ile Thr
          130            135            140
Met Arg Glu Glu Val Gly Asn Ile Ser Ile Leu Gln Glu Asn Asp Phe
          145            150            155            160
Gly Asp Phe Gly Met Asp Asp Arg Glu Ile Met Arg Glu Gly Ser Ala
          165            170            175
Phe Glu Asp Asp Asp Met Leu Val Ser Thr Ser Ala Ser Asn Leu Leu
          180            185            190
Leu Glu Pro Glu Gln Ser Thr Ser Asn Leu Asn Glu Lys Met Asn His

```

195	200	205
Leu Glu Tyr Glu Asp Gln Tyr Lys Asp Asp Asn Phe Gly Glu Gly Asn		
210	215	220
Asp Gly Gly Ile Leu Asp Asp Lys Leu Ile Ser Asn Asn Asp Gly Gly		
225	230	235
Ile Phe Asp Asp Pro Pro Ala Leu Ser Glu Ala Gly Val Met Leu Pro		
245	250	255
Glu Gln Pro Ala His Asp Asp Met Asp Glu Asp Asp Asn Gly Ser Leu		
260	265	270
Gly Gly Pro Asp Ser Pro Asp Ser Val Asp Pro Val Glu Pro Met Pro		
275	280	285
Thr Met Thr Asp Gln Thr Thr Leu Val Pro Asn Glu Glu Glu Ala Phe		
290	295	300
Ala Leu Glu Pro Ile Asp Ile Thr Val Lys Glu Thr Lys Ala Lys Arg		
305	310	315
Lys Arg Lys Leu Ile Val Asp Ser Val Lys Glu Leu Asp Ser Lys Thr		
325	330	335
Ile Arg Ala Gln Leu Ser Asp Tyr Ser Asp Ile Val Thr Thr Leu Asp		
340	345	350
Leu Ala Pro Pro Thr Lys Lys Leu Met Met Trp Lys Glu Thr Gly Gly		
355	360	365
Val Glu Lys Leu Phe Ser Leu Pro Ala Gln Pro Leu Trp Asn Asn Arg		
370	375	380
Leu Leu Lys Leu Phe Thr Arg Cys Leu Thr Pro Leu Val Pro Glu Asp		
385	390	395
Leu Arg Lys Arg Arg Lys Gly Gly Glu Ala Asp Asn Leu Asp Glu Phe		
405	410	415
Leu Lys Glu Phe Glu Asn Pro Glu Val Pro Arg Glu Glu Gln Gln Pro		
420	425	430

Gln Gln Gln Gln Pro Gln Pro Gln Arg Asp Val Ile Asp Glu Pro Ile
 435 440 445
 Ile Glu Glu Pro Ser Arg Leu Gln Asp Ser Val Met Glu Ala Ser Arg
 450 455 460
 Thr Thr Ile Glu Glu Ser Ala Met Pro Pro Pro Pro Pro Gln Gly Val
 465 470 475 480
 Lys Arg Lys Ala Gly Gln Ile Asp Pro Glu Pro Ser Ile Pro Pro Gln
 485 490 495
 Gln Val Glu Gln Met Glu Ile Pro Pro Val Glu Leu Pro Pro Glu Glu
 500 505 510
 Pro Pro Asn Ile Cys Gln Leu Ile Pro Glu Leu Glu Leu Leu Pro Glu
 515 520 525
 Lys Glu Lys Glu Lys Glu Lys Glu Lys Glu Glu Glu Glu Glu Glu Asp
 530 535 540
 Glu Asp Ala Ser Gly Gly Asp Gln Asp Gln Glu Glu Arg Arg Trp Asn
 545 550 555 560
 Lys Arg Thr Gln Gln Met Leu His Gly Leu Gln Arg Ala Leu Ala Lys
 565 570 575
 Thr Gly Ala Glu Ser Ile Ser Leu Leu Glu Leu Cys Arg Asn Thr Asn
 580 585 590
 Arg Lys Gln Ala Ala Ala Lys Phe Tyr Ser Phe Leu Val Leu Lys Lys
 595 600 605
 Gln Gln Ala Ile Glu Leu Thr Gln Glu Glu Pro Tyr Ser Asp Ile Ile
 610 615 620
 Ala Thr Pro Gly Pro Arg Phe His Ile Ile
 625 630

<210> 193

<211> 1350

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (205).. (1107)

<400> 193

```

taattaagga gacttttagaa gcagtccttc ttggattgca aagagtgttc agcaaaccat 60
cgccaaactg caagactgca gcctgacccc ctccccccag atttcaatgt ccgttccagc 120
tggaaggcta ggttggtgac ttctgatctt cactatgttc ttctttccag taagtgtgga 180
cattcctgca gtagagagag catc atg gtg gct ttc aaa gga gtc tgg act 231
Met Val Ala Phe Lys Gly Val Trp Thr
      1              5
cag gct ttc tgg aag gca gtc tca gca gaa ttt ctg gcc acg ctt atc 279
Gln Ala Phe Trp Lys Ala Val Ser Ala Glu Phe Leu Ala Thr Leu Ile
    10              15              20              25
ttt gtt ttg ggt gtg gga tcc acc ata aac tgg ggt ggc tca gaa aac 327
Phe Val Leu Gly Val Gly Ser Thr Ile Asn Trp Gly Gly Ser Glu Asn
      30              35              40
ccc tta cct gtg gac atg gtc ctc atc tcc ctt tgc ttt gga ctc agc 375
Pro Leu Pro Val Asp Met Val Leu Ile Ser Leu Cys Phe Gly Leu Ser
      45              50              55
att gca acc atg gtg cag tgc ctt ggc cac atc agc ggt ggc cac atc 423
Ile Ala Thr Met Val Gln Cys Leu Gly His Ile Ser Gly Gly His Ile
      60              65              70
aat cca gct gtg act gta gcc atg gtg tgc aca cga aag atc agc atc 471
Asn Pro Ala Val Thr Val Ala Met Val Cys Thr Arg Lys Ile Ser Ile
      75              80              85

```

gct aag tcc gtc ttc tac atc att gca cag tgc ctg ggg gcc atc att 519
 Ala Lys Ser Val Phe Tyr Ile Ile Ala Gln Cys Leu Gly Ala Ile Ile
 90 95 100 105
 gga gcc ggc atc ctc tac ctg gtc aca cct ccc agt gtg gtt gga gga 567
 Gly Ala Gly Ile Leu Tyr Leu Val Thr Pro Pro Ser Val Val Gly Gly
 110 115 120
 ttg gga gtc acc acg gtt cat gga aac ctc acc gct ggc cat ggg ctc 615
 Leu Gly Val Thr Thr Val His Gly Asn Leu Thr Ala Gly His Gly Leu
 125 130 135
 ctg gtg gag tta ata atc act ttc cag ttg gtg ttc act gtt ttt gcc 663
 Leu Val Glu Leu Ile Ile Thr Phe Gln Leu Val Phe Thr Val Phe Ala
 140 145 150
 agc tgt gat tcc aaa cgg act gat gtc act ggt tca ata gct tta gca 711
 Ser Cys Asp Ser Lys Arg Thr Asp Val Thr Gly Ser Ile Ala Leu Ala
 155 160 165
 att gga ttt tcc gtt gca att gga cat ttg ttt gca atc aat tat act 759
 Ile Gly Phe Ser Val Ala Ile Gly His Leu Phe Ala Ile Asn Tyr Thr
 170 175 180 185
 gga gcc agc atg aat cca gct cga tct ttt gga ccc gca gtt atc atg 807
 Gly Ala Ser Met Asn Pro Ala Arg Ser Phe Gly Pro Ala Val Ile Met
 190 195 200
 gga aac tgg gca aac cac tgg ata tat tgg gtt gga cca atc atg ggc 855
 Gly Asn Trp Ala Asn His Trp Ile Tyr Trp Val Gly Pro Ile Met Gly
 205 210 215
 gct gtg ctg gca ggt gcc ctt tat gag tat gtc ttc tgt cct gat gtg 903
 Ala Val Leu Ala Gly Ala Leu Tyr Glu Tyr Val Phe Cys Pro Asp Val
 220 225 230
 gag ctc aaa cgt cgc ctt aag gaa gcc ttc agc aaa gcc gcg cag cag 951
 Glu Leu Lys Arg Arg Leu Lys Glu Ala Phe Ser Lys Ala Ala Gln Gln

235 240 245
 aca aaa ggg agc tac atg gag gtg gag gac aac cgg agc caa gtg gag 999
 Thr Lys Gly Ser Tyr Met Glu Val Glu Asp Asn Arg Ser Gln Val Glu
 250 255 260 265
 acg gaa gac ttg atc ctg aag ccc gga gtg gtg cat gtg att gac att 1047
 Thr Glu Asp Leu Ile Leu Lys Pro Gly Val Val His Val Ile Asp Ile
 270 275 280
 gac cgt gga gaa gag aag aag gga agg gac tct tcg gga gag gta ttg 1095
 Asp Arg Gly Glu Glu Lys Lys Gly Arg Asp Ser Ser Gly Glu Val Leu
 285 290 295
 tct tcc gta tga ctagaggaca gcactgaagg cagaagagac tccctagacc 1147
 Ser Ser Val
 300
 tggcctcaga ttcttgccac ccattaagga acagatttgt tataaattag acacttgcgg 1207
 gtttcttctt cacacttggt acacagtta aatacacata ttctatatata catggggcct 1267
 ttttttaact ctaattcact ataatcctct cccctcaga atccaagaac ccatagggct 1327
 aaaagtaaaa aaaaaaaaaa aaa 1350

<210> 194

<211> 300

<212> PRT

<213> Mus musculus

<400> 194

Met Val Ala Phe Lys Gly Val Trp Thr Gln Ala Phe Trp Lys Ala Val
 1 5 10 15
 Ser Ala Glu Phe Leu Ala Thr Leu Ile Phe Val Leu Gly Val Gly Ser
 20 25 30
 Thr Ile Asn Trp Gly Gly Ser Glu Asn Pro Leu Pro Val Asp Met Val

35	40	45
Leu Ile Ser Leu Cys Phe Gly Leu Ser Ile Ala Thr Met Val Gln Cys		
50	55	60
Leu Gly His Ile Ser Gly Gly His Ile Asn Pro Ala Val Thr Val Ala		
65	70	75
Met Val Cys Thr Arg Lys Ile Ser Ile Ala Lys Ser Val Phe Tyr Ile		
85	90	95
Ile Ala Gln Cys Leu Gly Ala Ile Ile Gly Ala Gly Ile Leu Tyr Leu		
100	105	110
Val Thr Pro Pro Ser Val Val Gly Gly Leu Gly Val Thr Thr Val His		
115	120	125
Gly Asn Leu Thr Ala Gly His Gly Leu Leu Val Glu Leu Ile Ile Thr		
130	135	140
Phe Gln Leu Val Phe Thr Val Phe Ala Ser Cys Asp Ser Lys Arg Thr		
145	150	155
Asp Val Thr Gly Ser Ile Ala Leu Ala Ile Gly Phe Ser Val Ala Ile		
165	170	175
Gly His Leu Phe Ala Ile Asn Tyr Thr Gly Ala Ser Met Asn Pro Ala		
180	185	190
Arg Ser Phe Gly Pro Ala Val Ile Met Gly Asn Trp Ala Asn His Trp		
195	200	205
Ile Tyr Trp Val Gly Pro Ile Met Gly Ala Val Leu Ala Gly Ala Leu		
210	215	220
Tyr Glu Tyr Val Phe Cys Pro Asp Val Glu Leu Lys Arg Arg Leu Lys		
225	230	235
Glu Ala Phe Ser Lys Ala Ala Gln Gln Thr Lys Gly Ser Tyr Met Glu		
245	250	255
Val Glu Asp Asn Arg Ser Gln Val Glu Thr Glu Asp Leu Ile Leu Lys		
260	265	270

Pro Gly Val Val His Val Ile Asp Ile Asp Arg Gly Glu Glu Lys Lys

275

280

285

Gly Arg Asp Ser Ser Gly Glu Val Leu Ser Ser Val

290

295

300

<210> 195

<211> 2902

<212> DNA

<213> Mus musculus

<400> 195

cggcgccctcg aagagagagg gtctctacgc tgccccggct ccaactgcta gtgctgttgt 60
 tgctgccgct gatgcttgtg ccccagccca tagcaggcca tggcggcaag tactcgcgag 120
 agaagaacga gccggagatg gccgccaagc gcgagtcgg ggaggagttc cgcatggaga 180
 agctgaacca gctatgggag aaggccaagc ggcttcattt gtctcctgtg aggctggccg 240
 agctgcattc tgacctgaag atacaagaga gggatgaact caactggaaa aagctgaagg 300
 tggaaggctt ggataaggat ggggagaaaag aagcaaaact gatccacaac ctcaacgtca 360
 tcctggccag atacggactg gatgggagga aggacgcca gatggtgcac agcaacgccc 420
 tcaatgaaga caccagatg gagctggggg acccaggct ggaaaagctg tggcacaagg 480
 caaagacatc agggaaattc tccagtgaag agctggacaa gctgtggaga gagtttctgc 540
 attacaaaga gaagatccag gattacaatg tgctgctaga cacactgagc agagctgaag 600
 aaggttatga gaaccttctc agtccctcgg acatggccca catcaagagc gacacctga 660
 tcagcaagca cagtgaagct aaggacagac tgcgcagtat caaccagggc ttggaccgcc 720
 tgcggaaggt cagccaccag ggctatggct ccaccactga gtttgaagag ccccggtga 780
 tagatctgtg ggacctggct cagtctgcca acttactga gaaggaactg gattcattca 840
 gggaggagct caagcacttt gaggccaaaa ttgaaaagca caaccactac cagaagcagc 900
 tggagatttc ccaccagaag ctgaagcacg tggagagcat cggcgacccc gagcacatca 960
 gccgcaacaa ggagaaatag gtgctgtgtg aggagaagac caaggagctg ggctacaagg 1020
 tgaagaagca tctacaggac ctgtctagca gggcttcaag ggctcggcac aatgagctct 1080

gaggacCaga agccaccagc agcagcctag agagaacact tgaagacacc gggagctgtc 1140
agcatgtcat cggcttgcac agacctgagg tgactgggtg ggctgaccac cgtggcaagg 1200
aggatccctt gaaataccaa gctgaccta cagtggctgg caaggactta ttttctctca 1260
agcaagtgtg gttgtcacca cctggacga gggccttggg taccgctacc agtgagatag 1320
gactggactc cgagctgcag cacaacactt tataattgaaa tcacataaac ctgcctgcc 1380
ctggaaacat tctgtacaca tccttaata catggcagag ttttgagccc tcgagtcctt 1440
gccctggatc tcgaaggatg ggtccattga gccatggcaa agttaagtta cagatgaagg 1500
gggaaggcga agactagtct acccactgga agcatttccc tccctgcttc acgcaccctc 1560
tccctctctg gggatctggc cccagacagt tttaaatcaa gagatttcag gacaaagatg 1620
gcagagggtg aagcctgcag gtcttgacag gcgaacgttt tctggcccc tccaccccca 1680
aagaccctga tcagcttcca gatccagtct ctgttccctc acacagaata gccaaaattt 1740
tgtctgaccc cagcagctga tcctggaaga tcaggccatt gagtttgtta gccgctgaat 1800
ctcagcccag aaattggaat ctgcctatca ggggtgcgca gttaaccatg tttagaata 1860
tcacagccgg aaagaggctc agtgagtaaa atgttcatac agcaagcttg aggtctacag 1920
tttggatctg cagagccctg ctgtgtttac tiacctgcag tcccagcact tgagaggcag 1980
agaaagttaa tcccagccaa ataaacaaag gtggagtata tgggagaagg cactctccca 2040
ctctctgatg tgtgcataca cttacatgtg tacctgtaca caggtagca ctcatagata 2100
ctcatataatg ggtgaaactc ccagggcatc atcgtgcaag aagcccatgg gttaaggaca 2160
gcagccgcaa gaacagtagg cagtgtgggt cctcaccca tgcgtgtct gccaccatcc 2220
aggccaggcc agctgggatg tgtccctctg agcactagta gaatacttc ccagaaccct 2280
cagcagtgtc tgaggctcag agaaattctt gttgctaggg tctcagctct gcctttctgg 2340
ttcagcccaa caccaaagcc tctgtgcct cacagcccag gggactcagg ctcagagtca 2400
actgctgggg gagtgccctg ctgtcagatg cacccttact aatgtttgtc tccatcccta 2460
gagccagagc gcatggctgc atgctaagc ttagaaatgg gcacgttgaa gtaacatagc 2520
agtatacagc ccagtgaacc atctcagagt gagtgataga gagccacag ctatgttagg 2580
gagagggtgtg acctgtgtgg gagctgcctg cttctggagc agatctctag tcaggaggcc 2640
actcctgact aagctctcag atatcagatc ctgcaaactt cctgggtgag tgtgactccc 2700
accgcaaggg aacctcaagc tacaactta gatgcggctc tggctagcag ctctgccacc 2760
tagcaacagt gactgaaagt cctcaggctg acaggtcacc agtcacatta tggtaaacca 2820

gaacaggttc atgcaagttg tccctcact atgcgtgcta cggcacatgg gttcacacaa 2880
tgaataaaat atctttttaa gc 2902

<210> 196

<211> 1928

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (99).. (1784)

<400> 196

caagcggcct ccaaccggtc ttgtcactgc gctgcctctg ctccaccttc tctggccctg 60
gccgctagtgc ctgagagtgc ctgcagtcgg cctgtagc atg tgt ggc atc tgg gcc 116
Met Cys Gly Ile Trp Ala

1

5

ctc ttc ggc agc gat gac tgc ctt tcc gtg cag tgt ctg agt gcg atg 164
Leu Phe Gly Ser Asp Asp Cys Leu Ser Val Gln Cys Leu Ser Ala Met

10

15

20

aag atc gcg cac agg ggg cca gat gca ttt cgc ttt gag aat gtc aat 212
Lys Ile Ala His Arg Gly Pro Asp Ala Phe Arg Phe Glu Asn Val Asn

25

30

35

gga tac acc aac tgc tgc ttt ggc ttt cac cgc ttg gct gtg gtt gac 260
Gly Tyr Thr Asn Cys Cys Phe Gly Phe His Arg Leu Ala Val Val Asp

40

45

50

ccg ctg ttt gga atg cag ccg ata aga gtg agg aaa tac cct tat ttg 308
Pro Leu Phe Gly Met Gln Pro Ile Arg Val Arg Lys Tyr Pro Tyr Leu

55

60

65

70

tgg ctc tgt tac aat ggt gaa atc tac aac cac aag gcg cta cag caa	356
Trp Leu Cys Tyr Asn Gly Glu Ile Tyr Asn His Lys Ala Leu Gln Gln	
75 80 85	
cgt ttt gaa ttt gaa tat cag acc aat gtg gat ggt gag att atc ctc	404
Arg Phe Glu Phe Glu Tyr Gln Thr Asn Val Asp Gly Glu Ile Ile Leu	
90 95 100	
cac ctc tat gac aaa gga ggc atc gag aaa acc atc tgt atg ctg gac	452
His Leu Tyr Asp Lys Gly Gly Ile Glu Lys Thr Ile Cys Met Leu Asp	
105 110 115	
ggg gtg ttt gca ttc atc tta ctg gac act gcc aat aag aaa gta ttt	500
Gly Val Phe Ala Phe Ile Leu Leu Asp Thr Ala Asn Lys Lys Val Phe	
120 125 130	
ctg ggc aga gac acc tat gga gtc agg ccc ttg ttt aaa gcc atg aca	548
Leu Gly Arg Asp Thr Tyr Gly Val Arg Pro Leu Phe Lys Ala Met Thr	
135 140 145 150	
gaa gat ggg ttt ctg gct gtg tgt tca gaa gct aaa ggc ctt gtt tcc	596
Glu Asp Gly Phe Leu Ala Val Cys Ser Glu Ala Lys Gly Leu Val Ser	
155 160 165	
tta aaa cac tcc acc act ccc ttc tta aaa gtg gag ccc ttc ctt cct	644
Leu Lys His Ser Thr Thr Pro Phe Leu Lys Val Glu Pro Phe Leu Pro	
170 175 180	
gga cac tat gaa gtt ttg gat tta aaa cca aat ggc aaa gtt gcg tct	692
Gly His Tyr Glu Val Leu Asp Leu Lys Pro Asn Gly Lys Val Ala Ser	
185 190 195	
gtg gaa atg gtc aaa tac cat cac tgt acg gat gaa cca ttg cat gcc	740
Val Glu Met Val Lys Tyr His His Cys Thr Asp Glu Pro Leu His Ala	
200 205 210	
atc tat gac agc gtg gag aaa ctc ttc cca ggc ttt gac cta gag acc	788
Ile Tyr Asp Ser Val Glu Lys Leu Phe Pro Gly Phe Asp Leu Glu Thr	

215	220	225	230	
gtg aag aac aat ctg cgt atc ctt ttt gac aac gct atc aag aaa cgc				836
Val Lys Asn Asn Leu Arg Ile Leu Phe Asp Asn Ala Ile Lys Lys Arg				
	235	240	245	
ttg atg aca gac cgg agg att ggc tgc ctt tta tca ggg ggc ctg gac				884
Leu Met Thr Asp Arg Arg Ile Gly Cys Leu Leu Ser Gly Gly Leu Asp				
	250	255	260	
tcg agc ttg gtt gct gcc tct ctg ctg aag caa ctc aag gag gcc caa				932
Ser Ser Leu Val Ala Ala Ser Leu Leu Lys Gln Leu Lys Glu Ala Gln				
	265	270	275	
gtt cag tat cct ctc cag aca ttt gct att ggc atg gag gac agc ccc				980
Val Gln Tyr Pro Leu Gln Thr Phe Ala Ile Gly Met Glu Asp Ser Pro				
	280	285	290	
gat ctc ctg gcc gct aga aag gtg gca aat tat att gga agc gag cat				1028
Asp Leu Leu Ala Ala Arg Lys Val Ala Asn Tyr Ile Gly Ser Glu His				
	295	300	305	310
cat gaa gtc ctt ttt aac tct gaa gaa ggc att cag gcc ctg gat gaa				1076
His Glu Val Leu Phe Asn Ser Glu Glu Gly Ile Gln Ala Leu Asp Glu				
	315	320	325	
gtc ata ttt tcc ttg gaa act tat gat att acg aca gtt cgg gca tct				1124
Val Ile Phe Ser Leu Glu Thr Tyr Asp Ile Thr Thr Val Arg Ala Ser				
	330	335	340	
gtg ggc atg tat tta att tcc aag tat att cgg aag aac aca gac agc				1172
Val Gly Met Tyr Leu Ile Ser Lys Tyr Ile Arg Lys Asn Thr Asp Ser				
	345	350	355	
gtg gtg atc ttc tcc gga gag ggg tca gat gaa ctt aca cag ggc tat				1220
Val Val Ile Phe Ser Gly Glu Gly Ser Asp Glu Leu Thr Gln Gly Tyr				
	360	365	370	
ata tat ttc cac aag gct cct tcc cct gag aag gcc gag gag gag agt				1268

Ile Tyr Phe His Lys Ala Pro Ser Pro Glu Lys Ala Glu Glu Glu Ser
 375 380 385 390
 gag aga ctg ctg aag gaa ctc tac ctg ttt gat gtt ctc cgg gcc gac 1316
 Glu Arg Leu Leu Lys Glu Leu Tyr Leu Phe Asp Val Leu Arg Ala Asp
 395 400 405
 cgc act act gcc gca cat ggt ctc gaa ctg aga gtc ccc ttt ctg gat 1364
 Arg Thr Thr Ala Ala His Gly Leu Glu Leu Arg Val Pro Phe Leu Asp
 410 415 420
 cat cgg ttt tct tcc tat tac ctg tct ctg ccg cca gat atg aga att 1412
 His Arg Phe Ser Ser Tyr Tyr Leu Ser Leu Pro Pro Asp Met Arg Ile
 425 430 435
 cca aaa aat ggc ata gaa aaa cat ctc ctg aga gag act ttt gag gac 1460
 Pro Lys Asn Gly Ile Glu Lys His Leu Leu Arg Glu Thr Phe Glu Asp
 440 445 450
 tgc aac ctg cta ccc aaa gag att ctc tgg cga ccc aaa gaa gcc ttc 1508
 Cys Asn Leu Leu Pro Lys Glu Ile Leu Trp Arg Pro Lys Glu Ala Phe
 455 460 465 470
 agt gat ggg atc acc tca gtc aag aac tcc tgg ttc aag att ttg cag 1556
 Ser Asp Gly Ile Thr Ser Val Lys Asn Ser Trp Phe Lys Ile Leu Gln
 475 480 485
 gac tat gtt gaa cat cag gtt gat gat gaa atg atg tct gca gcc tcc 1604
 Asp Tyr Val Glu His Gln Val Asp Asp Glu Met Met Ser Ala Ala Ser
 490 495 500
 cag aag ttt ccc ttc aat act ccc aaa act aag gaa ggc tac ttc tac 1652
 Gln Lys Phe Pro Phe Asn Thr Pro Lys Thr Lys Glu Gly Tyr Phe Tyr
 505 510 515
 cgt cag atc ttt gaa cgc cat tac cca ggc cgg gct gat tgg ctg act 1700
 Arg Gln Ile Phe Glu Arg His Tyr Pro Gly Arg Ala Asp Trp Leu Thr
 520 525 530

cat tat tgg atg cct aag tgg atc aat gct act gac cct tct gcc cgc 1748
 His Tyr Trp Met Pro Lys Trp Ile Asn Ala Thr Asp Pro Ser Ala Arg
 535 540 545 550
 act ctg acc cat tat aag tca gct gcc aaa gct tag gcactctcta 1794
 Thr Leu Thr His Tyr Lys Ser Ala Ala Lys Ala
 555 560
 cactcttgtg taaaagtaaa tgtttcttcc ggctctgaag gtcgagacag cgacacaatc 1854
 agaaagaatg agactcagcc atcagtcacc caggcttact taggcatgaa aagaaataaa 1914
 agtttcacat ctga 1928

<210> 197

<211> 561

<212> PRT

<213> Mus musculus

<400> 197

Met Cys Gly Ile Trp Ala Leu Phe Gly Ser Asp Asp Cys Leu Ser Val
 1 5 10 15
 Gln Cys Leu Ser Ala Met Lys Ile Ala His Arg Gly Pro Asp Ala Phe
 20 25 30
 Arg Phe Glu Asn Val Asn Gly Tyr Thr Asn Cys Cys Phe Gly Phe His
 35 40 45
 Arg Leu Ala Val Val Asp Pro Leu Phe Gly Met Gln Pro Ile Arg Val
 50 55 60
 Arg Lys Tyr Pro Tyr Leu Trp Leu Cys Tyr Asn Gly Glu Ile Tyr Asn
 65 70 75 80
 His Lys Ala Leu Gln Gln Arg Phe Glu Phe Glu Tyr Gln Thr Asn Val
 85 90 95
 Asp Gly Glu Ile Ile Leu His Leu Tyr Asp Lys Gly Gly Ile Glu Lys

100	105	110
Thr Ile Cys Met Leu Asp Gly Val Phe Ala Phe Ile Leu Leu Asp Thr		
115	120	125
Ala Asn Lys Lys Val Phe Leu Gly Arg Asp Thr Tyr Gly Val Arg Pro		
130	135	140
Leu Phe Lys Ala Met Thr Glu Asp Gly Phe Leu Ala Val Cys Ser Glu		
145	150	155
Ala Lys Gly Leu Val Ser Leu Lys His Ser Thr Thr Pro Phe Leu Lys		
165	170	175
Val Glu Pro Phe Leu Pro Gly His Tyr Glu Val Leu Asp Leu Lys Pro		
180	185	190
Asn Gly Lys Val Ala Ser Val Glu Met Val Lys Tyr His His Cys Thr		
195	200	205
Asp Glu Pro Leu His Ala Ile Tyr Asp Ser Val Glu Lys Leu Phe Pro		
210	215	220
Gly Phe Asp Leu Glu Thr Val Lys Asn Asn Leu Arg Ile Leu Phe Asp		
225	230	235
Asn Ala Ile Lys Lys Arg Leu Met Thr Asp Arg Arg Ile Gly Cys Leu		
245	250	255
Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ala Ser Leu Leu Lys		
260	265	270
Gln Leu Lys Glu Ala Gln Val Gln Tyr Pro Leu Gln Thr Phe Ala Ile		
275	280	285
Gly Met Glu Asp Ser Pro Asp Leu Leu Ala Ala Arg Lys Val Ala Asn		
290	295	300
Tyr Ile Gly Ser Glu His His Glu Val Leu Phe Asn Ser Glu Glu Gly		
305	310	315
Ile Gln Ala Leu Asp Glu Val Ile Phe Ser Leu Glu Thr Tyr Asp Ile		
325	330	335

Thr Thr Val Arg Ala Ser Val Gly Met Tyr Leu Ile Ser Lys Tyr Ile
 340 345 350
 Arg Lys Asn Thr Asp Ser Val Val Ile Phe Ser Gly Glu Gly Ser Asp
 355 360 365
 Glu Leu Thr Gln Gly Tyr Ile Tyr Phe His Lys Ala Pro Ser Pro Glu
 370 375 380
 Lys Ala Glu Glu Glu Ser Glu Arg Leu Leu Lys Glu Leu Tyr Leu Phe
 385 390 395 400
 Asp Val Leu Arg Ala Asp Arg Thr Thr Ala Ala His Gly Leu Glu Leu
 405 410 415
 Arg Val Pro Phe Leu Asp His Arg Phe Ser Ser Tyr Tyr Leu Ser Leu
 420 425 430
 Pro Pro Asp Met Arg Ile Pro Lys Asn Gly Ile Glu Lys His Leu Leu
 435 440 445
 Arg Glu Thr Phe Glu Asp Cys Asn Leu Leu Pro Lys Glu Ile Leu Trp
 450 455 460
 Arg Pro Lys Glu Ala Phe Ser Asp Gly Ile Thr Ser Val Lys Asn Ser
 465 470 475 480
 Trp Phe Lys Ile Leu Gln Asp Tyr Val Glu His Gln Val Asp Asp Glu
 485 490 495
 Met Met Ser Ala Ala Ser Gln Lys Phe Pro Phe Asn Thr Pro Lys Thr
 500 505 510
 Lys Glu Gly Tyr Phe Tyr Arg Gln Ile Phe Glu Arg His Tyr Pro Gly
 515 520 525
 Arg Ala Asp Trp Leu Thr His Tyr Trp Met Pro Lys Trp Ile Asn Ala
 530 535 540
 Thr Asp Pro Ser Ala Arg Thr Leu Thr His Tyr Lys Ser Ala Ala Lys
 545 550 555 560
 Ala

<210> 198

<211> 1101

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (105).. (1058)

<400> 198

ggcacgagcc acagggcgt ggtggcagcc gctgtggtgc ttggctctct gagctatccg 60
 gtgccatcct tgtcgctgcg gcgaccctcg catcaactgc agcc atg acc gag cag 116

Met Thr Glu Gln

1

atg acc ctt cgc ggg acc ctt aag ggc cac aat gga tgg gta aca cag 164
 Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly Trp Val Thr Gln

5

10

15

20

atc gca acc aca ccg cag ttc ccg gac atg atc ctg tct gcg tct cga 212
 Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu Ser Ala Ser Arg

25

30

35

gac aag acc atc atc atg tgg aag ctg acc aga gat gag acc aac tat 260
 Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp Glu Thr Asn Tyr

40

45

50

ggc ata cca cag cgt gct ctg aga ggt cac tcc cac ttc gtt agt gat 308
 Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His Phe Val Ser Asp

55

60

65

gtt gtt atc tcc tct gat ggt cag ttt gcg ctc tcg ggc tcc tgg gac 356
 Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser Gly Ser Trp Asp

70	75	80	
gga acg ctg cgc ctc tgg gat ctc aca acg ggc acc acc aca agg cga	404		
Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr Thr Thr Arg Arg			
85	90	95	100
ttt gtc ggc cac acc aag gat gtg ttg agc gtg gcc ttc tcc tct gac	452		
Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala Phe Ser Ser Asp			
105	110	115	
aac cgg cag att gtc tct ggg tcc cga gac aag acc ata aag tta tgg	500		
Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr Ile Lys Leu Trp			
120	125	130	
aat act ctg ggt gtc tgc aag tac acg gtc cag gat gag agt cat tca	548		
Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp Glu Ser His Ser			
135	140	145	
gaa tgg gtg tct tgt gtc cgc ttc tcc ccg aac agc agc aac cct atc	596		
Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser Ser Asn Pro Ile			
150	155	160	
atc gtc tcc tgc gga tgg gac aag ctg gtc aag gtg tgg aat ctg gct	644		
Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val Trp Asn Leu Ala			
165	170	175	180
aac tgc aag cta aag acc aac cac att ggc cac act ggc tac ctg aac	692		
Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr Gly Tyr Leu Asn			
185	190	195	
aca gtg act gtc tct cca gat gga tcc ctc tgt gct tct gga ggc aag	740		
Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala Ser Gly Gly Lys			
200	205	210	
gat ggc cag gct atg ctg tgg gat ctc aat gaa ggc aag cac ctc tac	788		
Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly Lys His Leu Tyr			
215	220	225	
act tta gat ggt ggg gac atc atc aat gcc ttg tgc ttc agc ccc aac	836		

Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys Phe Ser Pro Asn
 230 235 240
 cgc tac tgg ctc tgc gct gcc act ggc ccc agc atc aag atc tgg gac 884
 Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile Lys Ile Trp Asp
 245 250 255 260
 ttg gag ggc aag atc att gta gat gaa ttg aag caa gaa gtt atc agc 932
 Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln Glu Val Ile Ser
 265 270 275
 acc agc agc aag gca gag cca ccc cag tgt acc tct ttg gca tgg tct 980
 Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser Leu Ala Trp Ser
 280 285 290
 gct gat ggc cag act ctg ttt gct ggc tat aca gac aac ttg gtg cga 1028
 Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp Asn Leu Val Arg
 295 300 305
 gta tgg cag gta act att ggt acc cgc taa aagttttatg acaaagtctt 1078
 Val Trp Gln Val Thr Ile Gly Thr Arg
 310 315
 agaaataaac tggcctcgtg ccg 1101

<210> 199

<211> 317

<212> PRT

<213> Mus musculus

<400> 199

Met Thr Glu Gln Met Thr Leu Arg Gly Thr Leu Lys Gly His Asn Gly
 1 5 10 15
 Trp Val Thr Gln Ile Ala Thr Thr Pro Gln Phe Pro Asp Met Ile Leu
 20 25 30

Ser Ala Ser Arg Asp Lys Thr Ile Ile Met Trp Lys Leu Thr Arg Asp
 35 40 45
 Glu Thr Asn Tyr Gly Ile Pro Gln Arg Ala Leu Arg Gly His Ser His
 50 55 60
 Phe Val Ser Asp Val Val Ile Ser Ser Asp Gly Gln Phe Ala Leu Ser
 65 70 75 80
 Gly Ser Trp Asp Gly Thr Leu Arg Leu Trp Asp Leu Thr Thr Gly Thr
 85 90 95
 Thr Thr Arg Arg Phe Val Gly His Thr Lys Asp Val Leu Ser Val Ala
 100 105 110
 Phe Ser Ser Asp Asn Arg Gln Ile Val Ser Gly Ser Arg Asp Lys Thr
 115 120 125
 Ile Lys Leu Trp Asn Thr Leu Gly Val Cys Lys Tyr Thr Val Gln Asp
 130 135 140
 Glu Ser His Ser Glu Trp Val Ser Cys Val Arg Phe Ser Pro Asn Ser
 145 150 155 160
 Ser Asn Pro Ile Ile Val Ser Cys Gly Trp Asp Lys Leu Val Lys Val
 165 170 175
 Trp Asn Leu Ala Asn Cys Lys Leu Lys Thr Asn His Ile Gly His Thr
 180 185 190
 Gly Tyr Leu Asn Thr Val Thr Val Ser Pro Asp Gly Ser Leu Cys Ala
 195 200 205
 Ser Gly Gly Lys Asp Gly Gln Ala Met Leu Trp Asp Leu Asn Glu Gly
 210 215 220
 Lys His Leu Tyr Thr Leu Asp Gly Gly Asp Ile Ile Asn Ala Leu Cys
 225 230 235 240
 Phe Ser Pro Asn Arg Tyr Trp Leu Cys Ala Ala Thr Gly Pro Ser Ile
 245 250 255
 Lys Ile Trp Asp Leu Glu Gly Lys Ile Ile Val Asp Glu Leu Lys Gln

	260	265	270
Glu Val Ile Ser Thr Ser Ser Lys Ala Glu Pro Pro Gln Cys Thr Ser			
275	280	285	
Leu Ala Trp Ser Ala Asp Gly Gln Thr Leu Phe Ala Gly Tyr Thr Asp			
290	295	300	
Asn Leu Val Arg Val Trp Gln Val Thr Ile Gly Thr Arg			
305	310	315	

<210> 200

<211> 364

<212> DNA

<213> Mus musculus

<400> 200

```

attcggcacg acggagaagg tctcggagta ggagtcgcag aagcagccgc agtagatctc 60
gaagtatctc aaaaagtcgc tcccgatcta ggtctcggag caaaggtcga tcccgatccc 120
gctcaaaagg caggaaatcc agatcaaaga gcaaatcgaa gccaagtct gaccggggct 180
cccattccca ctcaagaagc aggtctaagg ataagtatgg gaagtcacgt agtaggtcac 240
ggtctcggtc ccccaaagag aacggcaaag gagacataaa gtcaaagtcc agatcccgga 300
gccagtctcg gtcccactcg cctctacctg ctccaccctc aaaggctcgg tccatgtccc 360
ctcc

```

364

<210> 201

<211> 1785

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (51).. (1580)

<400> 201

```

ccgtctcctt caggtcctga gccccgagag ccccttcgc gcacgcggac atg ggc      56
                                     Met Gly
                                     1
ggc agc tcc agg gcg cgc tgg gtg gcc ttg ggg ttg ggc gcc ctg ggg      104
Gly Ser Ser Arg Ala Arg Trp Val Ala Leu Gly Leu Gly Ala Leu Gly
      5              10              15
ctg ctg ttt gct gcg ctc ggc gtt gtc atg atc ctc atg gtg ccc tcc      152
Leu Leu Phe Ala Ala Leu Gly Val Val Met Ile Leu Met Val Pro Ser
      20              25              30
ctc atc aag cag cag gig ctc aag aat gtc cgc ata gac ccg agc agc      200
Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro Ser Ser
      35              40              45              50
ctg tcc ttc ggg atg tgg aag gag atc ccc gtc cct ttc tac ttg tct      248
Leu Ser Phe Gly Met Trp Lys Glu Ile Pro Val Pro Phe Tyr Leu Ser
      55              60              65
gtc tac ttc ttc gaa gtg gtc aac cca aac gag gtc ctc aac ggc cag      296
Val Tyr Phe Phe Glu Val Val Asn Pro Asn Glu Val Leu Asn Gly Gln
      70              75              80
aag cca gta gtc cgg gag cgt gga ccc tat gtc tac agg gag ttc aga      344
Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu Phe Arg
      85              90              95
caa aag gtc aac atc acc ttc aat gac aac gac acc gtg tcc ttc gtg      392
Gln Lys Val Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser Phe Val
      100             105             110
gag aac cgc agc ctc cat ttc cag cct gac aag tcg cat ggc tca gag      440
Glu Asn Arg Ser Leu His Phe Gln Pro Asp Lys Ser His Gly Ser Glu

```

115	120	125	130	
agt gac tac att gta ctg cct aac atc ttg gtc ctg ggg ggc tcg ata	488			
Ser Asp Tyr Ile Val Leu Pro Asn Ile Leu Val Leu Gly Gly Ser Ile				
135	140	145		
ttg atg gag agc aag cct gtg agc ctg aag ctg atg atg acc ttg gcg	536			
Leu Met Glu Ser Lys Pro Val Ser Leu Lys Leu Met Met Thr Leu Ala				
150	155	160		
ctg gtc acc atg ggc cag cgt gct ttt atg aac cgc aca gtt ggt gag	584			
Leu Val Thr Met Gly Gln Arg Ala Phe Met Asn Arg Thr Val Gly Glu				
165	170	175		
atc ctg tgg ggc tat gac gat ccc ttc gtg cat ttt ctc aac acg tac	632			
Ile Leu Trp Gly Tyr Asp Asp Pro Phe Val His Phe Leu Asn Thr Tyr				
180	185	190		
ctc cca gac atg ctt ccc ata aag ggc aaa ttt ggc ctg ttt gtt ggg	680			
Leu Pro Asp Met Leu Pro Ile Lys Gly Lys Phe Gly Leu Phe Val Gly				
195	200	205	210	
atg aac aac tcg aat tct ggg gtc ttc act gtc ttc acg ggc gtc cag	728			
Met Asn Asn Ser Asn Ser Gly Val Phe Thr Val Phe Thr Gly Val Gln				
215	220	225		
aat ttc agc agg atc cat ctg gtg gac aaa tgg aac gga ctc agc aag	776			
Asn Phe Ser Arg Ile His Leu Val Asp Lys Trp Asn Gly Leu Ser Lys				
230	235	240		
atc gat tat tgg cat tca gag cag tgt aac atg atc aat ggg act tcc	824			
Ile Asp Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly Thr Ser				
245	250	255		
ggg cag atg tgg gca ccc ttc atg aca ccc gaa tcc tcg ctg gaa ttc	872			
Gly Gln Met Trp Ala Pro Phe Met Thr Pro Glu Ser Ser Leu Glu Phe				
260	265	270		
ttc agc ccg gag gca tgc agg tcc atg aag ctg acc tac aac gaa tca	920			

Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr Asn Glu Ser	
275	280
agg gtg ttt gaa ggc att ccc acg tat cgc ttc acg gcc ccc gat act	968
Arg Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro Asp Thr	
295	300
ctg ttt gcc aac ggg tcc gtc tac cca ccc aac gaa ggc ttc tgc cca	1016
Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe Cys Pro	
310	315
tgc cga gag tct ggc att cag aat gtc agc acc tgc agg ttt ggt gcg	1064
Cys Arg Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe Gly Ala	
325	330
cct ctg ttt ctc tcc cac ccc cac ttt tac aac gcc gac cct gtg ttg	1112
Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro Val Leu	
340	345
tca gaa gct gtt ctt ggt ctg aac cct aac cca aag gag cat tcc ttg	1160
Ser Glu Ala Val Leu Gly Leu Asn Pro Asn Pro Lys Glu His Ser Leu	
355	360
ttc cta gac atc cat ccg gtc act ggg atc ccc atg aac tgt tct gtg	1208
Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys Ser Val	
375	380
aag atg cag ctg agc ctc tac atc aaa tct gtc aag ggc atc ggg caa	1256
Lys Met Gln Leu Ser Leu Tyr Ile Lys Ser Val Lys Gly Ile Gly Gln	
390	395
aca ggg aag atc gag cca gta gtt ctg ccg ttg ctg tgg ttc gaa cag	1304
Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe Glu Gln	
405	410
agc gga gca atg ggt ggc aag ccc ctg agc acg ttc tac acg cag ctg	1352
Ser Gly Ala Met Gly Gly Lys Pro Leu Ser Thr Phe Tyr Thr Gln Leu	
420	425
	430

gtg ctg atg ccc cag gtt ctt cac tac gcg cag tat gtg ctg ctg ggg 1400
 Val Leu Met Pro Gln Val Leu His Tyr Ala Gln Tyr Val Leu Leu Gly
 435 440 445 450
 ctt gga ggc ctc ctg ttg ctg gtg ccc atc atc tgc caa ctg cgc agc 1448
 Leu Gly Gly Leu Leu Leu Leu Val Pro Ile Ile Cys Gln Leu Arg Ser
 455 460 465
 cag gag aaa tgc ttt ttg ttt tgg agt ggt agt aaa aag ggc tcc cag 1496
 Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly Ser Gln
 470 475 480
 gat aag gag gcc att cag gcc tac tct gag tcc ctg atg tca cca gct 1544
 Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser Pro Ala
 485 490 495
 gcc aag ggc acg gtg ctg caa gaa gcc aag cta tag ggtcctgaag 1590
 Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu
 500 505 510
 acactataag ccccccaaac ctgatagctt ggtcagacca gccacccagt ccctacaccc 1650
 cgcttcttga ggactctctc agcggacagc ccaccagtgc catggcctga gccccagat 1710
 gtcacacctg tccgcacgca cggcacatgg atgccacgc atgtgcaaaa acaactcagg 1770
 gaccagggac agacc 1785

<210> 202

<211> 509

<212> PRT

<213> Mus musculus

<400> 202

Met Gly Gly Ser Ser Arg Ala Arg Trp Val Ala Leu Gly Leu Gly Ala

1

5

10

15

Leu Gly Leu Leu Phe Ala Ala Leu Gly Val Val Met Ile Leu Met Val

	20	25	30
Pro Ser Leu Ile Lys Gln Gln Val Leu Lys Asn Val Arg Ile Asp Pro			
35	40	45	
Ser Ser Leu Ser Phe Gly Met Trp Lys Glu Ile Pro Val Pro Phe Tyr			
50	55	60	
Leu Ser Val Tyr Phe Phe Glu Val Val Asn Pro Asn Glu Val Leu Asn			
65	70	75	80
Gly Gln Lys Pro Val Val Arg Glu Arg Gly Pro Tyr Val Tyr Arg Glu			
85	90	95	
Phe Arg Gln Lys Val Asn Ile Thr Phe Asn Asp Asn Asp Thr Val Ser			
100	105	110	
Phe Val Glu Asn Arg Ser Leu His Phe Gln Pro Asp Lys Ser His Gly			
115	120	125	
Ser Glu Ser Asp Tyr Ile Val Leu Pro Asn Ile Leu Val Leu Gly Gly			
130	135	140	
Ser Ile Leu Met Glu Ser Lys Pro Val Ser Leu Lys Leu Met Met Thr			
145	150	155	160
Leu Ala Leu Val Thr Met Gly Gln Arg Ala Phe Met Asn Arg Thr Val			
165	170	175	
Gly Glu Ile Leu Trp Gly Tyr Asp Asp Pro Phe Val His Phe Leu Asn			
180	185	190	
Thr Tyr Leu Pro Asp Met Leu Pro Ile Lys Gly Lys Phe Gly Leu Phe			
195	200	205	
Val Gly Met Asn Asn Ser Asn Ser Gly Val Phe Thr Val Phe Thr Gly			
210	215	220	
Val Gln Asn Phe Ser Arg Ile His Leu Val Asp Lys Trp Asn Gly Leu			
225	230	235	240
Ser Lys Ile Asp Tyr Trp His Ser Glu Gln Cys Asn Met Ile Asn Gly			
245	250	255	

Thr Ser Gly Gln Met Trp Ala Pro Phe Met Thr Pro Glu Ser Ser Leu
 260 265 270
 Glu Phe Phe Ser Pro Glu Ala Cys Arg Ser Met Lys Leu Thr Tyr Asn
 275 280 285
 Glu Ser Arg Val Phe Glu Gly Ile Pro Thr Tyr Arg Phe Thr Ala Pro
 290 295 300
 Asp Thr Leu Phe Ala Asn Gly Ser Val Tyr Pro Pro Asn Glu Gly Phe
 305 310 315 320
 Cys Pro Cys Arg Glu Ser Gly Ile Gln Asn Val Ser Thr Cys Arg Phe
 325 330 335
 Gly Ala Pro Leu Phe Leu Ser His Pro His Phe Tyr Asn Ala Asp Pro
 340 345 350
 Val Leu Ser Glu Ala Val Leu Gly Leu Asn Pro Asn Pro Lys Glu His
 355 360 365
 Ser Leu Phe Leu Asp Ile His Pro Val Thr Gly Ile Pro Met Asn Cys
 370 375 380
 Ser Val Lys Met Gln Leu Ser Leu Tyr Ile Lys Ser Val Lys Gly Ile
 385 390 395 400
 Gly Gln Thr Gly Lys Ile Glu Pro Val Val Leu Pro Leu Leu Trp Phe
 405 410 415
 Glu Gln Ser Gly Ala Met Gly Gly Lys Pro Leu Ser Thr Phe Tyr Thr
 420 425 430
 Gln Leu Val Leu Met Pro Gln Val Leu His Tyr Ala Gln Tyr Val Leu
 435 440 445
 Leu Gly Leu Gly Gly Leu Leu Leu Leu Val Pro Ile Ile Cys Gln Leu
 450 455 460
 Arg Ser Gln Glu Lys Cys Phe Leu Phe Trp Ser Gly Ser Lys Lys Gly
 465 470 475 480
 Ser Gln Asp Lys Glu Ala Ile Gln Ala Tyr Ser Glu Ser Leu Met Ser

485 490 495
 Pro Ala Ala Lys Gly Thr Val Leu Gln Glu Ala Lys Leu
 500 505

<210> 203

<211> 1714

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (267).. (1451)

<400> 203

ctcatgtaat attgtctttt ccagctctgt ccattttacat gcaaattgta tgatctcatt 60
 tttcttttatg gctgaataaa attctagtgt atatgtagca gcttttcggt ccatccgtct 120
 atgcagacat ccaggctgac actgtttccct tgcttgctcg cgctttcctc gcggatcgaa 180
 gagactctag ctacagcctg tggctgggaa gggagacgga ggccgcagct cagggaaagt 240
 gaagctgcag tagtagcagt aggaag atg tcg ggc gaa gac gag cag cag gag 293

Met Ser Gly Glu Asp Glu Gln Gln Glu

1

5

caa act atc gcc gag gac ctg gtc gtg acc aag tat aag atg ggg ggc 341

Gln Thr Ile Ala Glu Asp Leu Val Val Thr Lys Tyr Lys Met Gly Gly

10

15

20

25

gac atc gcc aac cgg gtg ctt cga tct ttg gtg gag gct tcc agc tca 389

Asp Ile Ala Asn Arg Val Leu Arg Ser Leu Val Glu Ala Ser Ser Ser

30

35

40

ggg gtg tct gtg ctg agc ttg tgt gag aaa ggt gat gcc atg att atg 437

Gly Val Ser Val Leu Ser Leu Cys Glu Lys Gly Asp Ala Met Ile Met

45	50	55	
gaa gag aca ggg aag atc ttc aag aag gaa aag gag atg aag aaa ggt			485
Glu Glu Thr Gly Lys Ile Phe Lys Lys Glu Lys Glu Met Lys Lys Gly			
60	65	70	
att gcc ttt cct acc agc att tcc gta aat aac tgt gtg tgt cac ttc			533
Ile Ala Phe Pro Thr Ser Ile Ser Val Asn Asn Cys Val Cys His Phe			
75	80	85	
tcc cct ttg aag agt gac cag gac tat ata ctc aag gaa ggt gac ttg			581
Ser Pro Leu Lys Ser Asp Gln Asp Tyr Ile Leu Lys Glu Gly Asp Leu			
90	95	100	105
gta aaa att gac ctt ggg gtt cat gtg gat ggc ttc att gcc aat gtg			629
Val Lys Ile Asp Leu Gly Val His Val Asp Gly Phe Ile Ala Asn Val			
110	115	120	
gct cac act ttt gta att ggt gta gct cag ggg acc cag gta aca ggg			677
Ala His Thr Phe Val Ile Gly Val Ala Gln Gly Thr Gln Val Thr Gly			
125	130	135	
cgg aaa gca gat gtc att aag gcc gct cac cta tgt gct gaa gct gcc			725
Arg Lys Ala Asp Val Ile Lys Ala Ala His Leu Cys Ala Glu Ala Ala			
140	145	150	
tta cga ctg gtc aaa cct gga aac cag aac aca caa gtg act gaa gca			773
Leu Arg Leu Val Lys Pro Gly Asn Gln Asn Thr Gln Val Thr Glu Ala			
155	160	165	
tgg aac aag gtt gct cac tca ttt aac tgc aca cca ata gaa ggt atg			821
Trp Asn Lys Val Ala His Ser Phe Asn Cys Thr Pro Ile Glu Gly Met			
170	175	180	185
ctg tca cac caa ttg aag cag cat gtg att gat gga gag aag acg att			869
Leu Ser His Gln Leu Lys Gln His Val Ile Asp Gly Glu Lys Thr Ile			
190	195	200	
atc cag aac cct aca gac cag cag aag aag gac cat gaa aag gca gaa			917

Ile Gln Asn Pro Thr Asp Gln Gln Lys Lys Asp His Glu Lys Ala Glu
 205 210 215
 ttt gag gtg cat gag gtt tat gct gta gat gtc ctc gtc agc tca gga 965
 Phe Glu Val His Glu Val Tyr Ala Val Asp Val Leu Val Ser Ser Gly
 220 225 230
 gaa ggc aag gcc aaa gat gca gga cag aga acc acc atc tac aag cga 1013
 Glu Gly Lys Ala Lys Asp Ala Gly Gln Arg Thr Thr Ile Tyr Lys Arg
 235 240 245
 gac ccc tct aaa caa tat ggc ctg aaa atg aaa act tca cgt gcc ttt 1061
 Asp Pro Ser Lys Gln Tyr Gly Leu Lys Met Lys Thr Ser Arg Ala Phe
 250 255 260 265
 ttc agt gag gtg gaa cgg cgt ttt gat gcc atg ccg ttt act tta aga 1109
 Phe Ser Glu Val Glu Arg Arg Phe Asp Ala Met Pro Phe Thr Leu Arg
 270 275 280
 gca ttt gaa gat gag aag aag gct cga atg ggt gtg gta gag tgt gcc 1157
 Ala Phe Glu Asp Glu Lys Lys Ala Arg Met Gly Val Val Glu Cys Ala
 285 290 295
 aaa cat gag tta cta cag cca ttt aac gtt ctc tat gag aag gag ggt 1205
 Lys His Glu Leu Leu Gln Pro Phe Asn Val Leu Tyr Glu Lys Glu Gly
 300 305 310
 gaa ttt gtt gcc cag ttt aaa ttt aca gtt cta ctc atg ccc aac ggc 1253
 Glu Phe Val Ala Gln Phe Lys Phe Thr Val Leu Leu Met Pro Asn Gly
 315 320 325
 ccc atg cgg ata acc agt ggt ccc ttt gag cct gac ctg tac aag tct 1301
 Pro Met Arg Ile Thr Ser Gly Pro Phe Glu Pro Asp Leu Tyr Lys Ser
 330 335 340 345
 gag atg gag gtt caa gat gca gag ctg aag gct ctt ctc cag agt tct 1349
 Glu Met Glu Val Gln Asp Ala Glu Leu Lys Ala Leu Leu Gln Ser Ser
 350 355 360

gca agt aga aaa acc cag aaa aag aag aaa aag aag gcc tcc aag act 1397
 Ala Ser Arg Lys Thr Gln Lys Lys Lys Lys Lys Lys Ala Ser Lys Thr

365

370

375

gta gag aat gcc acc agt gga gaa acc tta gaa gag aat gga gct ggg 1445
 Val Glu Asn Ala Thr Ser Gly Glu Thr Leu Glu Glu Asn Gly Ala Gly

380

385

390

gac tga ggtgggtccc ctccccagct tgtcattcct gcctcacccc ctccccaccgc 1501
 Asp

395

accccaggct ctgtcaagtc gagttcgtct tctccacca agactaccag cagagcgggg 1561
 ggctttcagc cctcatcccg gtccccaacc caccaccca ctcttttcaa caaaaaacca 1621
 gctccgactg actcigggtg tgggaggcca ggcttccag ccaccgaaga ctacttttag 1681
 tagaaaagaa attgaataat aaaatcagga gtc 1714

<210> 204

<211> 394

<212> PRT

<213> Mus musculus

<400> 204

Met Ser Gly Glu Asp Glu Gln Gln Glu Gln Thr Ile Ala Glu Asp Leu

1

5

10

15

Val Val Thr Lys Tyr Lys Met Gly Gly Asp Ile Ala Asn Arg Val Leu

20

25

30

Arg Ser Leu Val Glu Ala Ser Ser Ser Gly Val Ser Val Leu Ser Leu

35

40

45

Cys Glu Lys Gly Asp Ala Met Ile Met Glu Glu Thr Gly Lys Ile Phe

50

55

60

Lys Lys Glu Lys Glu Met Lys Lys Gly Ile Ala Phe Pro Thr Ser Ile

65	70	75	80
Ser Val Asn Asn Cys Val Cys His Phe Ser Pro Leu Lys Ser Asp Gln			
	85	90	95
Asp Tyr Ile Leu Lys Glu Gly Asp Leu Val Lys Ile Asp Leu Gly Val			
	100	105	110
His Val Asp Gly Phe Ile Ala Asn Val Ala His Thr Phe Val Ile Gly			
	115	120	125
Val Ala Gln Gly Thr Gln Val Thr Gly Arg Lys Ala Asp Val Ile Lys			
	130	135	140
Ala Ala His Leu Cys Ala Glu Ala Ala Leu Arg Leu Val Lys Pro Gly			
145	150	155	160
Asn Gln Asn Thr Gln Val Thr Glu Ala Trp Asn Lys Val Ala His Ser			
	165	170	175
Phe Asn Cys Thr Pro Ile Glu Gly Met Leu Ser His Gln Leu Lys Gln			
	180	185	190
His Val Ile Asp Gly Glu Lys Thr Ile Ile Gln Asn Pro Thr Asp Gln			
	195	200	205
Gln Lys Lys Asp His Glu Lys Ala Glu Phe Glu Val His Glu Val Tyr			
	210	215	220
Ala Val Asp Val Leu Val Ser Ser Gly Glu Gly Lys Ala Lys Asp Ala			
225	230	235	240
Gly Gln Arg Thr Thr Ile Tyr Lys Arg Asp Pro Ser Lys Gln Tyr Gly			
	245	250	255
Leu Lys Met Lys Thr Ser Arg Ala Phe Phe Ser Glu Val Glu Arg Arg			
	260	265	270
Phe Asp Ala Met Pro Phe Thr Leu Arg Ala Phe Glu Asp Glu Lys Lys			
	275	280	285
Ala Arg Met Gly Val Val Glu Cys Ala Lys His Glu Leu Leu Gln Pro			
	290	295	300

Phe Asn Val Leu Tyr Glu Lys Glu Gly Glu Phe Val Ala Gln Phe Lys
 305 310 315 320
 Phe Thr Val Leu Leu Met Pro Asn Gly Pro Met Arg Ile Thr Ser Gly
 325 330 335
 Pro Phe Glu Pro Asp Leu Tyr Lys Ser Glu Met Glu Val Gln Asp Ala
 340 345 350
 Glu Leu Lys Ala Leu Leu Gln Ser Ser Ala Ser Arg Lys Thr Gln Lys
 355 360 365
 Lys Lys Lys Lys Lys Ala Ser Lys Thr Val Glu Asn Ala Thr Ser Gly
 370 375 380
 Glu Thr Leu Glu Glu Asn Gly Ala Gly Asp
 385 390

<210> 205

<211> 512

<212> DNA

<213> Mus musculus

<400> 205

ctggggctta tcttcatgaa aggcaacacc atcaccgaga ctgaggtctg ggacttcctg 60
 cgacggctcg gagtgtaccc cactaagaaa cacttaattt ttggcgaccc aaagaaactc 120
 attaccgaag actttgtgcg gcacgtact tggagtaccg gaggataccc cacaccgatac 180
 ctgtggacta tgaattacag tggggcccgc gaaccaacct ggaaaccagc aagatgaaag 240
 ttcttaagtt tgtggccaaa gtccataacc aggaccccaa agactggccc acacaatact 300
 gcgaggcttt ggcagatgag gagagtaggg ctagacctgc aactgctagt gcccagcca 360
 catcctcttg aactcittga gttatggctt gagggactct ggagatccag tataaaagaa 420
 cagggggaat gggggtcgga ggaagcittga ttctgctacg cataaaggcc ttggagcggt 480
 aggatgtgtt gcagggtttt ttgtttgatt tt 512

<210> 206

<211> 961

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (90).. (605)

<400> 206

gctcccggga aacgaatgag gaaccacctc ctccctgctgt tcaagtacag gggcctgggtg 60
 cgcaaaggga agaaaagcaa aagacgaaa atg gct aaa ttt aag atc cgt cca 113

Met Ala Lys Phe Lys Ile Arg Pro

1

5

gcc act gcc tct gac tgc agt gac atc ctg cga ctg atc aag gaa ctg 161
 Ala Thr Ala Ser Asp Cys Ser Asp Ile Leu Arg Leu Ile Lys Glu Leu

10

15

20

gct aaa tat gaa tac atg gaa gat caa gtc att tta act gag aaa gat 209
 Ala Lys Tyr Glu Tyr Met Glu Asp Gln Val Ile Leu Thr Glu Lys Asp

25

30

35

40

ctc caa gag gat ggc ttt gga gaa cac ccc ttc tac cac tgc ctg gtt 257
 Leu Gln Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Val

45

50

55

gca gaa gtg cct aaa gag cac tgg acc cct gaa gga cat agc att gtt 305
 Ala Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly His Ser Ile Val

60

65

70

ggg ttc gcc atg tac tat ttt acc tat gac cca tgg att ggc aag ttg 353
 Gly Phe Ala Met Tyr Tyr Phe Thr Tyr Asp Pro Trp Ile Gly Lys Leu

75

80

85

ctg tat ctt gaa gac ttc ttc gtg atg agt gat tac aga ggc ttt ggt 401
 Leu Tyr Leu Glu Asp Phe Phe Val Met Ser Asp Tyr Arg Gly Phe Gly

90

95

100

ata gga tca gaa att ttg aag aat cta agc cag gtt gcc atg aag tgt 449

Ile Gly Ser Glu Ile Leu Lys Asn Leu Ser Gln Val Ala Met Lys Cys

105

110

115

120

cgc tgc agc agt atg cac ttc ttg gta gca gaa tgg aat gaa cca tct 497

Arg Cys Ser Ser Met His Phe Leu Val Ala Glu Trp Asn Glu Pro Ser

125

130

135

atc aac ttc tac aaa aga aga ggt gct tgc gat ctg tcc agt gaa gag 545

Ile Asn Phe Tyr Lys Arg Arg Gly Ala Ser Asp Leu Ser Ser Glu Glu

140

145

150

gga tgg agg ctc ttc aag att gac aaa gag tac ttg cta aaa atg gca 593

Gly Trp Arg Leu Phe Lys Ile Asp Lys Glu Tyr Leu Leu Lys Met Ala

155

160

165

gca gag gag tga ggcgtgccgg ttagacaat gacaacctcc attgtgcttt 645

Ala Glu Glu

170

agaataattc tcagcttccc ttgctttcta tcttgttgt agtgaaataa tagagcgagc 705

accattcca aagctttatt accagtgcg ttgttgcag ttgaaattc ggtctgttta 765

aagtggcagt catgtatgtg gtttgaggc agaattcttg aacatctttt gatgaagaac 825

aaggtggtat gatcttacta tataagaaaa acaaaacttc attcttgtga gtcatttaaa 885

tgtgtacaat gtacacactg gtacttagag ttctgtttt gattcttttt ttttaataa 945

actcgtcttt tgattt 961

<210> 207

<211> 171

<212> PRT

<213> Mus musculus

<400> 207

Met Ala Lys Phe Lys Ile Arg Pro Ala Thr Ala Ser Asp Cys Ser Asp
 1 5 10 15
 Ile Leu Arg Leu Ile Lys Glu Leu Ala Lys Tyr Glu Tyr Met Glu Asp
 20 25 30
 Gln Val Ile Leu Thr Glu Lys Asp Leu Gln Glu Asp Gly Phe Gly Glu
 35 40 45
 His Pro Phe Tyr His Cys Leu Val Ala Glu Val Pro Lys Glu His Trp
 50 55 60
 Thr Pro Glu Gly His Ser Ile Val Gly Phe Ala Met Tyr Tyr Phe Thr
 65 70 75 80
 Tyr Asp Pro Trp Ile Gly Lys Leu Leu Tyr Leu Glu Asp Phe Phe Val
 85 90 95
 Met Ser Asp Tyr Arg Gly Phe Gly Ile Gly Ser Glu Ile Leu Lys Asn
 100 105 110
 Leu Ser Gln Val Ala Met Lys Cys Arg Cys Ser Ser Met His Phe Leu
 115 120 125
 Val Ala Glu Trp Asn Glu Pro Ser Ile Asn Phe Tyr Lys Arg Arg Gly
 130 135 140
 Ala Ser Asp Leu Ser Ser Glu Glu Gly Trp Arg Leu Phe Lys Ile Asp
 145 150 155 160
 Lys Glu Tyr Leu Leu Lys Met Ala Ala Glu Glu
 165 170

<210> 208

<211> 2740

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (54).. (791)

<400> 208

```

ggtcgagccg cgtccgtgtg ccgccaccca ctccggacac agaatatcca gtt atg      56
                                                    Met
                                                    1
gat aaa aat gag ctg gtg cag aag gcc aag ctg gcc gag cag gca gag      104
Asp Lys Asn Glu Leu Val Gln Lys Ala Lys Leu Ala Glu Gln Ala Glu
           5                10                15
cga tat gat gac atg gca gcc tgc atg aag tct gtc act gag cag gga      152
Arg Tyr Asp Asp Met Ala Ala Cys Met Lys Ser Val Thr Glu Gln Gly
           20                25                30
gct gag ctg tcg aat gag gag aga aac ctt ctc tct gtt gct tat aaa      200
Ala Glu Leu Ser Asn Glu Glu Arg Asn Leu Leu Ser Val Ala Tyr Lys
           35                40                45
aac gtt gta gga gcc cgt agg tca tcg tgg agg gtc gtc tca agt att      248
Asn Val Val Gly Ala Arg Arg Ser Ser Trp Arg Val Val Ser Ser Ile
           50                55                60                65
gag cag aag acg gaa ggt gct gag aaa aag cag cag atg gct cga gaa      296
Glu Gln Lys Thr Glu Gly Ala Glu Lys Lys Gln Gln Met Ala Arg Glu
           70                75                80
tac aga gag aag atc gag acg gag ctg cgt gac atc tgc aac gat gta      344
Tyr Arg Glu Lys Ile Glu Thr Glu Leu Arg Asp Ile Cys Asn Asp Val
           85                90                95
ctg tct ctt ttg gaa aag ttc ttg atc ccc aat gct tcg caa cca gaa      392
Leu Ser Leu Leu Glu Lys Phe Leu Ile Pro Asn Ala Ser Gln Pro Glu

```

100	105	110	
agc aaa gtc ttc tat ttg aaa atg aag ggt gac tac tac cgt tac ttg			440
Ser Lys Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr Arg Tyr Leu			
115	120	125	
gcc gag gtt gct gct ggt gat gac aag aaa gga att gtg gac cag tca			488
Ala Glu Val Ala Ala Gly Asp Asp Lys Lys Gly Ile Val Asp Gln Ser			
130	135	140	145
cag caa gca tac caa gaa gca ttt gaa atc agc aaa aag gag atg cag			536
Gln Gln Ala Tyr Gln Glu Ala Phe Glu Ile Ser Lys Lys Glu Met Gln			
150	155	160	
ccg aca cac ccc atc aga ctg ggt ctg gcc ctc aac ttc tct gtg ttc			584
Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val Phe			
165	170	175	
tat tac gag atc ctg aac tcc cca gag aaa gcc tgc tct ctt gca aaa			632
Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Lys Ala Cys Ser Leu Ala Lys			
180	185	190	
aca gct ttc gat gaa gcc att gct gaa ctt gat aca tta agt gaa gag			680
Thr Ala Phe Asp Glu Ala Ile Ala Glu Leu Asp Thr Leu Ser Glu Glu			
195	200	205	
tcg tac aaa gac agc acg cta ata atg cag tta ctg aga gac aac tta			728
Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn Leu			
210	215	220	225
aca ttg tgg aca tcg gat acc caa gga gat gaa gca gaa gca gga gaa			776
Thr Leu Trp Thr Ser Asp Thr Gln Gly Asp Glu Ala Glu Ala Gly Glu			
230	235	240	
gga ggg gaa aat taa ccggccttcc aacctttgtc tgcctcattc taaaatttac			831
Gly Gly Glu Asn			
245			
acagtagacc atttgtcatc catgctgtcc cacagatagt ttttttgitt acgatttatg			891

acaggtttat gttacttcta tttgaatttc tatatttccc atgtggtttt tatgttttaa 951
tattaggga gtagagccag ttaacttttag ggagttactc attttcatct tgaggtagcc 1011
aatatgggat giggaatttt tacatgagtt acacatgttt ggcataglac ttttggtaca 1071
ttgtggcttc agaaggcca gtgttaaac tgcctccatg tctaagcaaa gaaaactgcc 1131
tacata ttgg tgtgtgctgg cggggaataa tcaggataat gggtccagt catgagtgt 1191
gtctttgtgg gtactgtaag ggctggagca ctgtgaggc tgtgacacaa acacctgtg 1251
gatgcacgt aggatcgtgt gtgtctgctg gcacactctt gaccacagct ccagaagttg 1311
tctctagaca aagtcgtgac ccaatttact ctggttaagg cagaaacgg tccattcca 1371
ttatttgtaa agttacctgc tgtttgcttt cattattttt gctacacatt ttatttgtat 1431
ttaaagtgtt taggcaatct aagaacaaat gtaaaagtaa agatgcagta aaaacgagtt 1491
gtttggtgtg cccggctcca tacgtatcaa gcacagcgg aaacaaaatc ccatgtattt 1551
aactttttct tttttttttt ttttttttaa agtttttgg tttgtttgt ttttgctttt 1611
gtgatttttt ttttttcttt tggatacttg cctaacatgc atgtgctgta aaaatagtta 1671
acagggaat aacttgagat gacggctagc tttgttttaa tgtcttaaga aattttcatg 1731
aacaatccaa gcataattgt taagaacaca tgtattaaag ttcatgtaag tggaataaaa 1791
gttttatgaa tggacttttc aactactttt ctctacagct ttcatgttaa attagtcttt 1851
tggttttgag acttctccaa aaggaaattg tctccttatt cctcttggc agctaattgg 1911
cttttacc aa ttttgaatgc agagtttata ataaaaaaaa aaaaaccgct aatgtagctt 1971
ccatcctcag ccacctcca cattttccc ttactcctca acaattgaag tggactttta 2031
tggggtgggg ggtgattgcc aaaaggtaat gtgttcatt tataattttg gtctatggag 2091
ttttctaact taggaagcca caatgttctt ggcccatgtg actgacactg ggcagcatta 2151
actgttaagt tctgtgcttc caagtcgtg ttggttttaa gaatttcctg atgctcttac 2211
agtctgctg ggattctatt cctctatttc catgttgggc acaggctcac ttccctttta 2271
ctgtctgtc accaaccatt ccaacttgg ggccatgtat ttgggaaaag ggccgcatga 2331
tctttctggc tccactcagt gtctaagata cccgctccc ctgcttgct cccacagcct 2391
cccccatcc tctctacagc ccagctgcc tcagttgagc ttgtgtttat ctccctggaa 2451
gtcctgccct aaatggctg tcaccgtct cctttaaaat ccttccctc cctcttctc 2511
ctctctctc tctcacata atgatggggc taagtcacac ccaaagctca caccctaccg 2571
agtatttct cagtactta cagaaaacac caaacaaaa tgccatttta caagagggtg 2631

attttttttt cttttagaat gtaagctcgt ctagagacag gggcaatgtt ttctgtatgt 2691
 tctattgtgc ctagtacact gtaaagctc aataaatatt gatgatggg 2740

<210> 209

<211> 245

<212> PRT

<213> Mus musculus

<400> 209

Met	Asp	Lys	Asn	Glu	Leu	Val	Gln	Lys	Ala	Lys	Leu	Ala	Glu	Gln	Ala
1				5					10					15	
Glu	Arg	Tyr	Asp	Asp	Met	Ala	Ala	Cys	Met	Lys	Ser	Val	Thr	Glu	Gln
				20					25					30	
Gly	Ala	Glu	Leu	Ser	Asn	Glu	Glu	Arg	Asn	Leu	Leu	Ser	Val	Ala	Tyr
				35					40					45	
Lys	Asn	Val	Val	Gly	Ala	Arg	Arg	Ser	Ser	Trp	Arg	Val	Val	Ser	Ser
				50					55					60	
Ile	Glu	Gln	Lys	Thr	Glu	Gly	Ala	Glu	Lys	Lys	Gln	Gln	Met	Ala	Arg
				65					70					75	
Glu	Tyr	Arg	Glu	Lys	Ile	Glu	Thr	Glu	Leu	Arg	Asp	Ile	Cys	Asn	Asp
				85					90					95	
Val	Leu	Ser	Leu	Leu	Glu	Lys	Phe	Leu	Ile	Pro	Asn	Ala	Ser	Gln	Pro
				100					105					110	
Glu	Ser	Lys	Val	Phe	Tyr	Leu	Lys	Met	Lys	Gly	Asp	Tyr	Tyr	Arg	Tyr
				115					120					125	
Leu	Ala	Glu	Val	Ala	Ala	Gly	Asp	Asp	Lys	Lys	Gly	Ile	Val	Asp	Gln
				130					135					140	
Ser	Gln	Gln	Ala	Tyr	Gln	Glu	Ala	Phe	Glu	Ile	Ser	Lys	Lys	Glu	Met
				145					150					155	
															160

Gln Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe Ser Val
 165 170 175
 Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Lys Ala Cys Ser Leu Ala
 180 185 190
 Lys Thr Ala Phe Asp Glu Ala Ile Ala Glu Leu Asp Thr Leu Ser Glu
 195 200 205
 Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg Asp Asn
 210 215 220
 Leu Thr Leu Trp Thr Ser Asp Thr Gln Gly Asp Glu Ala Glu Ala Gly
 225 230 235 240
 Glu Gly Gly Glu Asn.
 245

<210> 210

<211> 2643

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (148).. (1518)

<400> 210

gtccggcgcg cggtgagcg accgagcgtg cggacggagc ggcggcctgc tggcgggct 60
 gagcggcgcg cgcggcggcg gagagacgcg gagcgaggga cgcggcggcg gcggacgcgg 120
 cgacaggict tctacttaca aaggaca atg act act gat gag ggc acc agt aac 174
 Met Thr Thr Asp Glu Gly Thr Ser Asn

1

5

aat gga gag aac cca gca gcc acc atg act gag cag ggt gaa gat atc 222

Asn Gly Glu Asn Pro Ala Ala Thr Met Thr Glu Gln Gly Glu Asp Ile
 10 15 20 25
 act acg aag aaa gac aga gga gta tta aag att gtc aaa aga gtg ggg 270
 Thr Thr Lys Lys Asp Arg Gly Val Leu Lys Ile Val Lys Arg Val Gly
 30 35 40
 act agt gac gag gcc cca atg ttt ggt gac aaa gtt tat gtc cac tac 318
 Thr Ser Asp Glu Ala Pro Met Phe Gly Asp Lys Val Tyr Val His Tyr
 45 50 55
 aaa ggg atg ttg tca gat gga aag aag ttt gat tcc agt cat gac aga 366
 Lys Gly Met Leu Ser Asp Gly Lys Lys Phe Asp Ser Ser His Asp Arg
 60 65 70
 aag aag cca ttt gcc ttt agc ctt ggc caa ggc cag gtt atc aaa gcc 414
 Lys Lys Pro Phe Ala Phe Ser Leu Gly Gln Gly Gln Val Ile Lys Ala
 75 80 85
 tgg gac att ggg gtg tct act atg aag aaa ggc gag atc tgc cat tta 462
 Trp Asp Ile Gly Val Ser Thr Met Lys Lys Gly Glu Ile Cys His Leu
 90 95 100 105
 tta tgt aaa cca gaa tat gct tat ggc tcg gct ggc cac ctc caa aaa 510
 Leu Cys Lys Pro Glu Tyr Ala Tyr Gly Ser Ala Gly His Leu Gln Lys
 110 115 120
 att cca tca aat gca act ctc ttt ttt gag att gag ctc ctt gat ttc 558
 Ile Pro Ser Asn Ala Thr Leu Phe Phe Glu Ile Glu Leu Leu Asp Phe
 125 130 135
 aaa ggt gag gat tta ttt gaa gat tca ggc gtt atc cgt aga atc aaa 606
 Lys Gly Glu Asp Leu Phe Glu Asp Ser Gly Val Ile Arg Arg Ile Lys
 140 145 150
 cgg aaa ggc gag gga tac tca aac cca aac gaa gga gca acg gta aaa 654
 Arg Lys Gly Glu Gly Tyr Ser Asn Pro Asn Glu Gly Ala Thr Val Lys
 155 160 165

gtc cac ctg gaa ggc tgc tgt ggt gga agg aca ttt gat tgc cga gat	702
Val His Leu Glu Gly Cys Cys Gly Gly Arg Thr Phe Asp Cys Arg Asp	
170 175 180 185	
gtg gtg ttc gtt gtt ggg gaa gga gaa gac cac gac att ccg att ggg	750
Val Val Phe Val Val Gly Glu Gly Glu Asp His Asp Ile Pro Ile Gly	
190 195 200	
atc gac aaa gcc ctg gtg aag atg cag aga gaa gaa cag tgt att cta	798
Ile Asp Lys Ala Leu Val Lys Met Gln Arg Glu Glu Gln Cys Ile Leu	
205 210 215	
tat ctt gga cca cgc tat ggt ttt gga gaa gcc ggg aag cct aag ttt	846
Tyr Leu Gly Pro Arg Tyr Gly Phe Gly Glu Ala Gly Lys Pro Lys Phe	
220 225 230	
ggc att gac ccc aat gct gag ctt atg tac gag gtc acc ctt aag agc	894
Gly Ile Asp Pro Asn Ala Glu Leu Met Tyr Glu Val Thr Leu Lys Ser	
235 240 245	
ttc gag aag gcc aaa gaa tct tgg gag atg gac acc aaa gaa aag ctg	942
Phe Glu Lys Ala Lys Glu Ser Trp Glu Met Asp Thr Lys Glu Lys Leu	
250 255 260 265	
acg cag gct gcc atc gtg aaa gag aag gga act gtg tac ttc aag gga	990
Thr Gln Ala Ala Ile Val Lys Glu Lys Gly Thr Val Tyr Phe Lys Gly	
270 275 280	
ggc aag tac acg cag gcc gtg att cag tac agg aag ata gtg tcc tgg	1038
Gly Lys Tyr Thr Gln Ala Val Ile Gln Tyr Arg Lys Ile Val Ser Trp	
285 290 295	
ctg gag atg gaa tac ggc ctg tca gag aag gag tcc aaa gcc tca gag	1086
Leu Glu Met Glu Tyr Gly Leu Ser Glu Lys Glu Ser Lys Ala Ser Glu	
300 305 310	
tcg ttc ctc ctc gca gcc ttc ctg aac ctg gcc atg tgc tac ctg aag	1134
Ser Phe Leu Leu Ala Ala Phe Leu Asn Leu Ala Met Cys Tyr Leu Lys	

315	320	325	
ctc cga gag tac aac aaa gcc gtg gag tgc tgc gac aag gcc ctt gga			1182
Leu Arg Glu Tyr Asn Lys Ala Val Glu Cys Cys Asp Lys Ala Leu Gly			
330	335	340	345
ctg gac agt gcc aat gag aaa ggc ttg tac aga agg ggc gag gcc cag			1230
Leu Asp Ser Ala Asn Glu Lys Gly Leu Tyr Arg Arg Gly Glu Ala Gln			
	350	355	360
ctg ctc atg aat gac ttt gag tgc gcc aag ggc gac ttc gag aag gtg			1278
Leu Leu Met Asn Asp Phe Glu Ser Ala Lys Gly Asp Phe Glu Lys Val			
	365	370	375
ttg gca gtc aat cct cag aac agg gcc gct cgc ctg cag atc tcc atg			1326
Leu Ala Val Asn Pro Gln Asn Arg Ala Ala Arg Leu Gln Ile Ser Met			
	380	385	390
tgc cag agg aag gcg aag gag cac aac gag cgg gac cgc agg gtg tac			1374
Cys Gln Arg Lys Ala Lys Glu His Asn Glu Arg Asp Arg Arg Val Tyr			
	395	400	405
gcc aac atg ttc aag aag ttc gca gag cgg gac gca aag gag gaa gcc			1422
Ala Asn Met Phe Lys Lys Phe Ala Glu Arg Asp Ala Lys Glu Glu Ala			
410	415	420	425
agc aaa gct ggg agc aag aag gct gta gaa gga gcc gct ggc aaa caa			1470
Ser Lys Ala Gly Ser Lys Lys Ala Val Glu Gly Ala Ala Gly Lys Gln			
	430	435	440
cac gag agt cag gcc atg gaa gaa gga aag gcc aaa ggc cat gta tga			1518
His Glu Ser Gln Ala Met Glu Glu Gly Lys Ala Lys Gly His Val			
	445	450	455
cgctgcgcca cggagggaag agagtcctaa tgaactcggc cctcctcgct gggctcgcct			1578
ccaactcagg actgaacagt gtttagtgta aggtttgtta cagtctctgt gattctggaa			1638
gcaaatggca taccagtagc ttcccaaagt accacctgct gctgcggggg ggtgggggtg			1698
ggggacatgc caggaaacag cagagaaggc cgctgggtgig aagagaccag gccagcagct			1758

cagtccagcc catttcagtt tgtcaccttt cagtgtccag cacagcatcc ctgtgaacct 1818
 agggcccagc tgctgtgggt tctacatcgg cactagggtc acactgcaga aaccgttgat 1878
 aaaacaaact cagtgatctc tgctttccta ttgggtgggca tggcaggggc gggtagatgag 1938
 atttgccttag cactgactga ctggcctgct aagaacacaa gcccacagcc aggggctccc 1998
 tgggccacag ctgggtctca ggcccccttac ctgccctcca agtcctttcg cagactcttg 2058
 agtgtggcctt tctgtcctag ccagcatgtc ccacagactc tgttgttctt ccaacgcccc 2118
 tcattagtga cagctttctc tctgagtttc tgtgggtgtg agagtgggta gaagtaggtt 2178
 tatctttccc gctgtctgcc ccactcaagg acgatgttag cgctcagcca tccctgcccc 2238
 gcacagctgc tcagcctcat gctcccaccc gcacccttgc tgtgcagaac ctaaggcttg 2298
 ctcccgtccc agactcgagt ggacggacat ccatgtccac ccaggattga cgaaggaagg 2358
 aacttcacac tcctctatca tgcaaaaata gttttcaatt ttacttttt agcttggggtt 2418
 ttgaaaggca aactctagga ggcttaaaac gggcagttac tcttaaggcg aggtagatac 2478
 ctcaccttgc accgcagcct ctgtattctg gtgggagctg taagggttgc gggcttcggg 2538
 tgtccatgca tcaagccaaa gtctccaaaa ctggggcatt gaattagggc aaatcttaaa 2598
 tagttttggg gttggatttt agtcctacag gtgatgattg aacgt 2643

<210> 211

<211> 456

<212> PRT

<213> Mus musculus

<400> 211

Met	Thr	Thr	Asp	Glu	Gly	Thr	Ser	Asn	Asn	Gly	Glu	Asn	Pro	Ala	Ala
1					5					10				15	
Thr	Met	Thr	Glu	Gln	Gly	Glu	Asp	Ile	Thr	Thr	Lys	Lys	Asp	Arg	Gly
				20						25				30	
Val	Leu	Lys	Ile	Val	Lys	Arg	Val	Gly	Thr	Ser	Asp	Glu	Ala	Pro	Met
				35						40				45	
Phe	Gly	Asp	Lys	Val	Tyr	Val	His	Tyr	Lys	Gly	Met	Leu	Ser	Asp	Gly

50	55	60
Lys Lys Phe Asp Ser Ser His Asp Arg Lys Lys Pro Phe Ala Phe Ser		
65	70	75
Leu Gly Gln Gly Gln Val Ile Lys Ala Trp Asp Ile Gly Val Ser Thr		
	85	90
Met Lys Lys Gly Glu Ile Cys His Leu Leu Cys Lys Pro Glu Tyr Ala		
	100	105
Tyr Gly Ser Ala Gly His Leu Gln Lys Ile Pro Ser Asn Ala Thr Leu		
	115	120
Phe Phe Glu Ile Glu Leu Leu Asp Phe Lys Gly Glu Asp Leu Phe Glu		
	130	135
Asp Ser Gly Val Ile Arg Arg Ile Lys Arg Lys Gly Glu Gly Tyr Ser		
145	150	155
Asn Pro Asn Glu Gly Ala Thr Val Lys Val His Leu Glu Gly Cys Cys		
	165	170
Gly Gly Arg Thr Phe Asp Cys Arg Asp Val Val Phe Val Val Gly Glu		
	180	185
Gly Glu Asp His Asp Ile Pro Ile Gly Ile Asp Lys Ala Leu Val Lys		
	195	200
Met Gln Arg Glu Glu Gln Cys Ile Leu Tyr Leu Gly Pro Arg Tyr Gly		
	210	215
Phe Gly Glu Ala Gly Lys Pro Lys Phe Gly Ile Asp Pro Asn Ala Glu		
225	230	235
Leu Met Tyr Glu Val Thr Leu Lys Ser Phe Glu Lys Ala Lys Glu Ser		
	245	250
Trp Glu Met Asp Thr Lys Glu Lys Leu Thr Gln Ala Ala Ile Val Lys		
	260	265
Glu Lys Gly Thr Val Tyr Phe Lys Gly Gly Lys Tyr Thr Gln Ala Val		
	275	280
		285

Ile Gln Tyr Arg Lys Ile Val Ser Trp Leu Glu Met Glu Tyr Gly Leu
 290 295 300
 Ser Glu Lys Glu Ser Lys Ala Ser Glu Ser Phe Leu Leu Ala Ala Phe
 305 310 315 320
 Leu Asn Leu Ala Met Cys Tyr Leu Lys Leu Arg Glu Tyr Asn Lys Ala
 325 330 335
 Val Glu Cys Cys Asp Lys Ala Leu Gly Leu Asp Ser Ala Asn Glu Lys
 340 345 350
 Gly Leu Tyr Arg Arg Gly Glu Ala Gln Leu Leu Met Asn Asp Phe Glu
 355 360 365
 Ser Ala Lys Gly Asp Phe Glu Lys Val Leu Ala Val Asn Pro Gln Asn
 370 375 380
 Arg Ala Ala Arg Leu Gln Ile Ser Met Cys Gln Arg Lys Ala Lys Glu
 385 390 395 400
 His Asn Glu Arg Asp Arg Arg Val Tyr Ala Asn Met Phe Lys Lys Phe
 405 410 415
 Ala Glu Arg Asp Ala Lys Glu Glu Ala Ser Lys Ala Gly Ser Lys Lys
 420 425 430
 Ala Val Glu Gly Ala Ala Gly Lys Gln His Glu Ser Gln Ala Met Glu
 435 440 445
 Glu Gly Lys Ala Lys Gly His Val
 450 455

<210> 212

<211> 510

<212> DNA

<213> Mus musculus

<400> 212

ctggatgaacg agtggttcgta cagggctatg agaagggccca gccagatgag gagctcaagc 60
 ccaagaagaa agtctttgag aagctgcagg ccgactttta aatttctgag gagtgcatcg 120
 cacagtggaa gcaaaccaac ttcatgacca agctgggatt cgctcctgt aaatcactaa 180
 aagggggtaa catcagctag ccagctctgt gccctccac catcccgctt gccggctcga 240
 cttgttgcat ctctcaccgg ttccaacaag gtctgaactg ctgacaaggt gcaggacttg 300
 gaaagggaca gcttcacatt cctactgggtg tgggatcacc cagcctgggt gaaaggaaac 360
 ggattgcctg ggctaaggag atgctgcccc gcgcagactg gccctacatt ctcccttgg 420
 cagctgactt gagaaatctg gtttcaatag aaccacagaa aaagtttatt ccatgggtccc 480
 tgtaatggga aaaacactgg ttcccaagtt 510

<210> 213

<211> 405

<212> DNA

<213> Mus musculus

<400> 213

tgtgtaatgc cctcaacagc ttgtctgaaa accagtcatt gctgaggatg cccccctggg 60
 agaatatctg gctcgtgggc tccatctgct tgtccatgtc acttcacttc ttgatcctct 120
 acgtggaacc ttgtccgctc attttccaga tcacaccgct gaatctggac ccagtgtctg 180
 tgcttctgaa aattctcctt gctgggtgaat ccaatgatga gacgcttaag ttgttggtccc 240
 gaactaccta gaacaaccgg caatactgga gtaacggctt ctaaaccatg tgcagagata 300
 ttaggtgttc gggccgtga tgtgcgttgt tagcaacat tgacaagccc tctgatgact 360
 gaggtttggg gaaagagaag tgaaacagtt cccaattact gtgtg 405

<210> 214

<211> 489

<212> DNA

<213> Mus musculus

<400> 214

```

gtcgtcctag gagaagacaa gaagaaatit aaaacacgtt caggigaaac tgtgcgcctt 60
atggacctgc tggaagaagg gctgaaacgg tccatggaca agctaaagga gaaagagaga 120
gacaaggctt taactgaaga ggaattgaaa gcagctcaga catccgttgc atatggctgc 180
atcaaatacg ccgaccttgc tcataatcgc ctcaatgact acatcttctc ctttgacaag 240
atgctggaig acagagggaa cacagctgct tacctactgt atgccttcac cagaatcagg 300
tctattgcgc gcctcgccaa cattgatgag gcgatgctac agagagccgc tcgggaaacc 360
aagatcattt tggaccatga aaaggagtgg aagctggggc ggigcatctt acggttcccc 420
gagatcctcc agaagatctt agacgacctg tttctccaca cctctgtga ctacatttac 480
gagctggca                                         489

```

<210> 215

<211> 886

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (20).. (835)

<400> 215

```

tgtgagggct tcccggaag atg gtg ctg att aag gaa ttc cgt gtg gtt ttg 52
      Met Val Leu Ile Lys Glu Phe Arg Val Val Leu
              1              5              10
ccg tgt tct gtt caa gag tat cag gtt gga cag ctt tac tct gtt gca 100
Pro Cys Ser Val Gln Glu Tyr Gln Val Gly Gln Leu Tyr Ser Val Ala
              15              20              25
gaa gcg agt aag aat gaa act ggt ggt gga gaa gga atc gaa gtc ctg 148
Glu Ala Ser Lys Asn Glu Thr Gly Gly Gly Glu Gly Ile Glu Val Leu

```

30	35	40	
aag aat gaa cct tac gaa aac gat ggc gag aag gga cag tac aca cac			196
Lys Asn Glu Pro Tyr Glu Asn Asp Gly Glu Lys Gly Gln Tyr Thr His			
45	50	55	
aaa atc tac cac ctg aag agc aaa gtt cct gca ttt gtg agg atg att			244
Lys Ile Tyr His Leu Lys Ser Lys Val Pro Ala Phe Val Arg Met Ile			
60	65	70	75
gct ccg gag ggc tcc ctg gtg ttt cat gag aaa gcc tgg aat gcc tac			292
Ala Pro Glu Gly Ser Leu Val Phe His Glu Lys Ala Trp Asn Ala Tyr			
80	85	90	
ccc tac tgc aga aca att gta acg aat gaa tac atg aaa gat gac ttc			340
Pro Tyr Cys Arg Thr Ile Val Thr Asn Glu Tyr Met Lys Asp Asp Phe			
95	100	105	
ttc atc aaa att gaa aca tgg cac aaa cct gac ttg gga aca tta gaa			388
Phe Ile Lys Ile Glu Thr Trp His Lys Pro Asp Leu Gly Thr Leu Glu			
110	115	120	
aat gtt cac ggt tta gat ccc aac act tgg aaa act gtt gaa ata gtc			436
Asn Val His Gly Leu Asp Pro Asn Thr Trp Lys Thr Val Glu Ile Val			
125	130	135	
cac ata gac att gca gat cga agt caa gtt gaa cca gca gac tac aaa			484
His Ile Asp Ile Ala Asp Arg Ser Gln Val Glu Pro Ala Asp Tyr Lys			
140	145	150	155
gct gat gaa gac cct gca tta ttc cat tca gtc aag acc aag aga gga			532
Ala Asp Glu Asp Pro Ala Leu Phe His Ser Val Lys Thr Lys Arg Gly			
160	165	170	
ccc ctg gga cct aac tgg aag aag gag ctg gca aac acc cct gac tgt			580
Pro Leu Gly Pro Asn Trp Lys Lys Glu Leu Ala Asn Thr Pro Asp Cys			
175	180	185	
cct agg atg tgt gcc tat aag ctg gtg acc atc aag ttc aag tgg tgg			628

Pro Arg Met Cys Ala Tyr Lys Leu Val Thr Ile Lys Phe Lys Trp Trp
 190 195 200
 ggg ctg cag agc aaa gta gag aac ttt atc cag aag caa gaa aaa cgg 676
 Gly Leu Gln Ser Lys Val Glu Asn Phe Ile Gln Lys Gln Glu Lys Arg
 205 210 215
 ata ttt acg aac tta cat cgc cag ctc ttt tgt tgg att gac aag tgg 724
 Ile Phe Thr Asn Leu His Arg Gln Leu Phe Cys Trp Ile Asp Lys Trp
 220 225 230 235
 att gac ctg aca atg gaa gac att agg cga atg gag gat gag act cag 772
 Ile Asp Leu Thr Met Glu Asp Ile Arg Arg Met Glu Asp Glu Thr Gln
 240 245 250
 aaa gaa cta gaa aca atg cgt aag aag ggt tcc gtc cga ggc acg tcg 820
 Lys Glu Leu Glu Thr Met Arg Lys Lys Gly Ser Val Arg Gly Thr Ser
 255 260 265
 gct gct gat gcc tag atgagcccct gtaggtcaga gacattatca gactgtctac 875
 Ala Ala Asp Ala
 270
 ggagtcaagg c 886

<210> 216

<211> 271

<212> PRT

<213> Mus musculus

<400> 216

Met Val Leu Ile Lys Glu Phe Arg Val Val Leu Pro Cys Ser Val Gln

1

5

10

15

Glu Tyr Gln Val Gly Gln Leu Tyr Ser Val Ala Glu Ala Ser Lys Asn

20

25

30

Glu Thr Gly Gly Gly Glu Gly Ile Glu Val Leu Lys Asn Glu Pro Tyr
 35 40 45
 Glu Asn Asp Gly Glu Lys Gly Gln Tyr Thr His Lys Ile Tyr His Leu
 50 55 60
 Lys Ser Lys Val Pro Ala Phe Val Arg Met Ile Ala Pro Glu Gly Ser
 65 70 75 80
 Leu Val Phe His Glu Lys Ala Trp Asn Ala Tyr Pro Tyr Cys Arg Thr
 85 90 95
 Ile Val Thr Asn Glu Tyr Met Lys Asp Asp Phe Phe Ile Lys Ile Glu
 100 105 110
 Thr Trp His Lys Pro Asp Leu Gly Thr Leu Glu Asn Val His Gly Leu
 115 120 125
 Asp Pro Asn Thr Trp Lys Thr Val Glu Ile Val His Ile Asp Ile Ala
 130 135 140
 Asp Arg Ser Gln Val Glu Pro Ala Asp Tyr Lys Ala Asp Glu Asp Pro
 145 150 155 160
 Ala Leu Phe His Ser Val Lys Thr Lys Arg Gly Pro Leu Gly Pro Asn
 165 170 175
 Trp Lys Lys Glu Leu Ala Asn Thr Pro Asp Cys Pro Arg Met Cys Ala
 180 185 190
 Tyr Lys Leu Val Thr Ile Lys Phe Lys Trp Trp Gly Leu Gln Ser Lys
 195 200 205
 Val Glu Asn Phe Ile Gln Lys Gln Glu Lys Arg Ile Phe Thr Asn Leu
 210 215 220
 His Arg Gln Leu Phe Cys Trp Ile Asp Lys Trp Ile Asp Leu Thr Met
 225 230 235 240
 Glu Asp Ile Arg Arg Met Glu Asp Glu Thr Gln Lys Glu Leu Glu Thr
 245 250 255
 Met Arg Lys Lys Gly Ser Val Arg Gly Thr Ser Ala Ala Asp Ala

260

265

270

<210> 217

<211> 3652

<212> DNA

<213> Mus musculus:

<220>

<221> CDS

<222> (348).. (3119)

<400> 217

tttttttttt tttttttttt tttttttttt ttttctctcc ttctttcttct tcctgagaca 60
 tggcccgggc agtggctcct ggaagaggaa caagtgtggg aaaagggaga ggaaatcgga 120
 gctaaatgac aggatgcagg cgacttgaga cacaaaaaga gaagcgcttc tcgcgaattc 180
 aggcattgcc tcgccgctag ccttccccgc caagaccgcg tgaggatttt atggttctta 240
 ggccggactta agagcgcttc ggattgttaa gattatcggt tgctggtttt tcgtccgcgc 300
 aatcgtgttc tcctgcggct gcctggggac tggcttggcg aaggagg atg gag agg 356

Met Glu Arg

1

ggg ctg ccg ttg ctg tgc gcc acg ctc gcc ctt gcc ctc gcc ctg gcg 404
 Gly Leu Pro Leu Leu Cys Ala Thr Leu Ala Leu Ala Leu Ala

5

10

15

ggc gct ttc cgc agc gac aaa tgt ggc ggc acc ata aaa atc gaa aac 452
 Gly Ala Phe Arg Ser Asp Lys Cys Gly Gly Thr Ile Lys Ile Glu Asn

20

25

30

35

cca ggg tac ctc aca tct ccc ggt tac cct cat tct tac cat cca agt 500
 Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr His Pro Ser

40

45

50

gag aag tgt gaa tgg cta atc caa gct ccg gaa ccc tac cag aga atc 548
 Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr Gln Arg Ile
 55 60 65
 ata atc aac ttc aac cca cat ttc gat ttg gag gac aga gac tgc aag 596
 Ile Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg Asp Cys Lys
 70 75 80
 tat gac tac gtg gaa gta att gat ggg gag aat gaa ggc ggc cgc ctg 644
 Tyr Asp Tyr Val Glu Val Ile Asp Gly Glu Asn Glu Gly Gly Arg Leu
 85 90 95
 tgg ggg aag ttc tgt ggg aag att gca cct tct cct gtg gtg tct tca 692
 Trp Gly Lys Phe Cys Gly Lys Ile Ala Pro Ser Pro Val Val Ser Ser
 100 105 110 115
 ggg ccc ttt ctc ttc atc aaa ttt gtc tct gac tat gag aca cat ggg 740
 Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu Thr His Gly
 120 125 130
 gca ggg ttt tcc atc cgc tat gaa atc ttc aag aga ggg ccc gaa tgt 788
 Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly Pro Glu Cys
 135 140 145
 tct cag aac tat aca gca cct act gga gtg ata aag tcc cct ggg ttc 836
 Ser Gln Asn Tyr Thr Ala Pro Thr Gly Val Ile Lys Ser Pro Gly Phe
 150 155 160
 cct gaa aaa tac ccc aac tgc ttg gag tgc acc tac atc atc ttt gca 884
 Pro Glu Lys Tyr Pro Asn Cys Leu Glu Cys Thr Tyr Ile Ile Phe Ala
 165 170 175
 cca aag atg tct gag ata atc ctg gag ttt gaa agt ttt gac ctg gag 932
 Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe Asp Leu Glu
 180 185 190 195
 caa gac tcg aat cct ccc gga gga atg ttc tgt cgc tat gac cgg ctg 980
 Gln Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr Asp Arg Leu

200	205	210	
gag atc tgg gat gga ttc cct gaa gtt ggc cct cac att ggg cgt tat			1028
Glu Ile Trp Asp Gly Phe Pro Glu Val Gly Pro His Ile Gly Arg Tyr			
215	220	225	
tgt ggg cag aaa act cct ggc cgg atc cgc tcc tct tca ggc gtt cta			1076
Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser Gly Val Leu			
230	235	240	
tcc atg gtc ttt tac act gac agc gca ata gca aaa gaa ggt ttc tca			1124
Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu Gly Phe Ser			
245	250	255	
gcc aac tac agt gtg cta cag agc agc atc tct gaa gat ttt aag tgt			1172
Ala Asn Tyr Ser Val Leu Gln Ser Ser Ile Ser Glu Asp Phe Lys Cys			
260	265	270	275
atg gag gct ctg ggc atg gaa tct gga gag atc cat tct gat cag atc			1220
Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser Asp Gln Ile			
280	285	290	
act gca tct tca cag tat ggt acc aac tgg tct gta gag cgc tcc cgc			1268
Thr Ala Ser Ser Gln Tyr Gly Thr Asn Trp Ser Val Glu Arg Ser Arg			
295	300	305	
ctg aac tac cct gaa aat ggg tgg act cca gga gaa gac tcc tac aag			1316
Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp Ser Tyr Lys			
310	315	320	
gag tgg atc cag gtg gac ttg ggc ctc ctg cga ttc gtt act gct gta			1364
Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val Thr Ala Val			
325	330	335	
ggg aca cag ggt gcc att tcc aag gaa acc aag aag aaa tat tat gtc			1412
Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys Tyr Tyr Val			
340	345	350	355
aag act tac aga gta gac atc agc tcc aac gga gag gac tgg atc tcc			1460

Lys Thr Tyr Arg Val Asp Ile Ser Ser Asn Gly Glu Asp Trp Ile Ser
 360 365 370
 ctg aaa gag gga aat aaa gcc att atc ttt cag gga aac acc aac ccc 1508
 Leu Lys Glu Gly Asn Lys Ala Ile Ile Phe Gln Gly Asn Thr Asn Pro
 375 380 385
 aca gat gtt gtc tta gga gtt ttc tcc aaa cca ctg ata act cga ttt 1556
 Thr Asp Val Val Leu Gly Val Phe Ser Lys Pro Leu Ile Thr Arg Phe
 390 395 400
 gtc cga atc aaa cct gta tcc tgg gaa act ggt ata tct atg aga ttt 1604
 Val Arg Ile Lys Pro Val Ser Trp Glu Thr Gly Ile Ser Met Arg Phe
 405 410 415
 gaa gtt tat ggc tgc aag ata aca gat tat cct tgc tct gga atg ttg 1652
 Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser Gly Met Leu
 420 425 430 435
 ggc atg gtg tct gga ctt att tca gac tcc cag att aca gca tcc aat 1700
 Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr Ala Ser Asn
 440 445 450
 caa gcc gac agg aat tgg atg cca gaa aac atc cgt ctg gtg acc agt 1748
 Gln Ala Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu Val Thr Ser
 455 460 465
 cgt acc ggc tgg gca ctg cca ccc tca ccc cac cca tac acc aat gaa 1796
 Arg Thr Gly Trp Ala Leu Pro Pro Ser Pro His Pro Tyr Thr Asn Glu
 470 475 480
 tgg ctc caa gtg gac ctg gga gat gag aag ata gta aga ggt gtc atc 1844
 Trp Leu Gln Val Asp Leu Gly Asp Glu Lys Ile Val Arg Gly Val Ile
 485 490 495
 att cag ggt ggg aag cac cga gaa aac aag gtg ttc atg agg aag ttc 1892
 Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met Arg Lys Phe
 500 505 510 515

aag atc gcc tat agt aac aat ggc tct gac tgg aaa act atc atg gat 1940
Lys Ile Ala Tyr Ser Asn Asn Gly Ser Asp Trp Lys Thr Ile Met Asp
520 525 530
gac agc aag cgc aag gct aag tgc ttc gaa ggc aac aac aac tat gac 1988
Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn Asn Tyr Asp
535 540 545
aca cct gag ctt cgg acg ttt tca cct ctc tcc aca agg ttc atc agg 2036
Thr Pro Glu Leu Arg Thr Phe Ser Pro Leu Ser Thr Arg Phe Ile Arg
550 555 560
atc tac cct gag aga gcc aca cac agt ggg ctt ggg ctg agg atg gag 2084
Ile Tyr Pro Glu Arg Ala Thr His Ser Gly Leu Gly Leu Arg Met Glu
565 570 575
cta ctg ggc tgt gaa gtg gaa gca cct aca gct gga cca acc aca ccc 2132
Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro Thr Thr Pro
580 585 590 595
aat ggg aac cca gtg cat gag tgt gac gac gac cag gcc aac tgc cac 2180
Asn Gly Asn Pro Val His Glu Cys Asp Asp Asp Gln Ala Asn Cys His
600 605 610
agt ggc aca ggt gat gac ttc cag ctc aca gga ggc acc act gtc ctg 2228
Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr Thr Val Leu
615 620 625
gcc aca gag aag cca acc att ata gac agc acc atc caa tca gag ttc 2276
Ala Thr Glu Lys Pro Thr Ile Ile Asp Ser Thr Ile Gln Ser Glu Phe
630 635 640
ccg aca tac ggt ttt aac tgc gag ttt ggc tgg ggc tct cac aag aca 2324
Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser His Lys Thr
645 650 655
ttc tgc cac tgg gag cat gac agc cat gca cag ctc agg tgg agt gtg 2372
Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg Trp Ser Val

660	665	670	675	
ctg acc agc aag aca ggg ccg att cag gac cat aca gga gat ggc aac	2420			
Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly Asp Gly Asn				
680	685	690		
ttc atc tat tcc caa gct gat gaa aat cag aaa ggc aaa gta gcc cgc	2468			
Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys Val Ala Arg				
695	700	705		
ctg gtg agc cct gtg gtc tat tcc cag agc tct gcc cac tgt atg acc	2516			
Leu Val Ser Pro Val Val Tyr Ser Gln Ser Ser Ala His Cys Met Thr				
710	715	720		
ttc tgg tat cac atg tcc ggc tct cat gtg ggt aca ctg agg gtc aaa	2564			
Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu Arg Val Lys				
725	730	735		
cta cgc tac cag aag cca gag gaa tat gat caa ctg gtc tgg atg gtg	2612			
Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val Trp Met Val				
740	745	750	755	
gtt ggg cac caa gga gac cac tgg aaa gaa gga cgt gtc ttg ctg cac	2660			
Val Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val Leu Leu His				
760	765	770		
aaa tct ctg aaa cta tat cag gtt att ttt gaa ggt gaa atc gga aaa	2708			
Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu Ile Gly Lys				
775	780	785		
gga aac ctt ggt gga att gct gtg gat gat atc agt att aac aac cat	2756			
Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile Asn Asn His				
790	795	800		
att tct cag gaa gac tgt gca aaa cca aca gac cta gat aaa aag aac	2804			
Ile Ser Gln Glu Asp Cys Ala Lys Pro Thr Asp Leu Asp Lys Lys Asn				
805	810	815		
aca gaa att aaa att gat gaa aca ggg agc act cca gga tat gaa gga	2852			

Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly Tyr Glu Gly
 820 825 830 835
 gaa ggg gaa ggt gac aag aac atc tcc agg aag cca ggc aat gtg ctt 2900
 Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly Asn Val Leu
 840 845 850
 aag acc ctg gat ccc atc ctg atc acc atc ata gcc atg agt gcc ctg 2948
 Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met Ser Ala Leu
 855 860 865
 gga gta ctc ctg ggt gca gtc tgt gga gtt gtg ctg tac tgt gcc tgt 2996
 Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr Cys Ala Cys
 870 875 880
 tgg cac aat ggg atg tca gaa agg aac cta tct gcc ctg gag aac tat 3044
 Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu Glu Asn Tyr
 885 890 895
 aac ttt gaa ctt gtg gat ggt gta aag ttg aaa aaa gat aaa ctg aac 3092
 Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp Lys Leu Asn
 900 905 910 915
 cca cag agt aat tac tca gag gcg tga aggcacggag ctggagggaa 3139
 Pro Gln Ser Asn Tyr Ser Glu Ala
 920
 caagggagga gcacggcagg agaacaggtg gaggcattggg gactctgita ctctgctttc 3199
 actgtaagct gggaagggcg gggactctgt tactccgctt tcaactgtaag ctcggaaggg 3259
 catccacgat gccatgccag gcttttctca ggagcttcaa tgagcgtcac ctacagacac 3319
 aagcaggtga ctgcggtaac aacaggaatc atgtacaagc ctgctttctt ctcttggttt 3379
 catttgggtta atcagaagcc attttagacc aagtgtgact gacttcatgg ttcatcctac 3439
 tagccccctt ttttctctc tttctctta cctgtgggtg gattcttctc ggaaactgca 3499
 aaatccaaga tgctggcact aggcgttatt cagtgggccc ttttgatgga catgtgacct 3559
 gtagccagat gccagagca tattatcata accacatttc aggggacgcc aacgtccatc 3619
 caccittgca tcgtacctg cagcagcac agg 3652

<210> 218

<211> 923

<212> PRT

<213> Mus musculus

<400> 218

```

Met Glu Arg Gly Leu Pro Leu Leu Cys Ala Thr Leu Ala Leu Ala Leu
  1             5             10             15
Ala Leu Ala Gly Ala Phe Arg Ser Asp Lys Cys Gly Gly Thr Ile Lys
          20             25             30
Ile Glu Asn Pro Gly Tyr Leu Thr Ser Pro Gly Tyr Pro His Ser Tyr
      35             40             45
His Pro Ser Glu Lys Cys Glu Trp Leu Ile Gln Ala Pro Glu Pro Tyr
      50             55             60
Gln Arg Ile Ile Ile Asn Phe Asn Pro His Phe Asp Leu Glu Asp Arg
      65             70             75             80
Asp Cys Lys Tyr Asp Tyr Val Glu Val Ile Asp Gly Glu Asn Glu Gly
          85             90             95
Gly Arg Leu Trp Gly Lys Phe Cys Gly Lys Ile Ala Pro Ser Pro Val
          100             105             110
Val Ser Ser Gly Pro Phe Leu Phe Ile Lys Phe Val Ser Asp Tyr Glu
          115             120             125
Thr His Gly Ala Gly Phe Ser Ile Arg Tyr Glu Ile Phe Lys Arg Gly
      130             135             140
Pro Glu Cys Ser Gln Asn Tyr Thr Ala Pro Thr Gly Val Ile Lys Ser
      145             150             155             160
Pro Gly Phe Pro Glu Lys Tyr Pro Asn Cys Leu Glu Cys Thr Tyr Ile
          165             170             175

```

Ile Phe Ala Pro Lys Met Ser Glu Ile Ile Leu Glu Phe Glu Ser Phe
 180 185 190
 Asp Leu Glu Gln Asp Ser Asn Pro Pro Gly Gly Met Phe Cys Arg Tyr
 195 200 205
 Asp Arg Leu Glu Ile Trp Asp Gly Phe Pro Glu Val Gly Pro His Ile
 210 215 220
 Gly Arg Tyr Cys Gly Gln Lys Thr Pro Gly Arg Ile Arg Ser Ser Ser
 225 230 235 240
 Gly Val Leu Ser Met Val Phe Tyr Thr Asp Ser Ala Ile Ala Lys Glu
 245 250 255
 Gly Phe Ser Ala Asn Tyr Ser Val Leu Gln Ser Ser Ile Ser Glu Asp
 260 265 270
 Phe Lys Cys Met Glu Ala Leu Gly Met Glu Ser Gly Glu Ile His Ser
 275 280 285
 Asp Gln Ile Thr Ala Ser Ser Gln Tyr Gly Thr Asn Trp Ser Val Glu
 290 295 300
 Arg Ser Arg Leu Asn Tyr Pro Glu Asn Gly Trp Thr Pro Gly Glu Asp
 305 310 315 320
 Ser Tyr Lys Glu Trp Ile Gln Val Asp Leu Gly Leu Leu Arg Phe Val
 325 330 335
 Thr Ala Val Gly Thr Gln Gly Ala Ile Ser Lys Glu Thr Lys Lys Lys
 340 345 350
 Tyr Tyr Val Lys Thr Tyr Arg Val Asp Ile Ser Ser Asn Gly Glu Asp
 355 360 365
 Trp Ile Ser Leu Lys Glu Gly Asn Lys Ala Ile Ile Phe Gln Gly Asn
 370 375 380
 Thr Asn Pro Thr Asp Val Val Leu Gly Val Phe Ser Lys Pro Leu Ile
 385 390 395 400
 Thr Arg Phe Val Arg Ile Lys Pro Val Ser Trp Glu Thr Gly Ile Ser

405	410	415
Met Arg Phe Glu Val Tyr Gly Cys Lys Ile Thr Asp Tyr Pro Cys Ser		
420	425	430
Gly Met Leu Gly Met Val Ser Gly Leu Ile Ser Asp Ser Gln Ile Thr		
435	440	445
Ala Ser Asn Gln Ala Asp Arg Asn Trp Met Pro Glu Asn Ile Arg Leu		
450	455	460
Val Thr Ser Arg Thr Gly Trp Ala Leu Pro Pro Ser Pro His Pro Tyr		
465	470	475
Thr Asn Glu Trp Leu Gln Val Asp Leu Gly Asp Glu Lys Ile Val Arg		
485	490	495
Gly Val Ile Ile Gln Gly Gly Lys His Arg Glu Asn Lys Val Phe Met		
500	505	510
Arg Lys Phe Lys Ile Ala Tyr Ser Asn Asn Gly Ser Asp Trp Lys Thr		
515	520	525
Ile Met Asp Asp Ser Lys Arg Lys Ala Lys Ser Phe Glu Gly Asn Asn		
530	535	540
Asn Tyr Asp Thr Pro Glu Leu Arg Thr Phe Ser Pro Leu Ser Thr Arg		
545	550	555
Phe Ile Arg Ile Tyr Pro Glu Arg Ala Thr His Ser Gly Leu Gly Leu		
565	570	575
Arg Met Glu Leu Leu Gly Cys Glu Val Glu Ala Pro Thr Ala Gly Pro		
580	585	590
Thr Thr Pro Asn Gly Asn Pro Val His Glu Cys Asp Asp Asp Gln Ala		
595	600	605
Asn Cys His Ser Gly Thr Gly Asp Asp Phe Gln Leu Thr Gly Gly Thr		
610	615	620
Thr Val Leu Ala Thr Glu Lys Pro Thr Ile Ile Asp Ser Thr Ile Gln		
625	630	635
		640

Ser Glu Phe Pro Thr Tyr Gly Phe Asn Cys Glu Phe Gly Trp Gly Ser
 645 650 655
 His Lys Thr Phe Cys His Trp Glu His Asp Ser His Ala Gln Leu Arg
 660 665 670
 Trp Ser Val Leu Thr Ser Lys Thr Gly Pro Ile Gln Asp His Thr Gly
 675 680 685
 Asp Gly Asn Phe Ile Tyr Ser Gln Ala Asp Glu Asn Gln Lys Gly Lys
 690 695 700
 Val Ala Arg Leu Val Ser Pro Val Val Tyr Ser Gln Ser Ser Ala His
 705 710 715 720
 Cys Met Thr Phe Trp Tyr His Met Ser Gly Ser His Val Gly Thr Leu
 725 730 735
 Arg Val Lys Leu Arg Tyr Gln Lys Pro Glu Glu Tyr Asp Gln Leu Val
 740 745 750
 Trp Met Val Val Gly His Gln Gly Asp His Trp Lys Glu Gly Arg Val
 755 760 765
 Leu Leu His Lys Ser Leu Lys Leu Tyr Gln Val Ile Phe Glu Gly Glu
 770 775 780
 Ile Gly Lys Gly Asn Leu Gly Gly Ile Ala Val Asp Asp Ile Ser Ile
 785 790 795 800
 Asn Asn His Ile Ser Gln Glu Asp Cys Ala Lys Pro Thr Asp Leu Asp
 805 810 815
 Lys Lys Asn Thr Glu Ile Lys Ile Asp Glu Thr Gly Ser Thr Pro Gly
 820 825 830
 Tyr Glu Gly Glu Gly Glu Gly Asp Lys Asn Ile Ser Arg Lys Pro Gly
 835 840 845
 Asn Val Leu Lys Thr Leu Asp Pro Ile Leu Ile Thr Ile Ile Ala Met
 850 855 860
 Ser Ala Leu Gly Val Leu Leu Gly Ala Val Cys Gly Val Val Leu Tyr

865	870	875	880
Cys Ala Cys Trp His Asn Gly Met Ser Glu Arg Asn Leu Ser Ala Leu			
885	890	895	
Glu Asn Tyr Asn Phe Glu Leu Val Asp Gly Val Lys Leu Lys Lys Asp			
900	905	910	
Lys Leu Asn Pro Gln Ser Asn Tyr Ser Glu Ala			
915	920		

<210> 219

<211> 314

<212> DNA

<213> Mus musculus

<400> 219

```

agccatgggt ctgcatagga gcttcatgct ctcctctgtc cticggtcag cagtctctgt 60
gcatttgaag aggaacattg ttgttacagc tgtggcctgt aataagtaac ttgacccgtg 120
acagaaactc ttcgtggaca agataggaga ttacgaatcg aggcgacagg catcttgaga 180
acctgttgat agttgccag agtatcagca agatctggac agagagcttt gtaagcittaa 240
acaaatgtat ggtaagaaga gagatggata catttcctag cticagattt gatgatccca 300
gatttgaagt atcg

```

314

<210> 220

<211> 512

<212> DNA

<213> Mus musculus

<400> 220

```

ctggaacggt tcagacagtg ccattatgac ggggtcctac aacaacttct ttagaatgtt 60
tgatagaaac actcggaggg atgttacact ggaagcctca agagagaaca gcaaaccg 120

```

agccagCctg aagccccgga aagtatgtac agggggtaag agaaagaaag acgagattag 180
 cgtggacAgc ttggacttca ataagaagat cctccacaca gcctggcacc ccatggagag 240
 cattattgct gtagctgcc acaataactt gtatatattc caggacaaaa ttaattaaga 300
 aaactgactg gaggaccaag tgttgtcttg cataatgtacg ccggtcaatt agttttcctg 360
 tcaaaaaagg cattgtcctc tccattgaga atagtggcgc acttctactt ccctaataga 420
 tacaggagaa gaagggctct cagctggagt cggaagagat gagtgccgct gctgaaggga 480
 aaacctgctc gaagctgaat tggtaggactc tg 512

<210> 221

<211> 1710

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (202).. (1671)

<400> 221

gaggagccgc cgccttctcg tcgctcgagc tctggacgac catggtcgct caggccccgt 60
 ccgcggggcc tccgcgctcc ccgtgaaggg tcggaagatg cgcgggaagt agcagccgtc 120
 tgctgggcga gcgggagacc gaccggacac ccctggggga cctctcgga tcaccgcgct 180
 tctcctgcgg cctccaggcc a atg tgc aat acc aac atg tct gtg tct acc 231
 Met Cys Asn Thr Asn Met Ser Val Ser Thr
 1 5 10
 gag ggt gct gca agc acc tca cag att cca gct tcg gaa caa gag act 279
 Glu Gly Ala Ala Ser Thr Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr
 15 20 25
 ctg gtt aga cca aaa cca ttg ctt ttg aag ttg tta aag tcc gtt gga 327
 Leu Val Arg Pro Lys Pro Leu Leu Leu Lys Leu Leu Lys Ser Val Gly

30	35	40	
gcg caa aac gac act tac act atg aaa gag att ata ttt tat att ggc	375		
Ala Gln Asn Asp Thr Tyr Thr Met Lys Glu Ile Ile Phe Tyr Ile Gly			
45	50	55	
cag tat att atg act aag agg tta tat gac gag aag cag cag cac att	423		
Gln Tyr Ile Met Thr Lys Arg Leu Tyr Asp Glu Lys Gln Gln His Ile			
60	65	70	
gtg tat tgt tca aat gat ctc cta gga gat gtg ttt gga gtc ccg agt	471		
Val Tyr Cys Ser Asn Asp Leu Leu Gly Asp Val Phe Gly Val Pro Ser			
75	80	85	90
ttc tct gtg aag gag cac agg aaa ata tat gca atg atc tac aga aat	519		
Phe Ser Val Lys Glu His Arg Lys Ile Tyr Ala Met Ile Tyr Arg Asn			
95	100	105	
tta gtg gct gta agt cag caa gac tct ggc aca tcg ctg agt gag agc	567		
Leu Val Ala Val Ser Gln Gln Asp Ser Gly Thr Ser Leu Ser Glu Ser			
110	115	120	
aga cgt cag cct gaa ggt ggg agt gat ctg aag gat cct ttg caa gcg	615		
Arg Arg Gln Pro Glu Gly Gly Ser Asp Leu Lys Asp Pro Leu Gln Ala			
125	130	135	
cca cca gaa gag aaa cct tca tct tct gat tta att tct aga ctg tct	663		
Pro Pro Glu Glu Lys Pro Ser Ser Ser Asp Leu Ile Ser Arg Leu Ser			
140	145	150	
acc tca tct aga agg aga tcc att agt gag aca gaa gag aac aca gat	711		
Thr Ser Ser Arg Arg Arg Ser Ile Ser Glu Thr Glu Glu Asn Thr Asp			
155	160	165	170
gag cta cct ggg gag cgg cac cgg aag cgc cgc agg tcc ctg tcc ttt	759		
Glu Leu Pro Gly Glu Arg His Arg Lys Arg Arg Arg Ser Leu Ser Phe			
175	180	185	
gat ccg agc ctg ggt ctg tgt gag ctg agg gag atg tgc agc ggc ggc	807		

Asp Pro Ser Leu Gly Leu Cys Glu Leu Arg Glu Met Cys Ser Gly Gly
 190 195 200
 acg agc agc agt agc agc agc agc agc gag tcc aca gag acg ccc tcg 855
 Thr Ser Ser Ser Ser Ser Ser Ser Ser Glu Ser Thr Glu Thr Pro Ser
 205 210 215
 cat cag gat ctt gac gat ggc gta agt gag cat tct ggt gat tgc ctg 903
 His Gln Asp Leu Asp Asp Gly Val Ser Glu His Ser Gly Asp Cys Leu
 220 225 230
 gat cag gat tca gtt tct gat cag ttt agc gtg gaa ttt gaa gtt gag 951
 Asp Gln Asp Ser Val Ser Asp Gln Phe Ser Val Glu Phe Glu Val Glu
 235 240 245 250
 tct ctg gac tcg gaa gat tac agc ctg agt gac gaa ggg cac gag ctc 999
 Ser Leu Asp Ser Glu Asp Tyr Ser Leu Ser Asp Glu Gly His Glu Leu
 255 260 265
 tca gat gag gat gat gag gtc tat cgg gtc aca gtc tat cag aca gga 1047
 Ser Asp Glu Asp Asp Glu Val Tyr Arg Val Thr Val Tyr Gln Thr Gly
 270 275 280
 gaa agc gat aca gac tct ttt gaa gga gat cct gag att tcc tta gct 1095
 Glu Ser Asp Thr Asp Ser Phe Glu Gly Asp Pro Glu Ile Ser Leu Ala
 285 290 295
 gac tat tgg aag tgt acc tca tgc aat gaa atg aat cct ccc ctt cca 1143
 Asp Tyr Trp Lys Cys Thr Ser Cys Asn Glu Met Asn Pro Pro Leu Pro
 300 305 310
 tca cac tgc aaa aga tgc tgg acc ctt cgt gag aac tgg ctt cca gac 1191
 Ser His Cys Lys Arg Cys Trp Thr Leu Arg Glu Asn Trp Leu Pro Asp
 315 320 325 330
 gat aag ggg aaa gat aaa gtg gaa atc tct gaa aaa gcc aaa ctg gaa 1239
 Asp Lys Gly Lys Asp Lys Val Glu Ile Ser Glu Lys Ala Lys Leu Glu
 335 340 345

aac tca gct cag gca gaa gaa ggc ttg gat gtg cct gat ggc aaa aag 1287
 Asn Ser Ala Gln Ala Glu Glu Gly Leu Asp Val Pro Asp Gly Lys Lys
 350 355 360
 ctg aca gag aat gat gct aaa gag cca tgt gct gag gag gac agc gag 1335
 Leu Thr Glu Asn Asp Ala Lys Glu Pro Cys Ala Glu Glu Asp Ser Glu
 365 370 375
 gag aag gcc gaa cag acg ccc ctg tcc cag gag agt gac gac tat tcc 1383
 Glu Lys Ala Glu Gln Thr Pro Leu Ser Gln Glu Ser Asp Asp Tyr Ser
 380 385 390
 caa cca tcg act tcc agc agc att gtt tat agc agc caa gaa agc gtg 1431
 Gln Pro Ser Thr Ser Ser Ser Ile Val Tyr Ser Ser Gln Glu Ser Val
 395 400 405 410
 aaa gag ttg aag gag gaa acg cag cac aaa gac gag agt gtg gaa tct 1479
 Lys Glu Leu Lys Glu Glu Thr Gln His Lys Asp Glu Ser Val Glu Ser
 415 420 425
 agc ttc tcc ctg aat gcc atc gaa cca tgt gtg atc tgc cag ggg cgg 1527
 Ser Phe Ser Leu Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg
 430 435 440
 cct aaa aat ggc tgc att gtt cac ggc aag act gga cac ctc atg tca 1575
 Pro Lys Asn Gly Cys Ile Val His Gly Lys Thr Gly His Leu Met Ser
 445 450 455
 tgt ttc acg tgt gca aag aag cta aaa aaa aga aac aag ccc tgc cca 1623
 Cys Phe Thr Cys Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro
 460 465 470
 gtg tgc aga cag cca atc caa atg att gtg cta agt tac ttc aac tag 1671
 Val Cys Arg Gln Pro Ile Gln Met Ile Val Leu Ser Tyr Phe Asn
 475 480 485 490
 ctgacctgct cacaaaaata gaattttata tttctaact 1710

<210> 222

<211> 489

<212> PRT

<213> Mus musculus

<400> 222

Met Cys Asn Thr Asn Met Ser Val Ser Thr Glu Gly Ala Ala Ser Thr

1 5 10 15

Ser Gln Ile Pro Ala Ser Glu Gln Glu Thr Leu Val Arg Pro Lys Pro

20 25 30

Leu Leu Leu Lys Leu Leu Lys Ser Val Gly Ala Gln Asn Asp Thr Tyr

35 40 45

Thr Met Lys Glu Ile Ile Phe Tyr Ile Gly Gln Tyr Ile Met Thr Lys

50 55 60

Arg Leu Tyr Asp Glu Lys Gln Gln His Ile Val Tyr Cys Ser Asn Asp

65 70 75 80

Leu Leu Gly Asp Val Phe Gly Val Pro Ser Phe Ser Val Lys Glu His

85 90 95

Arg Lys Ile Tyr Ala Met Ile Tyr Arg Asn Leu Val Ala Val Ser Gln

100 105 110

Gln Asp Ser Gly Thr Ser Leu Ser Glu Ser Arg Arg Gln Pro Glu Gly

115 120 125

Gly Ser Asp Leu Lys Asp Pro Leu Gln Ala Pro Pro Glu Glu Lys Pro

130 135 140

Ser Ser Ser Asp Leu Ile Ser Arg Leu Ser Thr Ser Ser Arg Arg Arg

145 150 155 160

Ser Ile Ser Glu Thr Glu Glu Asn Thr Asp Glu Leu Pro Gly Glu Arg

165 170 175

His Arg Lys Arg Arg Arg Ser Leu Ser Phe Asp Pro Ser Leu Gly Leu

180	185	190
Cys Glu Leu Arg Glu Met Cys Ser Gly Gly Thr Ser Ser Ser Ser Ser		
195	200	205
Ser Ser Ser Glu Ser Thr Glu Thr Pro Ser His Gln Asp Leu Asp Asp		
210	215	220
Gly Val Ser Glu His Ser Gly Asp Cys Leu Asp Gln Asp Ser Val Ser		
225	230	235
Asp Gln Phe Ser Val Glu Phe Glu Val Glu Ser Leu Asp Ser Glu Asp		
245	250	255
Tyr Ser Leu Ser Asp Glu Gly His Glu Leu Ser Asp Glu Asp Asp Glu		
260	265	270
Val Tyr Arg Val Thr Val Tyr Gln Thr Gly Glu Ser Asp Thr Asp Ser		
275	280	285
Phe Glu Gly Asp Pro Glu Ile Ser Leu Ala Asp Tyr Trp Lys Cys Thr		
290	295	300
Ser Cys Asn Glu Met Asn Pro Pro Leu Pro Ser His Cys Lys Arg Cys		
305	310	315
Trp Thr Leu Arg Glu Asn Trp Leu Pro Asp Asp Lys Gly Lys Asp Lys		
325	330	335
Val Glu Ile Ser Glu Lys Ala Lys Leu Glu Asn Ser Ala Gln Ala Glu		
340	345	350
Glu Gly Leu Asp Val Pro Asp Gly Lys Lys Leu Thr Glu Asn Asp Ala		
355	360	365
Lys Glu Pro Cys Ala Glu Glu Asp Ser Glu Glu Lys Ala Glu Gln Thr		
370	375	380
Pro Leu Ser Gln Glu Ser Asp Asp Tyr Ser Gln Pro Ser Thr Ser Ser		
385	390	395
Ser Ile Val Tyr Ser Ser Gln Glu Ser Val Lys Glu Leu Lys Glu Glu		
405	410	415

Thr Gln His Lys Asp Glu Ser Val Glu Ser Ser Phe Ser Leu Asn Ala
 420 425 430
 Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly Cys Ile
 435 440 445
 Val His Gly Lys Thr Gly His Leu Met Ser Cys Phe Thr Cys Ala Lys
 450 455 460
 Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln Pro Ile
 465 470 475 480
 Gln Met Ile Val Leu Ser Tyr Phe Asn
 485

<210> 223

<211> 6734

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (126).. (5840)

<400> 223

ggtgccggga gcagcatgcg gagccgcag acgctgccc tctggacacc tcagcctgag 60
 gccctctcgt gattcacggg ggtaccatcc cccaccaggg cagaggctgg aggccactgc 120
 caagc atg gcg ccc acc tgg agt ccc agc gtg gtg tct gtg gtg ggt cct 170
 Met Ala Pro Thr Trp Ser Pro Ser Val Val Ser Val Val Gly Pro
 1 5 10 15
 gtg ggg ctc ttc ctc gta ctg ctg gcc aga gga tgc ttg gct gaa gaa 218
 Val Gly Leu Phe Leu Val Leu Leu Ala Arg Gly Cys Leu Ala Glu Glu
 20 25 30

```

cca ccc agg ttt atc aga gag ccc aag gat cag att gga gtg tgc gga 266
Pro Pro Arg Phe Ile Arg Glu Pro Lys Asp Gln Ile Gly Val Ser Gly
      35              40              45

ggc gtg gcc tcc ttc gtg tgc cag gcc acg ggt gat cct aag cca cgg 314
Gly Val Ala Ser Phe Val Cys Gln Ala Thr Gly Asp Pro Lys Pro Arg
      50              55              60

gtg acc tgg aac aag aag ggc aag aaa gtg aac tca cag cgc ttc gag 362
Val Thr Trp Asn Lys Lys Gly Lys Lys Val Asn Ser Gln Arg Phe Glu
      65              70              75

acc att gac ttt gac gag agc tct ggg gcg gtc ctg agg atc cag cca 410
Thr Ile Asp Phe Asp Glu Ser Ser Gly Ala Val Leu Arg Ile Gln Pro
      80              85              90              95

ctt cgg acg cct cgg gat gag aac gtg tac gag tgt gtg gcc cag aac 458
Leu Arg Thr Pro Arg Asp Glu Asn Val Tyr Glu Cys Val Ala Gln Asn
      100              105              110

tcg gtg ggc gaa atc aca att cat gca aag ctc acc gtc ctt cga gag 506
Ser Val Gly Glu Ile Thr Ile His Ala Lys Leu Thr Val Leu Arg Glu
      115              120              125

gac cag ctg cct cct ggc ttc ccc aac att gac atg ggc ccc cag ttg 554
Asp Gln Leu Pro Pro Gly Phe Pro Asn Ile Asp Met Gly Pro Gln Leu
      130              135              140

aag gtt gta gag cgc aca cgc aca gcc acc atg ctc tgt gct gcc agc 602
Lys Val Val Glu Arg Thr Arg Thr Ala Thr Met Leu Cys Ala Ala Ser
      145              150              155

ggg aac ccg gac cct gag atc acc tgg ttt aag gac ttc ctg cct gtg 650
Gly Asn Pro Asp Pro Glu Ile Thr Trp Phe Lys Asp Phe Leu Pro Val
      160              165              170              175

gac ccc agt gcc agc aac ggg cgg atc aag cag ctt cga tca ggt gcc 698
Asp Pro Ser Ala Ser Asn Gly Arg Ile Lys Gln Leu Arg Ser Gly Ala

```

	180	185	190	
ctg cag att gag agc agc gag gag aca gac cag ggc aag tac gag tgt				746
Leu Gln Ile Glu Ser Ser Glu Glu Thr Asp Gln Gly Lys Tyr Glu Cys				
	195	200	205	
gtg gcc acc aac agc gct ggg gtg cgc tac tca tca cct gcc aac ctc				794
Val Ala Thr Asn Ser Ala Gly Val Arg Tyr Ser Ser Pro Ala Asn Leu				
	210	215	220	
tac gtg cga gtc cgc cgt gtg gcc cca cgc ttc tcc atc ctg ccc atg				842
Tyr Val Arg Val Arg Arg Val Ala Pro Arg Phe Ser Ile Leu Pro Met				
	225	230	235	
agc cac gag atc atg ccc ggt ggg aat gtg aat atc act tgt gtg gcc				890
Ser His Glu Ile Met Pro Gly Gly Asn Val Asn Ile Thr Cys Val Ala				
	240	245	250	255
gtg ggc tca ccc atg ccc tac gtg aaa tgg atg cag ggc gcc gag gac				938
Val Gly Ser Pro Met Pro Tyr Val Lys Trp Met Gln Gly Ala Glu Asp				
	260	265	270	
ctg acg cct gag gat gac atg ccc gtg ggt cgg aat gtt cta gaa ctc				986
Leu Thr Pro Glu Asp Asp Met Pro Val Gly Arg Asn Val Leu Glu Leu				
	275	280	285	
acg gat gtc aag gac tca gct aac tac act tgt gtg gcc atg tcc agc				1034
Thr Asp Val Lys Asp Ser Ala Asn Tyr Thr Cys Val Ala Met Ser Ser				
	290	295	300	
ctg ggt gtg atc gag gcc gtg gcc cag atc act gta aaa tct ctc ccc				1082
Leu Gly Val Ile Glu Ala Val Ala Gln Ile Thr Val Lys Ser Leu Pro				
	305	310	315	
aaa gcc cct ggg act cct gtg gtg acg gag aac act gcc acc agt atc				1130
Lys Ala Pro Gly Thr Pro Val Val Thr Glu Asn Thr Ala Thr Ser Ile				
	320	325	330	335
act gtc aca tgg gac tcg ggc aac cct gac ccc gtg tcc tac tac gta				1178

Thr Val Thr Trp Asp Ser Gly Asn Pro Asp Pro Val Ser Tyr Tyr Val
 340 345 350
 att gag tat aag tcc aaa agc cag gat ggg ccg tat cag atc aaa gaa 1226
 Ile Glu Tyr Lys Ser Lys Ser Gln Asp Gly Pro Tyr Gln Ile Lys Glu
 355 360 365
 gac atc acc acc acg cgc tac agc atc gga ggc ctg agc ccc aat tct 1274
 Asp Ile Thr Thr Thr Arg Tyr Ser Ile Gly Gly Leu Ser Pro Asn Ser
 370 375 380
 gag tat gag atc tgg gtg tca gct gtc aac tcc att ggc cag ggc cct 1322
 Glu Tyr Glu Ile Trp Val Ser Ala Val Asn Ser Ile Gly Gln Gly Pro
 385 390 395
 ccc agt gaa tcg gtg gtg acc cgc aca ggt gag cag gca cca gcc agc 1370
 Pro Ser Glu Ser Val Val Thr Arg Thr Gly Glu Gln Ala Pro Ala Ser
 400 405 410 415
 gct ccc agg aat gtt cag gcc cgc atg ctc agc gcc acc acc atg atc 1418
 Ala Pro Arg Asn Val Gln Ala Arg Met Leu Ser Ala Thr Thr Met Ile
 420 425 430
 gtg cag tgg gag gag cct gtg gag ccc aat ggc ctg atc cgt ggc tac 1466
 Val Gln Trp Glu Glu Pro Val Glu Pro Asn Gly Leu Ile Arg Gly Tyr
 435 440 445
 cgt gtc tac tat acc atg gag ccg gaa cac cca gtg ggc aac tgg cag 1514
 Arg Val Tyr Tyr Thr Met Glu Pro Glu His Pro Val Gly Asn Trp Gln
 450 455 460
 aaa cac aat gtg gac gac agt ctc ctg acc act gtg ggc agc ctg ctg 1562
 Lys His Asn Val Asp Asp Ser Leu Leu Thr Thr Val Gly Ser Leu Leu
 465 470 475
 gaa gac gag acc tac acc gtg cgc gtg ctc gcc ttc acg tcg gtg ggc 1610
 Glu Asp Glu Thr Tyr Thr Val Arg Val Leu Ala Phe Thr Ser Val Gly
 480 485 490 495

gac gga cca ctg tca gac ccc atc cag gtc aag acc cag cag gga gtt 1658
 Asp Gly Pro Leu Ser Asp Pro Ile Gln Val Lys Thr Gln Gln Gly Val
 500 505 510
 cct ggc cag ccc atg aac ttg cgg gct gag gcc aag tca gag acc agc 1706
 Pro Gly Gln Pro Met Asn Leu Arg Ala Glu Ala Lys Ser Glu Thr Ser
 515 520 525
 att ggg ctc tcg tgg agt gca cca cga cag gag agt gtc att aag tat 1754
 Ile Gly Leu Ser Trp Ser Ala Pro Arg Gln Glu Ser Val Ile Lys Tyr
 530 535 540
 gaa ctg ctc ttc cgg gag ggc gac cga ggc cga gag gtg ggg cga acc 1802
 Glu Leu Leu Phe Arg Glu Gly Asp Arg Gly Arg Glu Val Gly Arg Thr
 545 550 555
 ttc gac cca acc aca gcc ttt gtg gtg gag gac ctc aag ccc aat acg 1850
 Phe Asp Pro Thr Thr Ala Phe Val Val Glu Asp Leu Lys Pro Asn Thr
 560 565 570 575
 gag tat gcg ttc cgg ctg gcg gcg cgc tcg ccg cag ggc ctg ggc gcc 1898
 Glu Tyr Ala Phe Arg Leu Ala Ala Arg Ser Pro Gln Gly Leu Gly Ala
 580 585 590
 ttc acc gcg gtc gtg cgc cag cgc acg ctg cag gcc aaa ccg tca gcc 1946
 Phe Thr Ala Val Val Arg Gln Arg Thr Leu Gln Ala Lys Pro Ser Ala
 595 600 605
 ccc cct caa gac gtt aag tgc acc agc ttg cgc tcc acg gcc ata ttg 1994
 Pro Pro Gln Asp Val Lys Cys Thr Ser Leu Arg Ser Thr Ala Ile Leu
 610 615 620
 gta agt tgg cgc ccg cca ccg cca gaa act cac aac ggg gcc ctc gtg 2042
 Val Ser Trp Arg Pro Pro Pro Pro Glu Thr His Asn Gly Ala Leu Val
 625 630 635
 ggc tac agc gtc cgc tac cga ccg ctg ggc tca gag gac ccg gac ccc 2090
 Gly Tyr Ser Val Arg Tyr Arg Pro Leu Gly Ser Glu Asp Pro Asp Pro

640	645	650	655	
aag gag gtg aac aac ata ccc ccg acc acc act cag atc ctt ctg gaa	2138			
Lys Glu Val Asn Asn Ile Pro Pro Thr Thr Thr Gln Ile Leu Leu Glu				
660	665	670		
gct ttg gag aaa tgg acg gag tac cgt gtc acc gcc gtg gct tac aca	2186			
Ala Leu Glu Lys Trp Thr Glu Tyr Arg Val Thr Ala Val Ala Tyr Thr				
675	680	685		
gag gtg gga cca ggg ccc gag agc tcg ccc gtg gtc gtc cgc acc gat	2234			
Glu Val Gly Pro Gly Pro Glu Ser Ser Pro Val Val Val Arg Thr Asp				
690	695	700		
gag gac gtg ccc agc gcg ccc ccg cgg aag gtg gag gcg gag gcg ctc	2282			
Glu Asp Val Pro Ser Ala Pro Pro Arg Lys Val Glu Ala Glu Ala Leu				
705	710	715		
aac gcc aca gcc atc cga gtg ctg tgg cgc tcg ccc acg ccc ggc cgg	2330			
Asn Ala Thr Ala Ile Arg Val Leu Trp Arg Ser Pro Thr Pro Gly Arg				
720	725	730	735	
cag cac ggg cag atc cgc ggc tac cag gtc cac tat gtg cgc atg gag	2378			
Gln His Gly Gln Ile Arg Gly Tyr Gln Val His Tyr Val Arg Met Glu				
740	745	750		
ggt gcc gag gcc cgc ggg cca ccg cgc atc aag gac atc atg ctg gcg	2426			
Gly Ala Glu Ala Arg Gly Pro Pro Arg Ile Lys Asp Ile Met Leu Ala				
755	760	765		
gat gcc cag gaa atg gtg ata acg aac ctc cag cct gag act gct tac	2474			
Asp Ala Gln Glu Met Val Ile Thr Asn Leu Gln Pro Glu Thr Ala Tyr				
770	775	780		
tct atc aca gta gcc gcg tat acc atg aaa ggc gat ggc gct cgc agc	2522			
Ser Ile Thr Val Ala Ala Tyr Thr Met Lys Gly Asp Gly Ala Arg Ser				
785	790	795		

```

aaa ccg aag gtg gtg gtg acc aag gga gca gtg ctg ggc cgc ccc acc 2570
Lys Pro Lys Val Val Val Thr Lys Gly Ala Val Leu Gly Arg Pro Thr
800          805          810          815
ctg tcg gtg cag cag acc ccc gag ggc agc ctg ctg gcg cgc tgg gag 2618
Leu Ser Val Gln Gln Thr Pro Glu Gly Ser Leu Leu Ala Arg Trp Glu
820          825          830
ccc ccc gcg gac gcg gcc gag gac ccg gtg ctt ggc tac cgc ctg cag 2666
Pro Pro Ala Asp Ala Ala Glu Asp Pro Val Leu Gly Tyr Arg Leu Gln
835          840          845
ttt ggg cgc gaa gac gcg gcc ccg gcc acg ttg gag ctg gct gcg tgg 2714
Phe Gly Arg Glu Asp Ala Ala Pro Ala Thr Leu Glu Leu Ala Ala Trp
850          855          860
gag cgg cgg ttc gcg gcg cct gca cac aag ggc gcc acc tat gtg ttc 2762
Glu Arg Arg Phe Ala Ala Pro Ala His Lys Gly Ala Thr Tyr Val Phe
865          870          875
cgg ctg gca gcg cgg ggc cgc gcg ggg ttg ggc gag gag gcc gcg gca 2810
Arg Leu Ala Ala Arg Gly Arg Ala Gly Leu Gly Glu Glu Ala Ala Ala
880          885          890          895
gcg ctg agc atc ccc gag gac gct ccg cgc ggc ttc ccg cag atc ttg 2858
Ala Leu Ser Ile Pro Glu Asp Ala Pro Arg Gly Phe Pro Gln Ile Leu
900          905          910
ggc gcc gcg ggc aac gtg tcc gcg ggc tcc gtg cta ctg cgc tgg ctg 2906
Gly Ala Ala Gly Asn Val Ser Ala Gly Ser Val Leu Leu Arg Trp Leu
915          920          925
cca ccc gtg ccc gcc gag cgc aac ggc gcc atc atc aag tac acg gtg 2954
Pro Pro Val Pro Ala Glu Arg Asn Gly Ala Ile Ile Lys Tyr Thr Val
930          935          940
tcc gtg cgg gag gcc ggc gcc cct ggg ccc gcg acc gag acg gag ctg 3002
Ser Val Arg Glu Ala Gly Ala Pro Gly Pro Ala Thr Glu Thr Glu Leu

```

945	950	955	
gcg gcg gcc gcc cag ccg ggg gcc gag aca gcg ctc acg ctg cga ggg	3050		
Ala Ala Ala Ala Gln Pro Gly Ala Glu Thr Ala Leu Thr Leu Arg Gly			
960	965	970	975
ctg cgg ccg gag acg gcc tac gag tta cgc gtg cgc gca cac acg cgt	3098		
Leu Arg Pro Glu Thr Ala Tyr Glu Leu Arg Val Arg Ala His Thr Arg			
980	985	990	
cgc ggc ccg ggc ccc ttc tca ccc ccg ctg cgc tac agg ctc gcg cgg	3146		
Arg Gly Pro Gly Pro Phe Ser Pro Pro Leu Arg Tyr Arg Leu Ala Arg			
995	1000	1005	
gac cca gtc tcc cca aag aac ttc aag gtg aag atg atc atg aag act	3194		
Asp Pro Val Ser Pro Lys Asn Phe Lys Val Lys Met Ile Met Lys Thr			
1010	1015	1020	
tca gtg ctg ctg agc tgg gag ttc ccc gac aac tat aac tca ccc aca	3242		
Ser Val Leu Leu Ser Trp Glu Phe Pro Asp Asn Tyr Asn Ser Pro Thr			
1025	1030	1035	
ccc tac aag att cag tac aat ggg ctc acc ctg gat gtg gac ggc cgc	3290		
Pro Tyr Lys Ile Gln Tyr Asn Gly Leu Thr Leu Asp Val Asp Gly Arg			
1040	1045	1050	1055
acg acc aag aag ctg atc aca cac ctc aag cca cac acc ttc tat aat	3338		
Thr Thr Lys Lys Leu Ile Thr His Leu Lys Pro His Thr Phe Tyr Asn			
1060	1065	1070	
ttc gtg ctc acc aac cgt ggc agc agc ctg ggg ggc ctg cag cag acg	3386		
Phe Val Leu Thr Asn Arg Gly Ser Ser Leu Gly Gly Leu Gln Gln Thr			
1075	1080	1085	
gtc act gcc agg acc gcc ttt aac atg ctc agt ggc aag cct agc gtc	3434		
Val Thr Ala Arg Thr Ala Phe Asn Met Leu Ser Gly Lys Pro Ser Val			
1090	1095	1100	
gcc ccg aag ccc gac aat gac ggt ttc atc gtg gtc tac ctg cct gat	3482		

Ala Pro Lys Pro Asp Asn Asp Gly Phe Ile Val Val Tyr Leu Pro Asp
1105 1110 1115
ggc cag agt cct gtg acc gtg cag aac tac ttc att gtg atg gtc cca 3530
Gly Gln Ser Pro Val Thr Val Gln Asn Tyr Phe Ile Val Met Val Pro
1120 1125 1130 1135
ctt cgg aag tct cga ggt ggc cag ttc cct gtc cta cta ggt agt cca 3578
Leu Arg Lys Ser Arg Gly Gly Gln Phe Pro Val Leu Leu Gly Ser Pro
1140 1145 1150
gag gac atg gat ctg gag gag ctc atc cag gac atc tcc cgg ctg cag 3626
Glu Asp Met Asp Leu Glu Glu Leu Ile Gln Asp Ile Ser Arg Leu Gln
1155 1160 1165
agg cgc agc ctg cgc cac tcc aga cag ctg gag gtg cct cgg ccc tac 3674
Arg Arg Ser Leu Arg His Ser Arg Gln Leu Glu Val Pro Arg Pro Tyr
1170 1175 1180
atc gcc gct cga ttc tcc atc ctg cca gct gtc ttc cat cct ggg aac 3722
Ile Ala Ala Arg Phe Ser Ile Leu Pro Ala Val Phe His Pro Gly Asn
1185 1190 1195
cag aag caa tat ggt ggc ttt gac aac agg ggc ttg gag cca ggc cac 3770
Gln Lys Gln Tyr Gly Gly Phe Asp Asn Arg Gly Leu Glu Pro Gly His
1200 1205 1210 1215
cgc tat gtc ctc ttt gtg ctt gct gtg ttg cag aag aat gag cct aca 3818
Arg Tyr Val Leu Phe Val Leu Ala Val Leu Gln Lys Asn Glu Pro Thr
1220 1225 1230
ttt gca gcc agt ccc ttc tca gac ccc ttc cag ctg gac aac ccg gac 3866
Phe Ala Ala Ser Pro Phe Ser Asp Pro Phe Gln Leu Asp Asn Pro Asp
1235 1240 1245
cct cag ccc att gtg gac ggc gag gag ggc ctc atc tgg gtg att ggg 3914
Pro Gln Pro Ile Val Asp Gly Glu Glu Gly Leu Ile Trp Val Ile Gly
1250 1255 1260

cct gtg ctg gcc gtg gtc ttc atc atc tgc atc gtg att gcc atc ctg 3962
 Pro Val Leu Ala Val Val Phe Ile Ile Cys Ile Val Ile Ala Ile Leu
 1265 1270 1275
 ctg tac aag aac aaa cct gac agc aaa cgc aag gac tca gag ccc cgc 4010
 Leu Tyr Lys Asn Lys Pro Asp Ser Lys Arg Lys Asp Ser Glu Pro Arg
 1280 1285 1290 1295
 acc aaa tgc tta ctg aac aat gcc gac ctt gcc ccc cat cac ccc aag 4058
 Thr Lys Cys Leu Leu Asn Asn Ala Asp Leu Ala Pro His His Pro Lys
 1300 1305 1310
 gac cct gtg gaa atg cga cgc atc aac ttc cag aca cca ggt atg ctc 4106
 Asp Pro Val Glu Met Arg Arg Ile Asn Phe Gln Thr Pro Gly Met Leu
 1315 1320 1325
 agc cac cca ccc atc ccc atc aca gac atg gcg gag cac atg gag aga 4154
 Ser His Pro Pro Ile Pro Ile Thr Asp Met Ala Glu His Met Glu Arg
 1330 1335 1340
 ctc aaa gcc aac gac agc ctg aag ctc tcc cag gag tac gag tcc att 4202
 Leu Lys Ala Asn Asp Ser Leu Lys Leu Ser Gln Glu Tyr Glu Ser Ile
 1345 1350 1355
 gac ccc ggg cag caa ttc acg tgg gaa cat tgc aac ctg gag gcc aac 4250
 Asp Pro Gly Gln Gln Phe Thr Trp Glu His Ser Asn Leu Glu Ala Asn
 1360 1365 1370 1375
 aag ccc aag aac cgc tat gcc aac gtc atc gcc tat gac cac tca cga 4298
 Lys Pro Lys Asn Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg
 1380 1385 1390
 gtc atc ctg cag ccc cta gaa ggc atc atg ggt agt gat tac atc aat 4346
 Val Ile Leu Gln Pro Leu Glu Gly Ile Met Gly Ser Asp Tyr Ile Asn
 1395 1400 1405
 gcc aac tat gtg gac ggc tac cgg cgg cag aat gca tac att gcc acg 4394
 Ala Asn Tyr Val Asp Gly Tyr Arg Arg Gln Asn Ala Tyr Ile Ala Thr

1410	1415	1420	
cag ggg ccc ctg cct gag acc ttt ggg gac ttc tgg cgg atg gtg tgg			4442
Gln Gly Pro Leu Pro Glu Thr Phe Gly Asp Phe Trp Arg Met Val Trp			
1425	1430	1435	
gag cag cga tcg gcc act gtg gtc atg atg acg cga ctg gag gag aaa			4490
Glu Gln Arg Ser Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys			
1440	1445	1450	1455
tca cgg atc aaa tgt gac caa tac tgg cct aac cga ggc acc gag aca			4538
Ser Arg Ile Lys Cys Asp Gln Tyr Trp Pro Asn Arg Gly Thr Glu Thr			
	1460	1465	1470
tac ggc ttc atc cag gtc acc cta cta gat acc atg gag ctg gct acc			4586
Tyr Gly Phe Ile Gln Val Thr Leu Leu Asp Thr Met Glu Leu Ala Thr			
	1475	1480	1485
ttc tgc gtc agg act ttt tct cta cac aag aat ggc tct agc gag aag			4634
Phe Cys Val Arg Thr Phe Ser Leu His Lys Asn Gly Ser Ser Glu Lys			
	1490	1495	1500
cgt gag gtg cga cat ttc cag ttc acg gca tgg ccc gac cac ggg tac			4682
Arg Glu Val Arg His Phe Gln Phe Thr Ala Trp Pro Asp His Gly Tyr			
1505	1510	1515	
ccc acg ccc ttc ctg gca ttc ctg cga aga gtc aag acc tgc aac ccg			4730
Pro Thr Pro Phe Leu Ala Phe Leu Arg Arg Val Lys Thr Cys Asn Pro			
1520	1525	1530	1535
cct gat gct ggc ccc att gtg gtc cac tgc agc gcg ggt gtg ggg cgc			4778
Pro Asp Ala Gly Pro Ile Val Val His Cys Ser Ala Gly Val Gly Arg			
	1540	1545	1550
act ggc tgc ttc atc gta att gac gcc atg cta gag cgc atc aag aca			4826
Thr Gly Cys Phe Ile Val Ile Asp Ala Met Leu Glu Arg Ile Lys Thr			
	1555	1560	1565
gag aag acc gtg gat gtg tat gga cat gtg aca ctc atg cgg tcg cag			4874

Glu Lys Thr Val Asp Val Tyr Gly His Val Thr Leu Met Arg Ser Gln
 1570 1575 1580
 cgc aac tac atg gtg cag aca gag gat cag tat ggc ttc atc cac gag 4922
 Arg Asn Tyr Met Val Gln Thr Glu Asp Gln Tyr Gly Phe Ile His Glu
 1585 1590 1595
 gcg ctg ctg gag gct gtg ggc tgc ggc aat acc gag gtc cct gct cgc 4970
 Ala Leu Leu Glu Ala Val Gly Cys Gly Asn Thr Glu Val Pro Ala Arg
 1600 1605 1610 1615
 agc ctc tac acc tac atc cag aag ctg gcc cag gtg gag cct ggc gag 5018
 Ser Leu Tyr Thr Tyr Ile Gln Lys Leu Ala Gln Val Glu Pro Gly Glu
 1620 1625 1630
 cac gtc acg ggc atg gag ctt gag ttc aag agg ctc gcc agt tcc aag 5066
 His Val Thr Gly Met Glu Leu Glu Phe Lys Arg Leu Ala Ser Ser Lys
 1635 1640 1645
 gca cac act tcg cgc ttc atc acc gcc agc ctg cct tgc aac aag ttt 5114
 Ala His Thr Ser Arg Phe Ile Thr Ala Ser Leu Pro Cys Asn Lys Phe
 1650 1655 1660
 aag aac cga ctg gtg aac atc ctg ccg tac gag agc tcg cgt gtc tgc 5162
 Lys Asn Arg Leu Val Asn Ile Leu Pro Tyr Glu Ser Ser Arg Val Cys
 1665 1670 1675
 ctg cag ccc atc cgc ggt gtg gag ggc tct gac tac atc aat gcc agc 5210
 Leu Gln Pro Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser
 1680 1685 1690 1695
 ttt atc gac ggc tat aga cag cag aaa gcc tac att gca aca cag ggg 5258
 Phe Ile Asp Gly Tyr Arg Gln Gln Lys Ala Tyr Ile Ala Thr Gln Gly
 1700 1705 1710
 cca ctg gca gag acc aca gag gac ttc tgg cga gct ctg tgg gag aac 5306
 Pro Leu Ala Glu Thr Thr Glu Asp Phe Trp Arg Ala Leu Trp Glu Asn
 1715 1720 1725

aac tct act att gtc gta atg ctc acc aag ctc cga gaa atg ggc cgg 5354
 Asn Ser Thr Ile Val Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg
 1730 1735 1740
 gaa aag tgc cac cag tac tgg cca gcc gag cgc tct gcc cgc tac cag 5402
 Glu Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln
 1745 1750 1755
 tac ttt gtg gtt gac ccg atg gca gag tat aac atg cca cag tac att 5450
 Tyr Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile
 1760 1765 1770 1775
 ctg cgt gag ttt aag gtc aca gat gcc cgg gat ggc cag tcc cgg acc 5498
 Leu Arg Glu Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr
 1780 1785 1790
 gtc cga cag ttc cag ttc acg gac tgg cca gag cag ggt gca ccc aag 5546
 Val Arg Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Ala Pro Lys
 1795 1800 1805
 tca ggg gaa ggc ttc att gac ttc atc ggc caa gtg cat aag acc aag 5594
 Ser Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys
 1810 1815 1820
 gag cag ttt ggc cag gac gga ccc atc tca gtg cac tgc agc gcc gga 5642
 Glu Gln Phe Gly Gln Asp Gly Pro Ile Ser Val His Cys Ser Ala Gly
 1825 1830 1835
 gtg ggc agg acc gga gtg ttc atc acc ctg agc atc gtg ctt gag cgg 5690
 Val Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg
 1840 1845 1850 1855
 atg cgc tac gag ggc gtg gtg gac att ttc cag aca gtg aag gtg ctt 5738
 Met Arg Tyr Glu Gly Val Val Asp Ile Phe Gln Thr Val Lys Val Leu
 1860 1865 1870
 cgg acc cag agg cct gcc atg gtg cag aca gag gac gag tac cag ttc 5786
 Arg Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Glu Tyr Gln Phe

1875	1880	1885	
tgc ttc cag gcg gct ttg gaa tac ctg ggc agt ttt gat cat tat gca			5834
Cys Phe Gln Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala			
1890	1895	1900	
aca taa gccatggggc cgcaccaaca cctcagccct gcgccaagtgc ccttgatgt			5890
Thr			
1905			
gagcctaggc cgcgcgtgg gcaggatgcg gcccaggag acctcctctt cgcggagaca			5950
ggcgtgcct tctcattcc cttctgattc caaaacgagg ttccagggtg gggggttggg			6010
gtggagagag aaggagccac tgcctcccag gctgggggtca cacagggacc gacctctgct			6070
tccgcactcc cctgcctgcc ttttggcaac attttttttc ttattttttt ttaatagtgt			6130
atattttttt tctttttctt tttttctttt ttttttttaa gaaaaaaca aaatcgtgcc			6190
ggtaaaaact ttgaaaaaga aacaagatca ctgtttgtgc ctctgtggga ggcctatitt			6250
ttcatagtta gtgtgccgtg tggcggctat gtgcggccac ttcgacggct tctgtgtgtg			6310
catctttccc acatgcccgga cactgcccc atccccatgt gaatgggtgcg cttagttttt			6370
atttttaacc tttttacttt ttttttaatc aatcttcaga catatcagat atggagggtg			6430
aggcgttggg ggcactcggg ccagactaca gggacatggc caccaaggac acagtggctg			6490
gccttgcctg tcccagttcc tggcacacca gggagggtcc tegtctactc atgacctctg			6550
tgccccgcat ggaggacctg ggactacggg acacttgggg gatattcaac cccctggagc			6610
aactgaggtc tctctttgta ggagagtggg tcagtactcg tccccgtgt tttttgggca			6670
gaagcagcag gtgacgcccc tgtatgtaga taaaccaact ttgtattaaa gaaagattcg			6730
tccg			6734

<210> 224

<211> 1904

<212> PRT

<213> Mus musculus

<400> 224

Met Ala Pro Thr Trp Ser Pro Ser Val Val Ser Val Val Gly Pro Val
 1 5 10 15
 Gly Leu Phe Leu Val Leu Leu Ala Arg Gly Cys Leu Ala Glu Glu Pro
 20 25 30
 Pro Arg Phe Ile Arg Glu Pro Lys Asp Gln Ile Gly Val Ser Gly Gly
 35 40 45
 Val Ala Ser Phe Val Cys Gln Ala Thr Gly Asp Pro Lys Pro Arg Val
 50 55 60
 Thr Trp Asn Lys Lys Gly Lys Lys Val Asn Ser Gln Arg Phe Glu Thr
 65 70 75 80
 Ile Asp Phe Asp Glu Ser Ser Gly Ala Val Leu Arg Ile Gln Pro Leu
 85 90 95
 Arg Thr Pro Arg Asp Glu Asn Val Tyr Glu Cys Val Ala Gln Asn Ser
 100 105 110
 Val Gly Glu Ile Thr Ile His Ala Lys Leu Thr Val Leu Arg Glu Asp
 115 120 125
 Gln Leu Pro Pro Gly Phe Pro Asn Ile Asp Met Gly Pro Gln Leu Lys
 130 135 140
 Val Val Glu Arg Thr Arg Thr Ala Thr Met Leu Cys Ala Ala Ser Gly
 145 150 155 160
 Asn Pro Asp Pro Glu Ile Thr Trp Phe Lys Asp Phe Leu Pro Val Asp
 165 170 175
 Pro Ser Ala Ser Asn Gly Arg Ile Lys Gln Leu Arg Ser Gly Ala Leu
 180 185 190
 Gln Ile Glu Ser Ser Glu Glu Thr Asp Gln Gly Lys Tyr Glu Cys Val
 195 200 205
 Ala Thr Asn Ser Ala Gly Val Arg Tyr Ser Ser Pro Ala Asn Leu Tyr
 210 215 220
 Val Arg Val Arg Arg Val Ala Pro Arg Phe Ser Ile Leu Pro Met Ser

225	230	235	240
His Glu Ile Met Pro Gly Gly Asn Val Asn Ile Thr Cys Val Ala Val			
	245	250	255
Gly Ser Pro Met Pro Tyr Val Lys Trp Met Gln Gly Ala Glu Asp Leu			
	260	265	270
Thr Pro Glu Asp Asp Met Pro Val Gly Arg Asn Val Leu Glu Leu Thr			
	275	280	285
Asp Val Lys Asp Ser Ala Asn Tyr Thr Cys Val Ala Met Ser Ser Leu			
	290	295	300
Gly Val Ile Glu Ala Val Ala Gln Ile Thr Val Lys Ser Leu Pro Lys			
305	310	315	320
Ala Pro Gly Thr Pro Val Val Thr Glu Asn Thr Ala Thr Ser Ile Thr			
	325	330	335
Val Thr Trp Asp Ser Gly Asn Pro Asp Pro Val Ser Tyr Tyr Val Ile			
	340	345	350
Glu Tyr Lys Ser Lys Ser Gln Asp Gly Pro Tyr Gln Ile Lys Glu Asp			
	355	360	365
Ile Thr Thr Thr Arg Tyr Ser Ile Gly Gly Leu Ser Pro Asn Ser Glu			
	370	375	380
Tyr Glu Ile Trp Val Ser Ala Val Asn Ser Ile Gly Gln Gly Pro Pro			
385	390	395	400
Ser Glu Ser Val Val Thr Arg Thr Gly Glu Gln Ala Pro Ala Ser Ala			
	405	410	415
Pro Arg Asn Val Gln Ala Arg Met Leu Ser Ala Thr Thr Met Ile Val			
	420	425	430
Gln Trp Glu Glu Pro Val Glu Pro Asn Gly Leu Ile Arg Gly Tyr Arg			
	435	440	445
Val Tyr Tyr Thr Met Glu Pro Glu His Pro Val Gly Asn Trp Gln Lys			
	450	455	460

His Asn Val Asp Asp Ser Leu Leu Thr Thr Val Gly Ser Leu Leu Glu
 465 470 475 480
 Asp Glu Thr Tyr Thr Val Arg Val Leu Ala Phe Thr Ser Val Gly Asp
 485 490 495
 Gly Pro Leu Ser Asp Pro Ile Gln Val Lys Thr Gln Gln Gly Val Pro
 500 505 510
 Gly Gln Pro Met Asn Leu Arg Ala Glu Ala Lys Ser Glu Thr Ser Ile
 515 520 525
 Gly Leu Ser Trp Ser Ala Pro Arg Gln Glu Ser Val Ile Lys Tyr Glu
 530 535 540
 Leu Leu Phe Arg Glu Gly Asp Arg Gly Arg Glu Val Gly Arg Thr Phe
 545 550 555 560
 Asp Pro Thr Thr Ala Phe Val Val Glu Asp Leu Lys Pro Asn Thr Glu
 565 570 575
 Tyr Ala Phe Arg Leu Ala Ala Arg Ser Pro Gln Gly Leu Gly Ala Phe
 580 585 590
 Thr Ala Val Val Arg Gln Arg Thr Leu Gln Ala Lys Pro Ser Ala Pro
 595 600 605
 Pro Gln Asp Val Lys Cys Thr Ser Leu Arg Ser Thr Ala Ile Leu Val
 610 615 620
 Ser Trp Arg Pro Pro Pro Pro Glu Thr His Asn Gly Ala Leu Val Gly
 625 630 635 640
 Tyr Ser Val Arg Tyr Arg Pro Leu Gly Ser Glu Asp Pro Asp Pro Lys
 645 650 655
 Glu Val Asn Asn Ile Pro Pro Thr Thr Thr Gln Ile Leu Leu Glu Ala
 660 665 670
 Leu Glu Lys Trp Thr Glu Tyr Arg Val Thr Ala Val Ala Tyr Thr Glu
 675 680 685
 Val Gly Pro Gly Pro Glu Ser Ser Pro Val Val Val Arg Thr Asp Glu

690	695	700
Asp Val Pro Ser Ala Pro Pro Arg Lys Val Glu Ala Glu Ala Leu Asn		
705	710	715
Ala Thr Ala Ile Arg Val Leu Trp Arg Ser Pro Thr Pro Gly Arg Gln		
	725	730
His Gly Gln Ile Arg Gly Tyr Gln Val His Tyr Val Arg Met Glu Gly		
	740	750
Ala Glu Ala Arg Gly Pro Pro Arg Ile Lys Asp Ile Met Leu Ala Asp		
	755	760
Ala Gln Glu Met Val Ile Thr Asn Leu Gln Pro Glu Thr Ala Tyr Ser		
	770	780
Ile Thr Val Ala Ala Tyr Thr Met Lys Gly Asp Gly Ala Arg Ser Lys		
785	790	800
Pro Lys Val Val Val Thr Lys Gly Ala Val Leu Gly Arg Pro Thr Leu		
	805	810
Ser Val Gln Gln Thr Pro Glu Gly Ser Leu Leu Ala Arg Trp Glu Pro		
	820	830
Pro Ala Asp Ala Ala Glu Asp Pro Val Leu Gly Tyr Arg Leu Gln Phe		
	835	840
Gly Arg Glu Asp Ala Ala Pro Ala Thr Leu Glu Leu Ala Ala Trp Glu		
	850	860
Arg Arg Phe Ala Ala Pro Ala His Lys Gly Ala Thr Tyr Val Phe Arg		
865	870	880
Leu Ala Ala Arg Gly Arg Ala Gly Leu Gly Glu Glu Ala Ala Ala Ala		
	885	890
Leu Ser Ile Pro Glu Asp Ala Pro Arg Gly Phe Pro Gln Ile Leu Gly		
	900	910
Ala Ala Gly Asn Val Ser Ala Gly Ser Val Leu Leu Arg Trp Leu Pro		
	915	925

Pro Val Pro Ala Glu Arg Asn Gly Ala Ile Ile Lys Tyr Thr Val Ser
 930 935 940
 Val Arg Glu Ala Gly Ala Pro Gly Pro Ala Thr Glu Thr Glu Leu Ala
 945 950 955 960
 Ala Ala Ala Gln Pro Gly Ala Glu Thr Ala Leu Thr Leu Arg Gly Leu
 965 970 975
 Arg Pro Glu Thr Ala Tyr Glu Leu Arg Val Arg Ala His Thr Arg Arg
 980 985 990
 Gly Pro Gly Pro Phe Ser Pro Pro Leu Arg Tyr Arg Leu Ala Arg Asp
 995 1000 1005
 Pro Val Ser Pro Lys Asn Phe Lys Val Lys Met Ile Met Lys Thr Ser
 1010 1015 1020
 Val Leu Leu Ser Trp Glu Phe Pro Asp Asn Tyr Asn Ser Pro Thr Pro
 1025 1030 1035 1040
 Tyr Lys Ile Gln Tyr Asn Gly Leu Thr Leu Asp Val Asp Gly Arg Thr
 1045 1050 1055
 Thr Lys Lys Leu Ile Thr His Leu Lys Pro His Thr Phe Tyr Asn Phe
 1060 1065 1070
 Val Leu Thr Asn Arg Gly Ser Ser Leu Gly Gly Leu Gln Gln Thr Val
 1075 1080 1085
 Thr Ala Arg Thr Ala Phe Asn Met Leu Ser Gly Lys Pro Ser Val Ala
 1090 1095 1100
 Pro Lys Pro Asp Asn Asp Gly Phe Ile Val Val Tyr Leu Pro Asp Gly
 1105 1110 1115 1120
 Gln Ser Pro Val Thr Val Gln Asn Tyr Phe Ile Val Met Val Pro Leu
 1125 1130 1135
 Arg Lys Ser Arg Gly Gly Gln Phe Pro Val Leu Leu Gly Ser Pro Glu
 1140 1145 1150
 Asp Met Asp Leu Glu Glu Leu Ile Gln Asp Ile Ser Arg Leu Gln Arg

1155	1160	1165
Arg Ser Leu Arg His Ser Arg Gln Leu Glu Val Pro Arg Pro Tyr Ile		
1170	1175	1180
Ala Ala Arg Phe Ser Ile Leu Pro Ala Val Phe His Pro Gly Asn Gln		
185	1190	1195
Lys Gln Tyr Gly Gly Phe Asp Asn Arg Gly Leu Glu Pro Gly His Arg		1200
1205	1210	1215
Tyr Val Leu Phe Val Leu Ala Val Leu Gln Lys Asn Glu Pro Thr Phe		
1220	1225	1230
Ala Ala Ser Pro Phe Ser Asp Pro Phe Gln Leu Asp Asn Pro Asp Pro		
1235	1240	1245
Gln Pro Ile Val Asp Gly Glu Glu Gly Leu Ile Trp Val Ile Gly Pro		
1250	1255	1260
Val Leu Ala Val Val Phe Ile Ile Cys Ile Val Ile Ala Ile Leu Leu		
265	1270	1275
Tyr Lys Asn Lys Pro Asp Ser Lys Arg Lys Asp Ser Glu Pro Arg Thr		1280
1285	1290	1295
Lys Cys Leu Leu Asn Asn Ala Asp Leu Ala Pro His His Pro Lys Asp		
1300	1305	1310
Pro Val Glu Met Arg Arg Ile Asn Phe Gln Thr Pro Gly Met Leu Ser		
1315	1320	1325
His Pro Pro Ile Pro Ile Thr Asp Met Ala Glu His Met Glu Arg Leu		
1330	1335	1340
Lys Ala Asn Asp Ser Leu Lys Leu Ser Gln Glu Tyr Glu Ser Ile Asp		
345	1350	1355
Pro Gly Gln Gln Phe Thr Trp Glu His Ser Asn Leu Glu Ala Asn Lys		1360
1365	1370	1375
Pro Lys Asn Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val		
1380	1385	1390

Ile Leu Gln Pro Leu Glu Gly Ile Met Gly Ser Asp Tyr Ile Asn Ala
 1395 1400 1405
 Asn Tyr Val Asp Gly Tyr Arg Arg Gln Asn Ala Tyr Ile Ala Thr Gln
 1410 1415 1420
 Gly Pro Leu Pro Glu Thr Phe Gly Asp Phe Trp Arg Met Val Trp Glu
 425 1430 1435 1440
 Gln Arg Ser Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys Ser
 1445 1450 1455
 Arg Ile Lys Cys Asp Gln Tyr Trp Pro Asn Arg Gly Thr Glu Thr Tyr
 1460 1465 1470
 Gly Phe Ile Gln Val Thr Leu Leu Asp Thr Met Glu Leu Ala Thr Phe
 1475 1480 1485
 Cys Val Arg Thr Phe Ser Leu His Lys Asn Gly Ser Ser Glu Lys Arg
 1490 1495 1500
 Glu Val Arg His Phe Gln Phe Thr Ala Trp Pro Asp His Gly Tyr Pro
 505 1510 1515 1520
 Thr Pro Phe Leu Ala Phe Leu Arg Arg Val Lys Thr Cys Asn Pro Pro
 1525 1530 1535
 Asp Ala Gly Pro Ile Val Val His Cys Ser Ala Gly Val Gly Arg Thr
 1540 1545 1550
 Gly Cys Phe Ile Val Ile Asp Ala Met Leu Glu Arg Ile Lys Thr Glu
 1555 1560 1565
 Lys Thr Val Asp Val Tyr Gly His Val Thr Leu Met Arg Ser Gln Arg
 1570 1575 1580
 Asn Tyr Met Val Gln Thr Glu Asp Gln Tyr Gly Phe Ile His Glu Ala
 585 1590 1595 1600
 Leu Leu Glu Ala Val Gly Cys Gly Asn Thr Glu Val Pro Ala Arg Ser
 1605 1610 1615
 Leu Tyr Thr Tyr Ile Gln Lys Leu Ala Gln Val Glu Pro Gly Glu His

1620	1625	1630
Val Thr Gly Met Glu Leu Glu Phe Lys Arg Leu Ala Ser Ser Lys Ala		
1635	1640	1645
His Thr Ser Arg Phe Ile Thr Ala Ser Leu Pro Cys Asn Lys Phe Lys		
1650	1655	1660
Asn Arg Leu Val Asn Ile Leu Pro Tyr Glu Ser Ser Arg Val Cys Leu		
665	1670	1675
Gln Pro Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe		1680
1685	1690	1695
Ile Asp Gly Tyr Arg Gln Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro		
1700	1705	1710
Leu Ala Glu Thr Thr Glu Asp Phe Trp Arg Ala Leu Trp Glu Asn Asn		
1715	1720	1725
Ser Thr Ile Val Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg Glu		
1730	1735	1740
Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr		
745	1750	1755
Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu		1760
1765	1770	1775
Arg Glu Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr Val		
1780	1785	1790
Arg Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Ala Pro Lys Ser		
1795	1800	1805
Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu		
1810	1815	1820
Gln Phe Gly Gln Asp Gly Pro Ile Ser Val His Cys Ser Ala Gly Val		
825	1830	1835
Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg Met		1840
1845	1850	1855

Arg Tyr Glu Gly Val Val Asp Ile Phe Gln Thr Val Lys Val Leu Arg

1860

1865

1870

Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Glu Tyr Gln Phe Cys

1875

1880

1885

Phe Gln Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr

1890

1895

1900

<210> 225

<211> 432

<212> DNA

<213> Mus musculus

<400> 225

cgcatggaga gccaggcact gggcatcagg gtgctgggca gtggcagcct ggtgtccatg 60
 caggacgagg ccttccccgc ctgcaaggtg gagttctagc cccacgctgc agggcagcct 120
 gggaacaaca gticctcact gtgaccaggt ttgggtgctgt ggctccatgt gcaaagctag 180
 atcccggtgt taagttagcc accgtgtgac atcccagctt ccatctccag cactgagggt 240
 gagaactgcg cgctttatca ctgttccag ccccatcatg tgtcaggcac agctctctat 300
 gccttctacc ctagaactca ggttgcagag gcaggaggat ctatgcagag tccaggccag 360
 cctgggcttc atagtgaatc tttgtttcaa aaaccacaaa aaataaagct gttggctgag 420
 aaaaaaaaaa ag 432

<210> 226

<211> 566

<212> DNA

<213> Mus musculus

<400> 226

acgtgcagtt ctccctaagc agtgagctct acctgcactt ccaggagcat agccgtgatg 60

agcagtacct gtgccagttc tgtgagcacg agacagggga ccctgaggac ttgcacagcc 120
 acgttgtcaa cgagcacgct cgcagactga ttgagctgag tgacaagtgt ggcagtggtg 180
 gccatgggca gtgcagcctt ttaagcaaga tcacctttga caaatgtaaa aatttcttcg 240
 tgtgtcaagt atgtggcitt cggagcagac ttcacacaaa tgtcaacaga cacgtggcta 300
 tcgagcatac taaaatattc ccctcatgitt gtgatgactg tgggaagggc ttttcagca 360
 tgttggataa ttgcaagcat cttaaattcac atctatctga aggatattac ttatgccaat 420
 attgtgaata ttcaacagga caaatlgacg atcttaaaat tcacttagat ttcaagcatt 480
 cagctgactt gccatcataa tgtagtgagt gcttgatgag gtttggaac gaaagggact 540
 tactcgggtca cccctcagtc catgag 566

<210> 227

<211> 3387

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (140).. (2719)

<400> 227

gctgcgtgag agaggcgggc ggcggagagc ggtggcagag actgagcgca gtcttgcagg 60
 gtaagccgga cagtcttccc gactggtcga gcaggacgag cacgcagcgg acccgaggcg 120
 gaggcggacc gggccagcc atg tgc gtg gtt ggg cta gag cta ggc tca cag 172

Met Ser Val Val Gly Leu Glu Leu Gly Ser Gln

1

5

10

agc tgc tac att gcg gtg gcg cgg gcc ggg ggc atc gag acc atc gcc 220
 Ser Cys Tyr Ile Ala Val Ala Arg Ala Gly Gly Ile Glu Thr Ile Ala

15

20

25

aac gag ttc agc gac cgc tgc acc ccg tca gtc ata tca ttt gga tca 268

Asn	Glu	Phe	Ser	Asp	Arg	Cys	Thr	Pro	Ser	Val	Ile	Ser	Phe	Gly	Ser				
aaa	aac	aga	aca	att	gga	gtt	gca	gcc	aaa	aac	cag	caa	atc	act	cat				316
Lys	Asn	Arg	Thr	Ile	Gly	Val	Ala	Ala	Lys	Asn	Gln	Gln	Ile	Thr	His				
gca	aac	aat	acg	gtc	tct	agc	ttt	aag	aga	ttt	cat	ggc	aga	gca	ttc				364
Ala	Asn	Asn	Thr	Val	Ser	Ser	Phe	Lys	Arg	Phe	His	Gly	Arg	Ala	Phe				
aat	gac	ccc	ttc	att	cag	aag	gaa	aag	gag	aac	ctg	agc	tat	gat	ttg				412
Asn	Asp	Pro	Phe	Ile	Gln	Lys	Glu	Lys	Glu	Asn	Leu	Ser	Tyr	Asp	Leu				
gtc	cca	atg	aaa	aat	ggt	ggc	gtg	gga	ata	aag	gtc	atg	tac	atg	gat				460
Val	Pro	Met	Lys	Asn	Gly	Gly	Val	Gly	Ile	Lys	Val	Met	Tyr	Met	Asp				
gaa	gaa	cat	ttc	ttc	agt	gtg	gag	cag	ata	aca	gcc	atg	ctg	ctg	act				508
Glu	Glu	His	Phe	Phe	Ser	Val	Glu	Gln	Ile	Thr	Ala	Met	Leu	Leu	Thr				
aag	tta	aag	gaa	act	gca	gaa	aac	aac	ctc	aag	aag	cca	gtg	aca	gac				556
Lys	Leu	Lys	Glu	Thr	Ala	Glu	Asn	Asn	Leu	Lys	Lys	Pro	Val	Thr	Asp				
tgt	gtc	atc	tca	gtc	cca	tcc	ttc	ttc	aca	gat	gct	gag	cga	agg	tct				604
Cys	Val	Ile	Ser	Val	Pro	Ser	Phe	Phe	Thr	Asp	Ala	Glu	Arg	Arg	Ser				
gtg	ctg	gat	cgt	gcg	cag	att	gtg	ggc	ttg	aac	tgc	ttg	cgg	ctc	atg				652
Val	Leu	Asp	Arg	Ala	Gln	Ile	Val	Gly	Leu	Asn	Cys	Leu	Arg	Leu	Met				
aat	gac	atg	acg	gct	gtt	gct	ttg	aat	tat	ggg	att	tat	aag	caa	gat				700
Asn	Asp	Met	Thr	Ala	Val	Ala	Leu	Asn	Tyr	Gly	Ile	Tyr	Lys	Gln	Asp				

ctc ccg aat gcc gag gag aag cca cgg gtg gtg gtg ttt gtt gac atg 748
 Leu Pro Asn Ala Glu Glu Lys Pro Arg Val Val Val Phe Val Asp Met
 190 195 200
 gga cac tca tct ttc caa gtg tct gcc tgt gct ttt aac aaa gga aaa 796
 Gly His Ser Ser Phe Gln Val Ser Ala Cys Ala Phe Asn Lys Gly Lys
 205 210 215
 ctg aag gtt cta ggc aca gct ttt gat ccc ttc tta gga gga aag aac 844
 Leu Lys Val Leu Gly Thr Ala Phe Asp Pro Phe Leu Gly Gly Lys Asn
 220 225 230 235
 ttt gat gag aag cta gta gaa cat ttt tgt gct gaa ttt aaa acc aag 892
 Phe Asp Glu Lys Leu Val Glu His Phe Cys Ala Glu Phe Lys Thr Lys
 240 245 250
 tac aaa ttg gat gca aaa tcc aaa att cga gcc ctc ctt cgt ctc cat 940
 Tyr Lys Leu Asp Ala Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu His
 255 260 265
 cag gag tgt gaa aag ttg aaa aag ctc atg agt tct aac agc acg gac 988
 Gln Glu Cys Glu Lys Leu Lys Lys Leu Met Ser Ser Asn Ser Thr Asp
 270 275 280
 ctg ccg ctg aac atc gag tgc ttt atg aat gac aag gat gtc tct ggg 1036
 Leu Pro Leu Asn Ile Glu Cys Phe Met Asn Asp Lys Asp Val Ser Gly
 285 290 295
 aag atg aac agg tca cag ttt gaa gaa ctg tgt gct gag ctc ctg caa 1084
 Lys Met Asn Arg Ser Gln Phe Glu Glu Leu Cys Ala Glu Leu Leu Gln
 300 305 310 315
 aaa ata gag gtc ccc ctt cac tcg ttg atg gca cag act cag ctc aag 1132
 Lys Ile Glu Val Pro Leu His Ser Leu Met Ala Gln Thr Gln Leu Lys
 320 325 330
 gct gaa gat gtg agt gcc att gag ata gtg gga ggt gcc aca aga atc 1180
 Ala Glu Asp Val Ser Ala Ile Glu Ile Val Gly Gly Ala Thr Arg Ile

335	340	345	
cca gct gtg aaa gaa aga att gcc aag ttc ttt gga aaa gat gtc agc			1228
Pro Ala Val Lys Glu Arg Ile Ala Lys Phe Phe Gly Lys Asp Val Ser			
350	355	360	
acc acg ctc aat gca gac gaa gct gtg cgc aga ggc tgt gca ctg cag			1276
Thr Thr Leu Asn Ala Asp Glu Ala Val Arg Arg Gly Cys Ala Leu Gln			
365	370	375	
tgt gca att ctt tct ccg gca ttt aaa gtt aga gag ttc tct gtc acc			1324
Cys Ala Ile Leu Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr			
380	385	390	395
gat gca gtt cct ttt cca ata tct ctg gtc tgg aac cac gac tcg gaa			1372
Asp Ala Val Pro Phe Pro Ile Ser Leu Val Trp Asn His Asp Ser Glu			
400	405	410	
gaa acg gaa ggt gtg cac gag gtg ttc agt cgg aac cat gct gct cct			1420
Glu Thr Glu Gly Val His Glu Val Phe Ser Arg Asn His Ala Ala Pro			
415	420	425	
ttc tcc aaa gtg ctc acc ttc ctg aga agg ggg ccc ttt gag cta gaa			1468
Phe Ser Lys Val Leu Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu			
430	435	440	
gct ttc tat tct gac cct caa gga gtt cca tat cca gaa gca aaa ata			1516
Ala Phe Tyr Ser Asp Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile			
445	450	455	
ggc cgt ttt gtt gtt cag aat gtt tct gca cag aaa gat gga gag aag			1564
Gly Arg Phe Val Val Gln Asn Val Ser Ala Gln Lys Asp Gly Glu Lys			
460	465	470	475
tcg aga gtg aag gtc aaa gtg cgt gtg aac aca cat ggc atc ttc acc			1612
Ser Arg Val Lys Val Lys Val Arg Val Asn Thr His Gly Ile Phe Thr			
480	485	490	
atc tcc acg gct tcc atg gtg gag aag gtc ccg acc gag gaa gag gat			1660

Ile Ser Thr Ala Ser Met Val Glu Lys Val Pro Thr Glu Glu Glu Asp .
 495 500 505
 ggc tcc tct ctc gag gca gac atg gaa tgc ttc caa aac cag agg cca 1708
 Gly Ser Ser Leu Glu Ala Asp Met Glu Cys Phe Gln Asn Gln Arg Pro
 510 515 520
 aca gaa agc tgc gat gtg gat aaa aat atc cag caa gac aac agt gaa 1756
 Thr Glu Ser Ser Asp Val Asp Lys Asn Ile Gln Gln Asp Asn Ser Glu
 525 530 535
 gct gga aca cag ccc cag gta caa act gat ggt caa caa acc tca cag 1804
 Ala Gly Thr Gln Pro Gln Val Gln Thr Asp Gly Gln Gln Thr Ser Gln
 540 545 550 555
 tct ccc cct tca cct gaa ctt acc tca gaa gaa agc aaa acc cca gat 1852
 Ser Pro Pro Ser Pro Glu Leu Thr Ser Glu Glu Ser Lys Thr Pro Asp
 560 565 570
 gct gac aaa gca aat gaa aag aaa gtt gat cag cct cca gaa gcc aag 1900
 Ala Asp Lys Ala Asn Glu Lys Lys Val Asp Gln Pro Pro Glu Ala Lys
 575 580 585
 aaa cct aaa ata aag gtg gta aat gtt gag ctg cct gta gaa gcc aac 1948
 Lys Pro Lys Ile Lys Val Val Asn Val Glu Leu Pro Val Glu Ala Asn
 590 595 600
 ttg gta tgg cag tta ggg aga gac ctt ctt aac atg tat att gag aca 1996
 Leu Val Trp Gln Leu Gly Arg Asp Leu Leu Asn Met Tyr Ile Glu Thr
 605 610 615
 gag ggc aag atg atc atg caa gac aag ctg gag aag gag cgg aac gac 2044
 Glu Gly Lys Met Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp
 620 625 630 635
 gcc aag aac gcc gtg gag gag tgt gta tat gag ttc agg gac aag cta 2092
 Ala Lys Asn Ala Val Glu Glu Cys Val Tyr Glu Phe Arg Asp Lys Leu
 640 645 650

tgt gga cca tat gag aaa ttc ata tgt gag cag gaa cat gag aag ttc	2140
Cys Gly Pro Tyr Glu Lys Phe Ile Cys Glu Gln Glu His Glu Lys Phe	
655 660 665	
ttg agg ctt cta aca gag acg gaa gac tgg ctg tat gag gaa ggg gag	2188
Leu Arg Leu Leu Thr Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu	
670 675 680	
gac cag gct aag cag gca tac att gac aag ttg gaa gag ctg atg aaa	2236
Asp Gln Ala Lys Gln Ala Tyr Ile Asp Lys Leu Glu Glu Leu Met Lys	
685 690 695	
atg ggc act cct gtt aaa gtc aga ttt caa gaa gct gag gaa cga ccg	2284
Met Gly Thr Pro Val Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro	
700 705 710 715	
aaa gtg ttg gag gag ctg ggg cag cgc ctg cag cac tat gcc aag att	2332
Lys Val Leu Glu Glu Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile	
720 725 730	
gca gcg gac ttc aga ggc aag gat gag aaa tac aac cac aat gat gaa	2380
Ala Ala Asp Phe Arg Gly Lys Asp Glu Lys Tyr Asn His Asn Asp Glu	
735 740 745	
tca gaa atg aag aag gtt gag aag tct gtt aat gag gtg atg gag tgg	2428
Ser Glu Met Lys Lys Val Glu Lys Ser Val Asn Glu Val Met Glu Trp	
750 755 760	
atg aat aat gtc atg aat gct cag gct aaa aga agt ctt gat caa gac	2476
Met Asn Asn Val Met Asn Ala Gln Ala Lys Arg Ser Leu Asp Gln Asp	
765 770 775	
cct gtt gtt cga act cat gaa atc aga gcg aag gtc aag gaa ttg aac	2524
Pro Val Val Arg Thr His Glu Ile Arg Ala Lys Val Lys Glu Leu Asn	
780 785 790 795	
aat gtt tgt gaa cct gtt gta act caa ccc aaa cca aaa atc gag tca	2572
Asn Val Cys Glu Pro Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser	

800 805 810
 cct aaa ctg gag aga act cca aat ggc cca aat att gac aag aaa gaa 2620
 Pro Lys Leu Glu Arg Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu
 815 820 825
 gat tta gaa ggc aaa aat aat ctt ggt gct gaa cgt ccg cat cag aat 2668
 Asp Leu Glu Gly Lys Asn Asn Leu Gly Ala Glu Arg Pro His Gln Asn
 830 835 840
 ggt gaa tgc cac cct aat gag aag ggc tct gtc aac atg gac ctg gac 2716
 Gly Glu Cys His Pro Asn Glu Lys Gly Ser Val Asn Met Asp Leu Asp
 845 850 855
 tag gctctgtgct ggctccctcc cccacttcat gagatgtgtt tgccatagta 2769
 860
 tgtgatcctg tataacagac tgagtctatt tattattttc ttttttttaa gactgtctag 2829
 atctagaaat tttgtgtatt atgaggggaa aaaaggaaaa gcttgaatct gtgtagtcctc 2889
 tgaccctaag tgagaatgac tttgggtgtca gggctcctgtg gagttgtgcc ccacactgag 2949
 ctctgtacag tattgctgct catacactga ggagggtggg tcgtcttctg aggatatgaa 3009
 ctacactgct tggtcacacg ctgggatcag aatcttaagc agttattctt gccaaagggtt 3069
 ttgttttggt ttgcattttg ctcttcattt ccgcatgtgt gtggctgtgg ttgtttataa 3129
 atgagactaa gtctgatttg cataagggtt ttcaaaaatt aagtctgtcc agtagagtga 3189
 ttttgctttc attattacca agtcaaggta caacagagct agtgaactgt agcagcatgc 3249
 gaagcagggc tgtgaactat caccacacag tgcattgtcc cgtggagggtg tgacacggga 3309
 gacacacgtg tggatcatgt gatcattgtg aacacctcgt gagcttttaa ataaagtcca 3369
 ccctgtggtg tcatttct 3387

<210> 228

<211> 859

<212> PRT

<213> Mus musculus

<400> 228

Met	Ser	Val	Val	Gly	Leu	Glu	Leu	Gly	Ser	Gln	Ser	Cys	Tyr	Ile	Ala
1				5					10					15	
Val	Ala	Arg	Ala	Gly	Gly	Ile	Glu	Thr	Ile	Ala	Asn	Glu	Phe	Ser	Asp
			20					25					30		
Arg	Cys	Thr	Pro	Ser	Val	Ile	Ser	Phe	Gly	Ser	Lys	Asn	Arg	Thr	Ile
		35					40					45			
Gly	Val	Ala	Ala	Lys	Asn	Gln	Gln	Ile	Thr	His	Ala	Asn	Asn	Thr	Val
	50					55					60				
Ser	Ser	Phe	Lys	Arg	Phe	His	Gly	Arg	Ala	Phe	Asn	Asp	Pro	Phe	Ile
65				70					75					80	
Gln	Lys	Glu	Lys	Glu	Asn	Leu	Ser	Tyr	Asp	Leu	Val	Pro	Met	Lys	Asn
				85					90					95	
Gly	Gly	Val	Gly	Ile	Lys	Val	Met	Tyr	Met	Asp	Glu	Glu	His	Phe	Phe
		100						105					110		
Ser	Val	Glu	Gln	Ile	Thr	Ala	Met	Leu	Leu	Thr	Lys	Leu	Lys	Glu	Thr
	115						120						125		
Ala	Glu	Asn	Asn	Leu	Lys	Lys	Pro	Val	Thr	Asp	Cys	Val	Ile	Ser	Val
	130					135					140				
Pro	Ser	Phe	Phe	Thr	Asp	Ala	Glu	Arg	Arg	Ser	Val	Leu	Asp	Arg	Ala
145					150					155				160	
Gln	Ile	Val	Gly	Leu	Asn	Cys	Leu	Arg	Leu	Met	Asn	Asp	Met	Thr	Ala
			165					170					175		
Val	Ala	Leu	Asn	Tyr	Gly	Ile	Tyr	Lys	Gln	Asp	Leu	Pro	Asn	Ala	Glu
		180						185					190		
Glu	Lys	Pro	Arg	Val	Val	Val	Phe	Val	Asp	Met	Gly	His	Ser	Ser	Phe
		195					200					205			
Gln	Val	Ser	Ala	Cys	Ala	Phe	Asn	Lys	Gly	Lys	Leu	Lys	Val	Leu	Gly
	210						215						220		

Thr Ala Phe Asp Pro Phe Leu Gly Gly Lys Asn Phe Asp Glu Lys Leu
 225 230 235 240
 Val Glu His Phe Cys Ala Glu Phe Lys Thr Lys Tyr Lys Leu Asp Ala
 245 250 255
 Lys Ser Lys Ile Arg Ala Leu Leu Arg Leu His Gln Glu Cys Glu Lys
 260 265 270
 Leu Lys Lys Leu Met Ser Ser Asn Ser Thr Asp Leu Pro Leu Asn Ile
 275 280 285
 Glu Cys Phe Met Asn Asp Lys Asp Val Ser Gly Lys Met Asn Arg Ser
 290 295 300
 Gln Phe Glu Glu Leu Cys Ala Glu Leu Leu Gln Lys Ile Glu Val Pro
 305 310 315 320
 Leu His Ser Leu Met Ala Gln Thr Gln Leu Lys Ala Glu Asp Val Ser
 325 330 335
 Ala Ile Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys Glu
 340 345 350
 Arg Ile Ala Lys Phe Phe Gly Lys Asp Val Ser Thr Thr Leu Asn Ala
 355 360 365
 Asp Glu Ala Val Arg Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu Ser
 370 375 380
 Pro Ala Phe Lys Val Arg Glu Phe Ser Val Thr Asp Ala Val Pro Phe
 385 390 395 400
 Pro Ile Ser Leu Val Trp Asn His Asp Ser Glu Glu Thr Glu Gly Val
 405 410 415
 His Glu Val Phe Ser Arg Asn His Ala Ala Pro Phe Ser Lys Val Leu
 420 425 430
 Thr Phe Leu Arg Arg Gly Pro Phe Glu Leu Glu Ala Phe Tyr Ser Asp
 435 440 445
 Pro Gln Gly Val Pro Tyr Pro Glu Ala Lys Ile Gly Arg Phe Val Val

450	455	460
Gln Asn Val Ser Ala	Gln Lys Asp Gly Glu Lys Ser Arg Val Lys Val	
465	470	475
Lys Val Arg Val Asn Thr His Gly Ile Phe Thr Ile Ser Thr Ala Ser		480
	485	490
Met Val Glu Lys Val Pro Thr Glu Glu Glu Asp Gly Ser Ser Leu Glu		495
500	505	510
Ala Asp Met Glu Cys Phe Gln Asn Gln Arg Pro Thr Glu Ser Ser Asp		
515	520	525
Val Asp Lys Asn Ile Gln Gln Asp Asn Ser Glu Ala Gly Thr Gln Pro		
530	535	540
Gln Val Gln Thr Asp Gly Gln Gln Thr Ser Gln Ser Pro Pro Ser Pro		
545	550	555
Glu Leu Thr Ser Glu Glu Ser Lys Thr Pro Asp Ala Asp Lys Ala Asn		560
	565	570
Glu Lys Lys Val Asp Gln Pro Pro Glu Ala Lys Lys Pro Lys Ile Lys		575
580	585	590
Val Val Asn Val Glu Leu Pro Val Glu Ala Asn Leu Val Trp Gln Leu		
595	600	605
Gly Arg Asp Leu Leu Asn Met Tyr Ile Glu Thr Glu Gly Lys Met Ile		
610	615	620
Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val		
625	630	635
Glu Glu Cys Val Tyr Glu Phe Arg Asp Lys Leu Cys Gly Pro Tyr Glu		640
	645	650
Lys Phe Ile Cys Glu Gln Glu His Glu Lys Phe Leu Arg Leu Leu Thr		655
660	665	670
Glu Thr Glu Asp Trp Leu Tyr Glu Glu Gly Glu Asp Gln Ala Lys Gln		
675	680	685

Ala Tyr Ile Asp Lys Leu Glu Glu Leu Met Lys Met Gly Thr Pro Val
690 695 700
Lys Val Arg Phe Gln Glu Ala Glu Glu Arg Pro Lys Val Leu Glu Glu
705 710 715 720
Leu Gly Gln Arg Leu Gln His Tyr Ala Lys Ile Ala Ala Asp Phe Arg
725 730 735
Gly Lys Asp Glu Lys Tyr Asn His Asn Asp Glu Ser Glu Met Lys Lys
740 745 750
Val Glu Lys Ser Val Asn Glu Val Met Glu Trp Met Asn Asn Val Met
755 760 765
Asn Ala Gln Ala Lys Arg Ser Leu Asp Gln Asp Pro Val Val Arg Thr
770 775 780
His Glu Ile Arg Ala Lys Val Lys Glu Leu Asn Asn Val Cys Glu Pro
785 790 795 800
Val Val Thr Gln Pro Lys Pro Lys Ile Glu Ser Pro Lys Leu Glu Arg
805 810 815
Thr Pro Asn Gly Pro Asn Ile Asp Lys Lys Glu Asp Leu Glu Gly Lys
820 825 830
Asn Asn Leu Gly Ala Glu Arg Pro His Gln Asn Gly Glu Cys His Pro
835 840 845
Asn Glu Lys Gly Ser Val Asn Met Asp Leu Asp
850 855

<210> 229

<211> 2558

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (30).. (1694)

<400> 229

```

ggattgcagc ctgcgaagtg aagcgcgcc atg tac gcc ctc gcc ctc ttc gcc 53
                                Met Tyr Ala Leu Ala Leu Phe Ala
                                1                      5

agc ctt ctg gcc acc gct ctg acc agc cct gtc caa gac ccg aag aca 101
Ser Leu Leu Ala Thr Ala Leu Thr Ser Pro Val Gln Asp Pro Lys Thr
    10                      15                      20

tgc tct ggg ggc tca gca gtg ctg tgc aga gat gtg aag acg gcg gtg 149
Cys Ser Gly Gly Ser Ala Val Leu Cys Arg Asp Val Lys Thr Ala Val
    25                      30                      35                      40

gac tgt ggg gcc gtg aag cac tgc cag cag atg gtc tgg agc aag ccc 197
Asp Cys Gly Ala Val Lys His Cys Gln Gln Met Val Trp Ser Lys Pro
                45                      50                      55

aca gcg aaa tcc ctt cct tgc gac ata tgc aaa act gtt gtc acc gaa 245
Thr Ala Lys Ser Leu Pro Cys Asp Ile Cys Lys Thr Val Val Thr Glu
                60                      65                      70

gct ggg aac ttg ctg aaa gat aat gct acg cag gag gag atc ctt cat 293
Ala Gly Asn Leu Leu Lys Asp Asn Ala Thr Gln Glu Glu Ile Leu His
                75                      80                      85

tac ctg gag aag acc tgt gag tgg att cat gac tcc agc ctg tcg gcc 341
Tyr Leu Glu Lys Thr Cys Glu Trp Ile His Asp Ser Ser Leu Ser Ala
    90                      95                      100

tcg tgc aag gag gtg gtt gac tct tac ctg cct gtc atc ctg gac atg 389
Ser Cys Lys Glu Val Val Asp Ser Tyr Leu Pro Val Ile Leu Asp Met
    105                      110                      115                      120

att aag ggc gag atg agc aac cct ggg gaa gtg tgc tct gcg ctc aac 437

```

Ile Lys Gly Glu Met Ser Asn Pro Gly Glu Val Cys Ser Ala Leu Asn
 125 130 135
 ctg tgc cag tcc ctt cag gag tac ttg gcc gag caa aac cag aaa cag 485
 Leu Cys Gln Ser Leu Gln Glu Tyr Leu Ala Glu Gln Asn Gln Lys Gln
 140 145 150
 ctt gag tcc aac aaa gtc ccg gag gtg gac atg gcc cgt gtg gtt gcc 533
 Leu Glu Ser Asn Lys Val Pro Glu Val Asp Met Ala Arg Val Val Ala
 155 160 165
 ccc ttc agt gcc aac atc cct ctc ctg ctg tac cct cag gat cac ccc 581
 Pro Phe Ser Ala Asn Ile Pro Leu Leu Leu Tyr Pro Gln Asp His Pro
 170 175 180
 cgc agc cag ccc caa cct aag gct aac gag gac gtc tgc cag gac tgt 629
 Arg Ser Gln Pro Gln Pro Lys Ala Asn Glu Asp Val Cys Gln Asp Cys
 185 190 195 200
 atg aag ctg gtg tct gat gtc cag act gct gtg aag acc aac tcc agc 677
 Met Lys Leu Val Ser Asp Val Gln Thr Ala Val Lys Thr Asn Ser Ser
 205 210 215
 ttt atc cag ggc ttc gtg gac cac gtg aag gag gat tgt gac cgc ttg 725
 Phe Ile Gln Gly Phe Val Asp His Val Lys Glu Asp Cys Asp Arg Leu
 220 225 230
 ggg cca ggc gtg tct gac ata tgc aag aac tac gtg gac cag tat tcc 773
 Gly Pro Gly Val Ser Asp Ile Cys Lys Asn Tyr Val Asp Gln Tyr Ser
 235 240 245
 gag gtc tgt gtc cag att ttg atg cac atg caa ccc aag gaa atc tgt 821
 Glu Val Cys Val Gln Ile Leu Met His Met Gln Pro Lys Glu Ile Cys
 250 255 260
 gtg ctg gct ggc ttc tgt aat gag gtc aag aga gtg cca atg aag act 869
 Val Leu Ala Gly Phe Cys Asn Glu Val Lys Arg Val Pro Met Lys Thr
 265 270 275 280

ctg gtc cct gcc acc gag acc att aag aac atc ctc cct gcc ctg gag	917
Leu Val Pro Ala Thr Glu Thr Ile Lys Asn Ile Leu Pro Ala Leu Glu	
285 290 295	
atg atg gac ccc tat gag cag aat ctg gtc cag gcc cac aat gtg att	965
Met Met Asp Pro Tyr Glu Gln Asn Leu Val Gln Ala His Asn Val Ile	
300 305 310	
tta tgc cag acc tgt cag ttt gtg atg aat aag ttt tct gag ctg att	1013
Leu Cys Gln Thr Cys Gln Phe Val Met Asn Lys Phe Ser Glu Leu Ile	
315 320 325	
gtc aat aat gcc act gag gag ctc cta gtt aaa ggt ttg agc aac gca	1061
Val Asn Asn Ala Thr Glu Glu Leu Leu Val Lys Gly Leu Ser Asn Ala	
330 335 340	
tgc gca ctg ctc ccc gat cct gcc aga acc aag tgc cag gaa gtg gtg	1109
Cys Ala Leu Leu Pro Asp Pro Ala Arg Thr Lys Cys Gln Glu Val Val	
345 350 355 360	
gga aca ttt gac ccc tcc ctg ttg gac gac ttt atc cat gag gta aac	1157
Gly Thr Phe Asp Pro Ser Leu Leu Asp Asp Phe Ile His Glu Val Asn	
365 370 375	
ccc agc tct ctg tgc ggt gtg atc ggc ctg tgt act gcc ctc ccg gag	1205
Pro Ser Ser Leu Cys Gly Val Ile Gly Leu Cys Thr Ala Leu Pro Glu	
380 385 390	
ttg gtg gag gca ctt gag cag cct gcg cca cgc att gta tct gca ctg	1253
Leu Val Glu Ala Leu Glu Gln Pro Ala Pro Arg Ile Val Ser Ala Leu	
395 400 405	
ctc aaa gag cct aca ccg cca aag cag ccc gca cag ccc aag cag tct	1301
Leu Lys Glu Pro Thr Pro Pro Lys Gln Pro Ala Gln Pro Lys Gln Ser	
410 415 420	
gca ttg ccc gcc cat gtg cct cct cag aag aat ggt ggg ttc tgt gag	1349
Ala Leu Pro Ala His Val Pro Pro Gln Lys Asn Gly Gly Phe Cys Glu	

425	430	435	440	
gtg ttc aag aaa ctg gtc ctc tat ttg gaa cat aac ctg gag aaa aac	1397			
Val Phe Lys Lys Leu Val Leu Tyr Leu Glu His Asn Leu Glu Lys Asn				
445	450	455		
agc acc aag gag gaa atc ctg gcc gca ctt gag aag ggc tgc agc ttc	1445			
Ser Thr Lys Glu Glu Ile Leu Ala Ala Leu Glu Lys Gly Cys Ser Phe				
460	465	470		
ctg cca gac cct tac cag aag cag tgc gat gac ttt gtg gct gag tat	1493			
Leu Pro Asp Pro Tyr Gln Lys Gln Cys Asp Asp Phe Val Ala Glu Tyr				
475	480	485		
gag ccc ttg cta ttg gag atc ctc gtg gaa gtg atg gat cct gga ttt	1541			
Glu Pro Leu Leu Leu Glu Ile Leu Val Glu Val Met Asp Pro Gly Phe				
490	495	500		
gtg tgc tcg aaa att gga gtt tgc cct tct gcc tat aag ctg ctg ctg	1589			
Val Cys Ser Lys Ile Gly Val Cys Pro Ser Ala Tyr Lys Leu Leu Leu				
505	510	515	520	
gga acc gag aag tgt gtc tgg ggc cct agc tac tgg tgt cag aac atg	1637			
Gly Thr Glu Lys Cys Val Trp Gly Pro Ser Tyr Trp Cys Gln Asn Met				
525	530	535		
gag act gcc gcc cga tgc aat gct gtc gat cat tgc aaa cgc cat gtg	1685			
Glu Thr Ala Ala Arg Cys Asn Ala Val Asp His Cys Lys Arg His Val				
540	545	550		
tgg aac tag tttcccagct gcagaagtca cctacttgtg ggtctagggt	1734			
Trp Asn				
555				
aatgaacaca tagatctatt tgaccttaat aagtaggaac cccctttgac ccttcccttc	1794			
tgtagcatitt ctgtcatgta agagggtgtg acagccactt ccgtctcccc tttctgctcg	1854			
aaggatgagg ataccttggg catcactccc cggctgccct tttcaccac ctgctggagg	1914			
ggggtcgtgc agccagaggg caggagcatt ttctgagccc ctttcttggt gtgtggggga	1974			

tctatggcca tctcctacca tgaggagct acccagcttc ctgtggtacc aaggagttat 2034
 tttggatgat tagaagcaca gaatgacag gcctttagag cgaatggaagt ggccattgtc 2094
 atagcacaga gatttcagaa gcacctgcag gtggcttgct tgggatgttg ctgtccctgg 2154
 gtcaccttc attctgcttt cctgttcttc ccgtctgcct tgttgggggtt ctgtggggta 2214
 ggggtggggag gggaaacttg tgaatgtaac ttgcctgtgc cgtgtgacgg tcacgtgggc 2274
 ctggcttttt gtgtgaggcc ctgaccgtg tcctctgcct ggcatgttgg ggtcctcctg 2334
 caacggactt tcccaccacc tgtagctctt gttgacctgc ctgttcacct catgagttaa 2394
 ggcgctgcc tggcagtggg ccatgaactg aggggtctct gtgtagagta caagcttcct 2454
 gtgctccggt tgccaggaga cagcctgtgc agttaaatgg acctagattt tgttttgcac 2514
 taaagtctct gtgacttaat aaagtctgt taaccaacaa aaag 2558

<210> 230

<211> 554

<212> PRT

<213> Mus musculus

<400> 230

Met	Tyr	Ala	Leu	Ala	Leu	Phe	Ala	Ser	Leu	Leu	Ala	Thr	Ala	Leu	Thr
1				5					10					15	
Ser	Pro	Val	Gln	Asp	Pro	Lys	Thr	Cys	Ser	Gly	Gly	Ser	Ala	Val	Leu
				20				25						30	
Cys	Arg	Asp	Val	Lys	Thr	Ala	Val	Asp	Cys	Gly	Ala	Val	Lys	His	Cys
				35				40						45	
Gln	Gln	Met	Val	Trp	Ser	Lys	Pro	Thr	Ala	Lys	Ser	Leu	Pro	Cys	Asp
				50				55						60	
Ile	Cys	Lys	Thr	Val	Val	Thr	Glu	Ala	Gly	Asn	Leu	Leu	Lys	Asp	Asn
				65				70						75	
Ala	Thr	Gln	Glu	Glu	Ile	Leu	His	Tyr	Leu	Glu	Lys	Thr	Cys	Glu	Trp
				85										95	

Ile His Asp Ser Ser Leu Ser Ala Ser Cys Lys Glu Val Val Asp Ser
 100 105 110
 Tyr Leu Pro Val Ile Leu Asp Met Ile Lys Gly Glu Met Ser Asn Pro
 115 120 125
 Gly Glu Val Cys Ser Ala Leu Asn Leu Cys Gln Ser Leu Gln Glu Tyr
 130 135 140
 Leu Ala Glu Gln Asn Gln Lys Gln Leu Glu Ser Asn Lys Val Pro Glu
 145 150 155 160
 Val Asp Met Ala Arg Val Val Ala Pro Phe Ser Ala Asn Ile Pro Leu
 165 170 175
 Leu Leu Tyr Pro Gln Asp His Pro Arg Ser Gln Pro Gln Pro Lys Ala
 180 185 190
 Asn Glu Asp Val Cys Gln Asp Cys Met Lys Leu Val Ser Asp Val Gln
 195 200 205
 Thr Ala Val Lys Thr Asn Ser Ser Phe Ile Gln Gly Phe Val Asp His
 210 215 220
 Val Lys Glu Asp Cys Asp Arg Leu Gly Pro Gly Val Ser Asp Ile Cys
 225 230 235 240
 Lys Asn Tyr Val Asp Gln Tyr Ser Glu Val Cys Val Gln Ile Leu Met
 245 250 255
 His Met Gln Pro Lys Glu Ile Cys Val Leu Ala Gly Phe Cys Asn Glu
 260 265 270
 Val Lys Arg Val Pro Met Lys Thr Leu Val Pro Ala Thr Glu Thr Ile
 275 280 285
 Lys Asn Ile Leu Pro Ala Leu Glu Met Met Asp Pro Tyr Glu Gln Asn
 290 295 300
 Leu Val Gln Ala His Asn Val Ile Leu Cys Gln Thr Cys Gln Phe Val
 305 310 315 320
 Met Asn Lys Phe Ser Glu Leu Ile Val Asn Asn Ala Thr Glu Glu Leu

	325		330		335
Leu Val Lys Gly Leu Ser Asn Ala Cys Ala Leu Leu Pro Asp Pro Ala					
	340		345		350
Arg Thr Lys Cys Gln Glu Val Val Gly Thr Phe Asp Pro Ser Leu Leu					
	355		360		365
Asp Asp Phe Ile His Glu Val Asn Pro Ser Ser Leu Cys Gly Val Ile					
	370		375		380
Gly Leu Cys Thr Ala Leu Pro Glu Leu Val Glu Ala Leu Glu Gln Pro					
385		390		395	400
Ala Pro Arg Ile Val Ser Ala Leu Leu Lys Glu Pro Thr Pro Pro Lys					
	405		410		415
Gln Pro Ala Gln Pro Lys Gln Ser Ala Leu Pro Ala His Val Pro Pro					
	420		425		430
Gln Lys Asn Gly Gly Phe Cys Glu Val Phe Lys Lys Leu Val Leu Tyr					
	435		440		445
Leu Glu His Asn Leu Glu Lys Asn Ser Thr Lys Glu Glu Ile Leu Ala					
	450		455		460
Ala Leu Glu Lys Gly Cys Ser Phe Leu Pro Asp Pro Tyr Gln Lys Gln					
465		470		475	480
Cys Asp Asp Phe Val Ala Glu Tyr Glu Pro Leu Leu Leu Glu Ile Leu					
	485		490		495
Val Glu Val Met Asp Pro Gly Phe Val Cys Ser Lys Ile Gly Val Cys					
	500		505		510
Pro Ser Ala Tyr Lys Leu Leu Leu Gly Thr Glu Lys Cys Val Trp Gly					
	515		520		525
Pro Ser Tyr Trp Cys Gln Asn Met Glu Thr Ala Ala Arg Cys Asn Ala					
	530		535		540
Val Asp His Cys Lys Arg His Val Trp Asn					
545		550			

<210> 231

<211> 419

<212> DNA

<213> Mus musculus

<400> 231

caagacccac cagagcaaca ccaggcggcc gtccgacagc cctcagtggc acaacctctg 60
ctgccccctgc agccccctgcc cggcgctcggg gtccggagtg cagtgagtg aagaagctct 120
tcagcacaga gacgtcacta caggctccatc ggcgcatcca cacaggtagc cggccatacc 180
cctgtccaga ctgtggcaag gccttcgcc agagtaccca tctgaaagac cacagacgcc 240
tacacacagg cgagcggccc ttgtcgtgtg aagtgtgtg caaggccttt gccatctcca 300
tgcgtctgga agaacatcgc cgcattccaca cgggtgagcg accctactcc tgtcctgact 360
gtggcaagag ctaccgttcc ttctccaatc tctggaagca cgcgaagatc caccagctt 419

<210> 232

<211> 277

<212> DNA

<213> Mus musculus

<400> 232

cacttcgcaa gtgtagtctc ccaccatggc atcgcgccta tccattttca aagaggcaat 60
gcattgatta agtctgagac tgagattttt gcactggtaa agttttgac tgtagtagtg 120
ctatttttat ttccatcata gatgaaaata tacgatttgt tcaacticca cttcacaac 180
atttcttcgg tgctttgcgc ctccacatta cggacgatgc aagggatgac cacagtttca 240
ttgcatgaag tgaactctat ggagttgacg ttactaa 277

<210> 233

<211> 3428

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (365).. (1114)

<400> 233

```

ccactgcccc gcgcagtcct tcgctgcgcg ctgacccccga ggaaggcagt acttggtcag 60
ggcgctgagg gacctccac cgggacgccg gcccctcccc gggcctctgc tcacttgacc 120
cccactccct agtccgtccc cttagtaggc ctgtcggatc ggggacgtgg ggcgagctga 180
gagcaggccc ggggtgggtg gtcaccgtgg tgaagacgtg gctgtcaaga tgatagaagt 240
actgacaact gactctcaga aactgctaca ccagctgaac accctgttgg aacaggagtc 300
tagatgtcag ccaaaggtct gcggcttgaa actaattgag tcggcccatg ataatggcct 360
caga atg act gca aga tta cgg gac ttt gaa gta aaa gat cta ctt agt 409
      Met Thr Ala Arg Leu Arg Asp Phe Glu Val Lys Asp Leu Leu Ser
          1             5             10             15
cta act cag ttc ttt ggc ttt gac acg gag aca ttt tcc cta gct gtg 457
Leu Thr Gln Phe Phe Gly Phe Asp Thr Glu Thr Phe Ser Leu Ala Val
          20             25             30
aat tta ctg gac aga ttc ttg tct aaa atg aag gta cag gcg aag cat 505
Asn Leu Leu Asp Arg Phe Leu Ser Lys Met Lys Val Gln Ala Lys His
          35             40             45
ctt ggg tgt gtt gga ctg agc tgc ttt tat ttg gct gtg aaa gcg act 553
Leu Gly Cys Val Gly Leu Ser Cys Phe Tyr Leu Ala Val Lys Ala Thr
          50             55             60
gaa gag gaa agg aat gtc cca ctg gcg act gat ttg atc cga ata agt 601
Glu Glu Glu Arg Asn Val Pro Leu Ala Thr Asp Leu Ile Arg Ile Ser
          65             70             75

```

cag tat agg ttc acg gtt tca gac ctg atg aga atg gag aag att gtg 649
 Gln Tyr Arg Phe Thr Val Ser Asp Leu Met Arg Met Glu Lys Ile Val
 80 85 90 95
 ttg gag aaa gtg tgt tgg aaa gtc aaa gct act act gcc ttt caa ttt 697
 Leu Glu Lys Val Cys Trp Lys Val Lys Ala Thr Thr Ala Phe Gln Phe
 100 105 110
 ctg cag ctc tat tat tca ctc gtt cac gac acc ttg cca ttt gag agg 745
 Leu Gln Leu Tyr Tyr Ser Leu Val His Asp Thr Leu Pro Phe Glu Arg
 115 120 125
 aga aac gat ctg aat ttt gaa aga cta gaa gcc caa ctt aag gcc tgc 793
 Arg Asn Asp Leu Asn Phe Glu Arg Leu Glu Ala Gln Leu Lys Ala Cys
 130 135 140
 cac tgc agg atc ata ttt tct aag gca aag cct tct gtg ctg gcg cta 841
 His Cys Arg Ile Ile Phe Ser Lys Ala Lys Pro Ser Val Leu Ala Leu
 145 150 155
 tct atc ctt gcg ttg gag atc caa gca ctg aaa tac gta gag tta aca 889
 Ser Ile Leu Ala Leu Glu Ile Gln Ala Leu Lys Tyr Val Glu Leu Thr
 160 165 170 175
 gaa gga gta gaa tgt att cag aaa cat tcc aag ata agt ggc cga gat 937
 Glu Gly Val Glu Cys Ile Gln Lys His Ser Lys Ile Ser Gly Arg Asp
 180 185 190
 ttg acc ttc tgg caa gag ctt gtt tcc aag tgt tta act gaa tat tca 985
 Leu Thr Phe Trp Gln Glu Leu Val Ser Lys Cys Leu Thr Glu Tyr Ser
 195 200 205
 tca aac aag tgc tcc aaa cct aac ggt cag aag ttg aaa tgg att gtg 1033
 Ser Asn Lys Cys Ser Lys Pro Asn Gly Gln Lys Leu Lys Trp Ile Val
 210 215 220
 tct gga cgc act gca cgg caa ctg aag cac agt tat tat aga ata act 1081
 Ser Gly Arg Thr Ala Arg Gln Leu Lys His Ser Tyr Tyr Arg Ile Thr

225

230

235

cac ctc cca acg att cct gag acc att tgt tag ttgataaatc tggttgttat 1134
 His Leu Pro Thr Ile Pro Glu Thr Ile Cys

240

245

250

tctctgtata cagaaaattt tccagtatga tcattttctg ctacaactga agaattgaaa 1194
 tactatcttc aatataaaga atatgggatg aaaacataaa ggaaaagtga attgttgact 1254
 ggtctagata gagaatactg gaaggcattc actgtgtaca gtcgtagca gttttaagag 1314
 aaaagacata tcaaaccctt agatatacgc taatactttt catcaaaaaga ttagcgtagt 1374
 agcaaagaga atacttttaa ctcgaatttt aaaagtagtt actgaaatag cacttcttta 1434
 aattacgtac caccceactg tagcttattt aaagttgcat aagcccatgc agaacaacaa 1494
 gcaatgtgac ccatataatga acaaatttta atctgcccat cgactatgaa aatgaagtac 1554
 aaacctgggt gatggactta caaagtaata tagggcatgc ccatgttagg tttctggaaa 1614
 ctgccagagt gtcttaattc tatagctagt attttacctc tatagcattt ggactaatac 1674
 aaagtaatta tatgcatgaa aatataaaat tggctctctga tacatacaca tttttgacat 1734
 ctcaatttct tcatcatacc aaagatttat ctttttaatga ttaaacacaa ttttttctt 1794
 aatgcatggc agcacatccc tttaatccca gcactagaga ggcagagaca ggtagatctc 1854
 tgagttcaaa gccaggctgg tctacacagt gagttccaag acagctagag accttgtctc 1914
 aaaaacactc aaaacaccca aacaccaggg gtaaattgtt ctgggaagtc agggaagatg 1974
 gtttagaagg gaagcctgac aacctgactt cattcttcag gaccacatg atggaaggag 2034
 agaacgaaga actcccaagt tctctcacat atgcacatac ctaccaccc ccgcaggaa 2094
 atacatgac atgcgtctga gatatacca gttcaccttt agcagctcgc agttttagg 2154
 cagatttctg ttaagttggg tctgtgttgt ttgcctatgt agcaggatta cagcagcagc 2214
 aaaaacggtc cctcaagtct tcttgccact ctgacctgag tttcctacgg tacaggattt 2274
 actctgagaa acctcagcac ctggccacag tagccttggc agaattggcct cacggtagg 2334
 gaaactcctg attctaagct tgggagagct acgcttagat ttgaattcac ccaggaagca 2394
 ttcaaatcaa ggctaaagac ataaatgtga aataaaactg tgaaccttca ttctaaagtt 2454
 catctgactt ccagatttg atcaatatat tcttaggttg tattaataat ggtaaactgc 2514
 ttaattttaa tctcaaaatt taaattatga ggtttacata aaaaccaaca tttcatgaat 2574
 gcacttttaa ggtattaaaa ggggtactta agcggtaa at ggtttcttgg caccataac 2634

caagtaatag ttaatttaca ggtgggattt ttttttattg ctatgagaat tacattttaa 2694
 attgtgggtg ttttatataa agcagatatc acaagttttg aaaatttggt acctttaata 2754
 tttcttctag agaatagggtg ttgtatcca taataaaaga aaaatttggtc agaactgctg 2814
 ctccaatcta atcccatitg agagaattgt ctttactgtc ttaataactg gatgaattat 2874
 cactctgaaa atgtatttat tgcactaaag ttagtttagg ctigataaaa cactccagac 2934
 atttttacta cagactgttt ctataaaact gccattgctt ctaatggaga attttatttt 2994
 aaaagaaata aaattgctga gtctatctgc aaaacccttc tctaagtcct atgggacgta 3054
 aggagacacc tccataattia taagagccgt tgtgctcaga gtctccaatgc tggcttgaat 3114
 gtaatgatcca cactgtttaa acataggcag cagctcaggg ccttgacag cctgagtcaa 3174
 cctagagtag ctggaaccat ttigacatgt aatggataag gaaattatcc attgagaagc 3234
 tgaacaataa accaaagaac ggggtgtattt tatccttaac ctctgtaaac cacgttacac 3294
 tgagaacact tcagttcttc ctaaagggtg ataggcttca gtctgaaaac aatattgatt 3354
 tggagtggac agaagttaac taaccaacta ccattatgtt ttgaatacac ctccaataa 3414
 aatgattgaa atgc 3428

<210> 234

<211> 249

<212> PRT

<213> Mus musculus

<400> 234

Met	Thr	Ala	Arg	Leu	Arg	Asp	Phe	Glu	Val	Lys	Asp	Leu	Leu	Ser	Leu
1				5					10					15	
Thr	Gln	Phe	Phe	Gly	Phe	Asp	Thr	Glu	Thr	Phe	Ser	Leu	Ala	Val	Asn
				20					25					30	
Leu	Leu	Asp	Arg	Phe	Leu	Ser	Lys	Met	Lys	Val	Gln	Ala	Lys	His	Leu
				35					40					45	
Gly	Cys	Val	Gly	Leu	Ser	Cys	Phe	Tyr	Leu	Ala	Val	Lys	Ala	Thr	Glu
				50					55					60	

<400> 235

gcgacgccgc tggccccgcc gccgttgcca ccgccgcctcc cgeccctcag ctccctcggcc 60
 gcgcatggga cccgcgacga cgagtiacgac tacctcttta aagtigtctt tattggagat 120
 tctggtgttg gaaagagtaa cctccigtct cgatttactc gaaatgagtt taatctggaa 180
 agcaagagta ccattggagt agagtttgca acaagaagca tccaggttga tgggaaaaca 240
 ataaaggcac agataitggga cacagcaggg caggagcggc acagggctat aacgtctgca 300
 tactatcgtg gagcagtagg tgccttattg gtttatgaca ttgctaagca tctcacatat 360
 gaaaatgtag agcgatggct gaaagaactg agagatcatg ctgatatgaa cattgtttatc 420
 atgcittgtg gcaataagag tgatttacgt catctcaggg cagttcctac agatgaagca 480
 agagcttttg cagagaagaa tgggtgtgca ttcattgaga catctgctct agattctaca 540
 aatgttgaag ctgcttttca gacaattcta acagagatat agggcattgt ttctcagaag 600
 ccatgtgccg acagacttga aatgacatgt ctccaagcac aatgggtgtcc tattcagttc 660

<210> 236

<211> 930

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1).. (930)

<400> 236

atg gac gac aag gcg ttc acc aag gag ctg gac cag tgg gtg gag cag 48
 Met Asp Asp Lys Ala Phe Thr Lys Glu Leu Asp Gln Trp Val Glu Gln
 1 5 10 15
 ctg aac gag tgt aag cag ctg aac gag aac caa gtg cgg acg ctg tgc 96
 Leu Asn Glu Cys Lys Gln Leu Asn Glu Asn Gln Val Arg Thr Leu Cys

20	25	30	
gag aag gct aag gaa att tta acg aaa gaa tca aat gtg caa gag gtc			144
Glu Lys Ala Lys Glu Ile Leu Thr Lys Glu Ser Asn Val Gln Glu Val			
35	40	45	
cgc tgt cct gtt acc gtc tgt gga gat gtg cat ggc caa ttc cat gac			192
Arg Cys Pro Val Thr Val Cys Gly Asp Val His Gly Gln Phe His Asp			
50	55	60	
ctt atg gag ctc ttc aga att ggt ggg aaa tca cca gat acg aac tac			240
Leu Met Glu Leu Phe Arg Ile Gly Gly Lys Ser Pro Asp Thr Asn Tyr			
65	70	75	80
cta ttc atg ggg gac tat gta gac aga ggc tac tac tct gtg gag act			288
Leu Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr			
85	90	95	
gtg act ctt ctt gta gca tta aag gtg cgc tat cca gag cgc atc aca			336
Val Thr Leu Leu Val Ala Leu Lys Val Arg Tyr Pro Glu Arg Ile Thr			
100	105	110	
ata itg cga gga aat cat gaa agc cgg cag atc aca caa gtg tat ggc			384
Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly			
115	120	125	
ttt tat gat gag tgc cta cgg aag tat gga aat gcc aac gtg tgg aaa			432
Phe Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys			
130	135	140	
tac ttt aca gat ctc ttt gat tat ctt cca ctt aca gct tta gta gat			480
Tyr Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Val Asp			
145	150	155	160
gga cag ata ttc tgc ctc cac ggt ggc ctg tct cca tcc ata gat aca			528
Gly Gln Ile Phe Cys Leu His Gly Gly Leu Ser Pro Ser Ile Asp Thr			
165	170	175	
ctg gac cac ata aga gcc ctg gat cgc ttg caa gaa gtt cca cat gag			576

Leu Asp His Ile Arg Ala Leu Asp Arg Leu Gln Glu Val Pro His Glu
 180 185 190
 ggc cca atg tgt gat ctc tta tgg tca gat ccg gat gac cgt ggc ggc 624
 Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Gly Gly
 195 200 205
 tgg ggc att tct cca cgt ggt gct ggc tac aca ttt gga caa gac att 672
 Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile
 210 215 220
 tct gaa aca ttt aac cat gcc aac ggt ctc aca ctg gtg tct cgt gct 720
 Ser Glu Thr Phe Asn His Ala Asn Gly Leu Thr Leu Val Ser Arg Ala
 225 230 235 240
 cac cag ctt gta atg gaa gga tat aac tgg tgc cat gat cgg aat gtg 768
 His Gln Leu Val Met Glu Gly Tyr Asn Trp Cys His Asp Arg Asn Val
 245 250 255
 gtc acc att ttt agt gcg ccc aat tac tgc tac cgt tgt ggg aac cag 816
 Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Gln
 260 265 270
 gct gct atc atg gaa tta gat gac act tta aaa tat tca ttt ctt cag 864
 Ala Ala Ile Met Glu Leu Asp Asp Thr Leu Lys Tyr Ser Phe Leu Gln
 275 280 285
 ttt gac cca gca cct cgt cgt gga gag cct cat gtg acc cgg cgc acc 912
 Phe Asp Pro Ala Pro Arg Arg Gly Glu Pro His Val Thr Arg Arg Thr
 290 295 300
 cca gac tac ttc cta taa 930
 Pro Asp Tyr Phe Leu
 305 310

<210> 237

<211> 309

<212> PRT

<213> Mus musculus

<400> 237

```

Met Asp Asp Lys Ala Phe Thr Lys Glu Leu Asp Gln Trp Val Glu Gln
  1           5           10           15
Leu Asn Glu Cys Lys Gln Leu Asn Glu Asn Gln Val Arg Thr Leu Cys
          20           25           30
Glu Lys Ala Lys Glu Ile Leu Thr Lys Glu Ser Asn Val Gln Glu Val
          35           40           45
Arg Cys Pro Val Thr Val Cys Gly Asp Val His Gly Gln Phe His Asp
          50           55           60
Leu Met Glu Leu Phe Arg Ile Gly Gly Lys Ser Pro Asp Thr Asn Tyr
          65           70           75           80
Leu Phe Met Gly Asp Tyr Val Asp Arg Gly Tyr Tyr Ser Val Glu Thr
          85           90           95
Val Thr Leu Leu Val Ala Leu Lys Val Arg Tyr Pro Glu Arg Ile Thr
          100          105          110
Ile Leu Arg Gly Asn His Glu Ser Arg Gln Ile Thr Gln Val Tyr Gly
          115          120          125
Phe Tyr Asp Glu Cys Leu Arg Lys Tyr Gly Asn Ala Asn Val Trp Lys
          130          135          140
Tyr Phe Thr Asp Leu Phe Asp Tyr Leu Pro Leu Thr Ala Leu Val Asp
          145          150          155          160
Gly Gln Ile Phe Cys Leu His Gly Gly Leu Ser Pro Ser Ile Asp Thr
          165          170          175
Leu Asp His Ile Arg Ala Leu Asp Arg Leu Gln Glu Val Pro His Glu
          180          185          190
Gly Pro Met Cys Asp Leu Leu Trp Ser Asp Pro Asp Asp Arg Gly Gly

```

195 200 205
 Trp Gly Ile Ser Pro Arg Gly Ala Gly Tyr Thr Phe Gly Gln Asp Ile
 210 215 220
 Ser Glu Thr Phe Asn His Ala Asn Gly Leu Thr Leu Val Ser Arg Ala
 225 230 235 240
 His Gln Leu Val Met Glu Gly Tyr Asn Trp Cys His Asp Arg Asn Val
 245 250 255
 Val Thr Ile Phe Ser Ala Pro Asn Tyr Cys Tyr Arg Cys Gly Asn Gln
 260 265 270
 Ala Ala Ile Met Glu Leu Asp Asp Thr Leu Lys Tyr Ser Phe Leu Gln
 275 280 285
 Phe Asp Pro Ala Pro Arg Arg Gly Glu Pro His Val Thr Arg Arg Thr
 290 295 300
 Pro Asp Tyr Phe Leu

305

<210> 238

<211> 1203

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (67).. (873)

<400> 238

acgagacgaa gacggaaccg gagccgggcg cgcggacggc ggacgcgggt cctgagaaag 60
 ccgaag atg gca gtg aat gtg tac tct acg tca gtc acc agt gat aac 108

Met Ala Val Asn Val Tyr Ser Thr Ser Val Thr Ser Asp Asn

1	5	10	
cta agt cga cat gac atg ctg gct tgg atc aat gaa tct ctg cag ttg	156		
Leu Ser Arg His Asp Met Leu Ala Trp Ile Asn Glu Ser Leu Gln Leu			
15	20	25	30
aat ctg aca aag ata gaa cag ttg tgt tca ggg gct gca tat tgt cag	204		
Asn Leu Thr Lys Ile Glu Gln Leu Cys Ser Gly Ala Ala Tyr Cys Gln			
35	40	45	
ttt atg gac atg ctc ttc cct gga tcc att gcc ttg aag aaa gtg aaa	252		
Phe Met Asp Met Leu Phe Pro Gly Ser Ile Ala Leu Lys Lys Val Lys			
50	55	60	
ttc caa gct aag cta gaa cat gaa tat atc cag aac ttc aaa ata cta	300		
Phe Gln Ala Lys Leu Glu His Glu Tyr Ile Gln Asn Phe Lys Ile Leu			
65	70	75	
caa gca ggc ttc aag agg atg ggc gtt gac aaa ata att cct gtg gat	348		
Gln Ala Gly Phe Lys Arg Met Gly Val Asp Lys Ile Ile Pro Val Asp			
80	85	90	
aaa tta gta aaa gga aaa ttt cag gac aat ttt gaa ttt gtt caa tgg	396		
Lys Leu Val Lys Gly Lys Phe Gln Asp Asn Phe Glu Phe Val Gln Trp			
95	100	105	110
ttc aag aag ttt ttt gat gca aat tat gat gga aaa gag tat gat cct	444		
Phe Lys Lys Phe Phe Asp Ala Asn Tyr Asp Gly Lys Glu Tyr Asp Pro			
115	120	125	
gta gct gcc aga caa ggt caa gaa act gca gtg gct cct tct ctt gtc	492		
Val Ala Ala Arg Gln Gly Gln Glu Thr Ala Val Ala Pro Ser Leu Val			
130	135	140	
gcc cca gct ttg agt aaa ccg aag aaa cct ctc ggc tcc agt act gca	540		
Ala Pro Ala Leu Ser Lys Pro Lys Lys Pro Leu Gly Ser Ser Thr Ala			
145	150	155	
gcc cca cag aga ccc att gca aca cag agg act act gca gct cct aag	588		

Ala Pro Gln Arg Pro Ile Ala Thr Gln Arg Thr Thr Ala Ala Pro Lys
 160 165 170
 gct ggc ccc gga atg gtg cga aag aat cct ggt gtg ggc aat gga gat 636
 Ala Gly Pro Gly Met Val Arg Lys Asn Pro Gly Val Gly Asn Gly Asp
 175 180 185 190
 gat gaa gca gct gaa ttg atg cag cag gtc aaa gta ctg aag ctt act 684
 Asp Glu Ala Ala Glu Leu Met Gln Gln Val Lys Val Leu Lys Leu Thr
 195 200 205
 gtt gaa gac ttg gag aag gag aga gac ttc tac ttc gga aag cta agg 732
 Val Glu Asp Leu Glu Lys Glu Arg Asp Phe Tyr Phe Gly Lys Leu Arg
 210 215 220
 aac att gaa ctg att tgc cag gag aac gag ggg gaa aac gac cct gta 780
 Asn Ile Glu Leu Ile Cys Gln Glu Asn Glu Gly Glu Asn Asp Pro Val
 225 230 235
 ctg cag agg att gta gat att ctt tat gcc aca gat gaa ggc ttt gtg 828
 Leu Gln Arg Ile Val Asp Ile Leu Tyr Ala Thr Asp Glu Gly Phe Val
 240 245 250
 ata cct gat gaa ggg ggc cca cag gag gaa caa gaa gag tat taa 873
 Ile Pro Asp Glu Gly Gly Pro Gln Glu Glu Gln Glu Glu Tyr
 255 260 265
 gcagcctgga ccagcagagc aacatccgaa gtcttcactc caaatcatgt gcttaactgt 933
 taatactccc ttttattaat cttagaggat tcaactggttt cttttcataa gcaaaaagta 993
 cctcttcttc aaagtgcact ttgcagaagt ctcaccttct ccgatgagtt tgagtttagga 1053
 gctttggcct tgtagcagag cagtattaac atctagttagg tttaccaggg gaacaagagg 1113
 ccaaccaatgg ggctcttcat gtggatgctg gccacactga ctgatggaga aggggggttta 1173
 taatacgaga ggtgacaacc tcagaaatgc 1203

<210> 239

<211> 268

<212> PRT

<213> Mus musculus

<400> 239

```

Met Ala Val Asn Val Tyr Ser Thr Ser Val Thr Ser Asp Asn Leu Ser
  1              5              10              15
Arg His Asp Met Leu Ala Trp Ile Asn Glu Ser Leu Gln Leu Asn Leu
      20              25              30
Thr Lys Ile Glu Gln Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met
      35              40              45
Asp Met Leu Phe Pro Gly Ser Ile Ala Leu Lys Lys Val Lys Phe Gln
      50              55              60
Ala Lys Leu Glu His Glu Tyr Ile Gln Asn Phe Lys Ile Leu Gln Ala
      65              70              75              80
Gly Phe Lys Arg Met Gly Val Asp Lys Ile Ile Pro Val Asp Lys Leu
      85              90              95
Val Lys Gly Lys Phe Gln Asp Asn Phe Glu Phe Val Gln Trp Phe Lys
      100              105              110
Lys Phe Phe Asp Ala Asn Tyr Asp Gly Lys Glu Tyr Asp Pro Val Ala
      115              120              125
Ala Arg Gln Gly Gln Glu Thr Ala Val Ala Pro Ser Leu Val Ala Pro
      130              135              140
Ala Leu Ser Lys Pro Lys Lys Pro Leu Gly Ser Ser Thr Ala Ala Pro
      145              150              155              160
Gln Arg Pro Ile Ala Thr Gln Arg Thr Thr Ala Ala Pro Lys Ala Gly
      165              170              175
Pro Gly Met Val Arg Lys Asn Pro Gly Val Gly Asn Gly Asp Asp Glu
      180              185              190
Ala Ala Glu Leu Met Gln Gln Val Lys Val Leu Lys Leu Thr Val Glu

```

195 200 205
 Asp Leu Glu Lys Glu Arg Asp Phe Tyr Phe Gly Lys Leu Arg Asn Ile
 210 215 220
 Glu Leu Ile Cys Gln Glu Asn Glu Gly Glu Asn Asp Pro Val Leu Gln
 225 230 235 240
 Arg Ile Val Asp Ile Leu Tyr Ala Thr Asp Glu Gly Phe Val Ile Pro
 245 250 255
 Asp Glu Gly Gly Pro Gln Glu Glu Gln Glu Glu Tyr
 260 265

<210> 240

<211> 667

<212> DNA

<213> Mus musculus

<400> 240

ttcaigggaa actcttagat ggattcttca ttcgaccatt ctacaagatg atgctgggga 60.
 agcagataac gctgaacgac atggagtccg tggacagcga gtactacaac tctttgaagt 120
 ggatctttaga aaacgacccc acggaacttg acctcatgtt ctgcatagac gaagagaact 180
 ttgggcagac ataccaagtg gatctgaagc ccaacgggtc agaaataatg gtaaccaatg 240
 agaacaaacg agaatacatt gacttagtca tccagiggag atttgtgaac aggggccaga 300
 agcaaatgaa tgccttcttg gagggattta cagaacttct tccaatcgac ttgattaaaa 360
 tttttgatga aaatgagctg gagttgctga tgtgcggcct tggatgatgc gacgtgaacg 420
 actggagaca gcactctatt tacaagaacg gctactgccc caaccaccct gtcattccagt 480
 ggttctggaa ggccgtgctc ctgatggatg ctgagaagcg catccggita ctacagtttg 540
 tcacaggcac ctccagagta cccatgaatg gatttgccga actctatggt tccaatggtc 600
 ctcagctggt tacaatagag caatggggca gtccgaaaaa ctaccagagc tctacatgct 660
 taatcgc 667

<210> 241

<211> 2089

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (157).. (780)

<400> 241

```

agcaaggccg gagctttgac cataaagccc aaggcggcgg cgttggcggc ggtgtttggg 60
gccgggcagc tccgaggagc ctgctggagc cggaatcgga cgtctctgtt gcggcctgcg 120
ttgtgtctcc tccctccgtg accctgcgct tcaagg atg acc tct agg aag aaa 174
                                     Met Thr Ser Arg Lys Lys
                                     1           5
gtg ttg ctg aag gtc atc atc ctg ggg gac tct ggt gtt gga aag acc 222
Val Leu Leu Lys Val Ile Ile Leu Gly Asp Ser Gly Val Gly Lys Thr
                10           15           20
tct ctc atg aac cag tat gtg aac aag aag ttc agt aac cag tac aaa 270
Ser Leu Met Asn Gln Tyr Val Asn Lys Lys Phe Ser Asn Gln Tyr Lys
                25           30           35
gcc aca ata gga gcg gac ttt ctg acc aag gag gtg atg gtg gac gac 318
Ala Thr Ile Gly Ala Asp Phe Leu Thr Lys Glu Val Met Val Asp Asp
                40           45           50
aga ctt gtt acc atg cag atc tgg gac aca gcc ggt caa gaa cgg ttc 366
Arg Leu Val Thr Met Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe
                55           60           65           70
cag tct ctt ggt gtg gcc ttc tac aga ggt gca gat tgc tgt gtt ctg 414
Gln Ser Leu Gly Val Ala Phe Tyr Arg Gly Ala Asp Cys Cys Val Leu

```

	75	80	85	
gtg ttt gat gtg act gcc ccc aac act ttc aaa acc ctc gac agc tgg				462
Val Phe Asp Val Thr Ala Pro Asn Thr Phe Lys Thr Leu Asp Ser Trp				
	90	95	100	
aga gac gag ttt ctc atc cag gcc agc ccc cgg gat ccc gag aac ttc				510
Arg Asp Glu Phe Leu Ile Gln Ala Ser Pro Arg Asp Pro Glu Asn Phe				
	105	110	115	
cct ttt gtt gtg ttg gga aac aag att gac ctg gaa aac aga caa gtg				558
Pro Phe Val Val Leu Gly Asn Lys Ile Asp Leu Glu Asn Arg Gln Val				
	120	125	130	
gcc aca aag agg gca cag gct tgg tgc tac agg aaa aac aac att cct				606
Ala Thr Lys Arg Ala Gln Ala Trp Cys Tyr Arg Lys Asn Asn Ile Pro				
	135	140	145	150
tac ttc gag acc agt gcc aag gag gcc atc aat gtg gag cag gcc ttc				654
Tyr Phe Glu Thr Ser Ala Lys Glu Ala Ile Asn Val Glu Gln Ala Phe				
	155	160	165	
cag aca att gct cgg aat gcc ctt aaa cag gaa aca gaa gtg gaa ctg				702
Gln Thr Ile Ala Arg Asn Ala Leu Lys Gln Glu Thr Glu Val Glu Leu				
	170	175	180	
tac aat gaa ttc cct gaa ccc atc aaa ctg gac aag aat gac cgg gcc				750
Tyr Asn Glu Phe Pro Glu Pro Ile Lys Leu Asp Lys Asn Asp Arg Ala				
	185	190	195	
aag gcc tcc gca gaa agc tgc agt tgt tga aggggcagtg agcacagagt				800
Lys Ala Ser Ala Glu Ser Cys Ser Cys				
	200	205		
ccttcacaga ccaagaacac acacgiaggc cttcaatatg cgtccctect cctccaaaca				860
gaccagaacg tgagctctca catccagctg ccaaaagaaa ctccaccgaa cagttaccca				920
acacacacac atacacaaaa cacactcgtg cacacaaaaa cacatacaca caacacacac				980
acagcaagca aactccagcc tgtgcctgtc agggctcctg gggcagctgc gcctcgtggg				1040

```

cctgtgtatg gcaggcataat ggcagagacc ctgggtgctc tgggggtgcag tgggcatgga 1100
aagcttactc tttttgtcca ctggagagtg agagaactgt tcacagtcca tctgtgtcta 1160
attatctgat ttttttttaa cggctcttggt gtcctttacc cctccctcct tgaaggtect 1220
gtgggaaggc tgggtcccag gctccgttct gagcaggtct ttttgtatgt atctgttaat 1280
gcttgttact ttttaactaat cagatctttt tacagtatcc atttattatg taatgcttct 1340
tagaaaagaa tcttatagta catgttaata tatgcaacca attaaaatgt ataaattagt 1400
gtaaggaatt cctggattgt gtgtttaagt cctctaacgc aggcgtgcaa ggtggagggt 1460
tgaaccctgt ctggattaca gagtgttaga gactcaagtt tggaagtcca gctagcggca 1520
gtattctgta cagtagacac aagaattatg tacgcccttt atcacagact taagagccaa 1580
aaagcttttc atctctctga agggaaaact gaacatgaac agttcccttc tgtgtctaaa 1640
ttttccaaaa ggttgatttt gcttaataata gtagtgtata caatggataa attgctgtta 1700
cttcaagaat taaaattctc attttctccc ttctgtttt ttttccttat attcaacact 1760
ttaatgatgcc cttttgtcac tatcttactc aaagaggaaa ggagaacca ccagacctgt 1820
cccagtact ctaccttgt tctagaaggc gctccttcca gggttgtggt acctgtaggt 1880
tagcagacce tcttctttc ccaccacca agtgtggccc agcactaacc caccgtctct 1940
tgggttgagc cctggcagtt ctgtcccttc ccgaggtcct gccctgcac atggcttgct 2000
tcttgagca ctcccccttc agaggtctac attctagggt gtaggctgag ttcttctgta 2060
aagagacgaa cgtgatgcc: ataaaattt 2089

```

<210> 242

<211> 207

<212> PRT

<213> Mus musculus

<400> 242

Met Thr Ser Arg Lys Lys Val Leu Leu Lys Val Ile Ile Leu Gly Asp

1

5

10

15

Ser Gly Val Gly Lys Thr Ser Leu Met Asn Gln Tyr Val Asn Lys Lys

20

25

30

Phe Ser Asn Gln Tyr Lys Ala Thr Ile Gly Ala Asp Phe Leu Thr Lys
 35 40 45
 Glu Val Met Val Asp Asp Arg Leu Val Thr Met Gln Ile Trp Asp Thr
 50 55 60
 Ala Gly Gln Glu Arg Phe Gln Ser Leu Gly Val Ala Phe Tyr Arg Gly
 65 70 75 80
 Ala Asp Cys Cys Val Leu Val Phe Asp Val Thr Ala Pro Asn Thr Phe
 85 90 95
 Lys Thr Leu Asp Ser Trp Arg Asp Glu Phe Leu Ile Gln Ala Ser Pro
 100 105 110
 Arg Asp Pro Glu Asn Phe Pro Phe Val Val Leu Gly Asn Lys Ile Asp
 115 120 125
 Leu Glu Asn Arg Gln Val Ala Thr Lys Arg Ala Gln Ala Trp Cys Tyr
 130 135 140
 Arg Lys Asn Asn Ile Pro Tyr Phe Glu Thr Ser Ala Lys Glu Ala Ile
 145 150 155 160
 Asn Val Glu Gln Ala Phe Gln Thr Ile Ala Arg Asn Ala Leu Lys Gln
 165 170 175
 Glu Thr Glu Val Glu Leu Tyr Asn Glu Phe Pro Glu Pro Ile Lys Leu
 180 185 190
 Asp Lys Asn Asp Arg Ala Lys Ala Ser Ala Glu Ser Cys Ser Cys
 195 200 205

<210> 243

<211> 2362

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (81).. (734)

<400> 243

```

cggctgagcc cagagctctt cagcagggaa gaticccttc cccctgctt caggctgctg 60
agcactgagc ggcgctcaga atg gaa gcc atc gcc aaa tat gac ttc aaa gct 113
      Met Glu Ala Ile Ala Lys Tyr Asp Phe Lys Ala
              1              5              10
act gct gac gat gag ctg agc ttc aaa agg ggg gac atc ctt aag gtt 161
Thr Ala Asp Asp Glu Leu Ser Phe Lys Arg Gly Asp Ile Leu Lys Val
              15              20              25
ttg aat gaa gaa tgt gac cag aac tgg tat aag gca gaa ctc aat ggg 209
Leu Asn Glu Glu Cys Asp Gln Asn Trp Tyr Lys Ala Glu Leu Asn Gly
              30              35              40
aaa gat ggc ttc atc ccc aag aat tac ata gaa atg aaa cca cat ccg 257
Lys Asp Gly Phe Ile Pro Lys Asn Tyr Ile Glu Met Lys Pro His Pro
              45              50              55
tgg ttt ttt ggc aaa atc ccc aga gcc aag gca gaa gaa atg ctc agc 305
Trp Phe Phe Gly Lys Ile Pro Arg Ala Lys Ala Glu Glu Met Leu Ser
              60              65              70              75
aaa cag cgg cat gac ggg gcc ttc ctg atc cga gag agc gag agc gct 353
Lys Gln Arg His Asp Gly Ala Phe Leu Ile Arg Glu Ser Glu Ser Ala
              80              85              90
cct ggg gac ttc tcc ctg tcc gtc aag ttt gga aat gat gtg cag cac 401
Pro Gly Asp Phe Ser Leu Ser Val Lys Phe Gly Asn Asp Val Gln His
              95              100              105
ttc aag gtg ctc cgc gac gga gcc ggg aag tat ttc ctg tgg gtg gtg 449
Phe Lys Val Leu Arg Asp Gly Ala Gly Lys Tyr Phe Leu Trp Val Val
              110              115              120

```


aag ttt aat tct ttg aat gag ctg gta gat tac cac aga tca aca tcc 497
Lys Phe Asn Ser Leu Asn Glu Leu Val Asp Tyr His Arg Ser Thr Ser
125 130 135
gtg tcc agg aac cag cag ata ttc tta cgg gac ata gaa cag atg cca 545
Val Ser Arg Asn Gln Gln Ile Phe Leu Arg Asp Ile Glu Gln Met Pro
140 145 150 155
cag cag cca acc tac gtc cag gcg ctc ttt gac ttt gac ccc cag gag 593
Gln Gln Pro Thr Tyr Val Gln Ala Leu Phe Asp Phe Asp Pro Gln Glu
160 165 170
gat ggc gag ctg ggc ttt cgc aga gga gac ttc att cat gtc atg gat 641
Asp Gly Glu Leu Gly Phe Arg Arg Gly Asp Phe Ile His Val Met Asp
175 180 185
aac tca gat ccc aat tgg tgg aaa ggg gcc tgc cac ggg cag acc ggc 689
Asn Ser Asp Pro Asn Trp Trp Lys Gly Ala Cys His Gly Gln Thr Gly
190 195 200
atg ttt ccc cgc aat tat gtc acc cca gtg aac cgg aac gtc taa 734
Met Phe Pro Arg Asn Tyr Val Thr Pro Val Asn Arg Asn Val
205 210 215
gaagcaaaag agattattta aagaaagtga aaagttaaga ccgttcacaa gaattacacc 794
cacacgctgc ctgtcacagc ctgtgaggga acgcagaaca cctggctggg tcccacgggt 854
gaccctctca ttgggtigca actttggggg gtggggtagg ggtgtttgat ttcataatgc 914
caaaacttaa cctattgaat gaattacagt ttttattacg gaatctcgcc gctacccttg 974
ttccccctct gtgtcctttt tctcgttctt tctttcctgt ccagtgcag atgtttaagg 1034
ccacatatag tccagctgat gccaataata aaagacaaga aaccaagtgg gctggatatt 1094
tctctatgca aaatgtctgt ggagatggat ggactgaaag agccggattc ctcacacaca 1154
ggggcagcca gtgcttcttg ggccctgggt ggggttcacc cgagatgcc aggggtaccg 1214
cctccagcct caggcctgga gcattccatc aaagtiggaa ttaggggaag gaggccact 1274
gacctccccg gtctcctgag agtcagactg caggccctcc cctctccac tgcttccctt 1334
caggtgtttt gacgtttttt tgtttgtttg ttgtttttt ttaaatagtg cctttgtctt 1394

atttcaaggg tgttcataaa tggatattgt accatititit tttttaataa gttaaagaca 1454
 gtccagagct tttcagtiga ttctgtctct atccctgtgta aatatititcc tctcagggca 1514
 ggggaaagag gacagagaaa ggagctggta gaagcagaga gtgtatitcc catcttgaat 1574
 gggccggagg tctcgaagcc tcagctitita ctttgtgagc tgcaacactc gcttcgactc 1634
 agactcagtg gacatcagag tctctgtctc cgtgtctcag ttatggctctg ctctctctat 1694
 gccctggagct actgatccaa acacaagacg gtcagaggag ccttggcctc cticactctt 1754
 ataggcctac atgcgatggg ctigaagaga attggccttc atttttcacg ctcgatttcc 1814
 ccacctgtcc aagggtgcag atagcaggat tgtggggctc gccgcctctc tcttggcagt 1874
 gggttgtgct gcccctcccc ccacccacc cctccatccc acaaagcctt tcgaggtagg 1934
 agagaccaag accagtgcac agctititaac tcttgtcttc tgtgagtttt ccgtcctctg 1994
 tagtcacgtg cctgcacacc gtctctctca ccttgcctcc ttcccacaga gaagcagggc 2054
 tccaccagg ccttcccttg gagtccgtgc atccatgggc tgctagactc ttgcgggtag 2114
 agtctccctt ggacttagca ttgtgagatg gactcagctc agggcgcccc taaggctcgg 2174
 aggccatggc cttctgggtc cccacctctc ctggttcgct gctgctctcc ctgctgatga 2234
 taaagtaatc tctggagtca cacctgggcc atgtgatgtt ttttatitig gaattggaga 2294
 tatcatgaag ccttgcctgaa ctaagttitg tgtgtatata tttaaagatc agtgittaaa 2354
 taaaaaaaa 2362

<210> 244

<211> 217

<212> PRT

<213> Mus musculus

<400> 244

Met	Glu	Ala	Ile	Ala	Lys	Tyr	Asp	Phe	Lys	Ala	Thr	Ala	Asp	Asp	Glu
1				5					10					15	
Leu	Ser	Phe	Lys	Arg	Gly	Asp	Ile	Leu	Lys	Val	Leu	Asn	Glu	Glu	Cys
				20					25					30	
Asp	Gln	Asn	Trp	Tyr	Lys	Ala	Glu	Leu	Asn	Gly	Lys	Asp	Gly	Phe	Ile

35	40	45
Pro Lys Asn Tyr Ile Glu Met Lys Pro His Pro Trp Phe Phe Gly Lys		
50	55	60
Ile Pro Arg Ala Lys Ala Glu Glu Met Leu Ser Lys Gln Arg His Asp		
65	70	75
Gly Ala Phe Leu Ile Arg Glu Ser Glu Ser Ala Pro Gly Asp Phe Ser		
85	90	95
Leu Ser Val Lys Phe Gly Asn Asp Val Gln His Phe Lys Val Leu Arg		
100	105	110
Asp Gly Ala Gly Lys Tyr Phe Leu Trp Val Val Lys Phe Asn Ser Leu		
115	120	125
Asn Glu Leu Val Asp Tyr His Arg Ser Thr Ser Val Ser Arg Asn Gln		
130	135	140
Gln Ile Phe Leu Arg Asp Ile Glu Gln Met Pro Gln Gln Pro Thr Tyr		
145	150	155
Val Gln Ala Leu Phe Asp Phe Asp Pro Gln Glu Asp Gly Glu Leu Gly		
165	170	175
Phe Arg Arg Gly Asp Phe Ile His Val Met Asp Asn Ser Asp Pro Asn		
180	185	190
Trp Trp Lys Gly Ala Cys His Gly Gln Thr Gly Met Phe Pro Arg Asn		
195	200	205
Tyr Val Thr Pro Val Asn Arg Asn Val		
210	215	

<210> 245

<211> 1220

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (111).. (671)

<400> 245

gcctggacag tgctgcgggg ttctgcctg ctcccaagct ggtagaatcc ccaaaagaag 60
 gtaaaggagg caagccttcc cgcgccctctg gaaagagcgc caaacggaaa atg gaa 116

Met Glu

1

ggc cca aag aaa gcc cag ggc cac agc cct gta aat ggc ttg ctg aaa 164
 Gly Pro Lys Lys Ala Gln Gly His Ser Pro Val Asn Gly Leu Leu Lys

5

10

15

ggg cag gag agt cga agt caa agc agg agt cgt gag cag agc tac tca 212
 Gly Gln Glu Ser Arg Ser Gln Ser Arg Ser Arg Glu Gln Ser Tyr Ser

20

25

30

agg tcc cca tca cgg tct gct tct cca aag aga agg aaa agt gat agt 260
 Arg Ser Pro Ser Arg Ser Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser

35

40

45

50

ggc tct acc tca ggt ggg tcc aag tca cag agt cgt tct cgg agc cga 308
 Gly Ser Thr Ser Gly Gly Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg

55

60

65

agt gac tct cct cca agg cag gta cac cga ggt gct ccc tac aaa ggc 356
 Ser Asp Ser Pro Pro Arg Gln Val His Arg Gly Ala Pro Tyr Lys Gly

70

75

80

tca gaa gtg agg ggc tcc cgg aaa tca aag gac tgc aag tac ctc acc 404
 Ser Glu Val Arg Gly Ser Arg Lys Ser Lys Asp Cys Lys Tyr Leu Thr

85

90

95

cag aag cca cac aag tct cgt agc cgg agc tcc tct cgt tcc cga agc 452
 Gln Lys Pro His Lys Ser Arg Ser Arg Ser Ser Arg Ser Arg Ser

100	105	110	
cgg tca cga gag cgg acg gac aat tct gga aaa tac aag aag aaa agt			500
Arg Ser Arg Glu Arg Thr Asp Asn Ser Gly Lys Tyr Lys Lys Lys Ser			
115	120	125	130
cat tac tat aga gat caa aga cgt gag cgc tca agg tca tat gag cgc			548
His Tyr Tyr Arg Asp Gln Arg Arg Glu Arg Ser Arg Ser Tyr Glu Arg			
	135	140	145
aca ggc cat cgc tat gag agg gac cac cct gga cac agc agg cat cgg			596
Thr Gly His Arg Tyr Glu Arg Asp His Pro Gly His Ser Arg His Arg			
	150	155	160
agg tgt gat agg atc tct ggt ggc tgc cct tgg tcc ctc cct gtt ggg			644
Arg Cys Asp Arg Ile Ser Gly Gly Cys Pro Trp Ser Leu Pro Val Gly			
	165	170	175
cac acc ttg gcg tca gtg gcc ttg tag catgatgttt ttcgaaagtg			691
His Thr Leu Ala Ser Val Ala Leu			
180	185		
tttttaattg gaccttgagg tgaatttgat tgatgagaca gtgggcaagg tgcccttcag			751
gctggccttg ggagtgtgtg gcatctgtcc cggttaatgg tccacctcaa ctgcagacct			811
tcaggtagct ggatggaaca gcaaaggcac acgtcccat tggcgtggct tgggtgctatt			871
gacaagctgt ctcttcactc ctaaactgat actcaattac gttaagccaa gaaagatgat			931
ttttgaaatc ttgcctata ttaggttgta cttgtgtaca tattttgcag tggttcaca			991
tgagaaaatg gccttaatag ccccttggt ctcctattcac gttgtaaata aacatgttta			1051
atacaagtaa aagctatata cgagaactca gaattttgat tctgttagct taacacttgt			1111
atagaaaatt gagattttta aaatgtgaag gtatttaggt ctgtgttgaa agtcatatat			1171
ttttatctgt gcaatgctga gtgcaggccc ttagagcac actggcggc			1220

<210> 246

<211> 186

<212> PRT

<213> Mus musculus

<400> 246

```

Met Glu Gly Pro Lys Lys Ala Gln Gly His Ser Pro Val Asn Gly Leu
  1           5           10           15
Leu Lys Gly Gln Glu Ser Arg Ser Gln Ser Arg Ser Arg Glu Gln Ser
          20           25           30
Tyr Ser Arg Ser Pro Ser Arg Ser Ala Ser Pro Lys Arg Arg Lys Ser
          35           40           45
Asp Ser Gly Ser Thr Ser Gly Gly Ser Lys Ser Gln Ser Arg Ser Arg
  50           55           60
Ser Arg Ser Asp Ser Pro Pro Arg Gln Val His Arg Gly Ala Pro Tyr
  65           70           75           80
Lys Gly Ser Glu Val Arg Gly Ser Arg Lys Ser Lys Asp Cys Lys Tyr
          85           90           95
Leu Thr Gln Lys Pro His Lys Ser Arg Ser Arg Ser Ser Ser Arg Ser
          100          105          110
Arg Ser Arg Ser Arg Glu Arg Thr Asp Asn Ser Gly Lys Tyr Lys Lys
          115          120          125
Lys Ser His Tyr Tyr Arg Asp Gln Arg Arg Glu Arg Ser Arg Ser Tyr
          130          135          140
Glu Arg Thr Gly His Arg Tyr Glu Arg Asp His Pro Gly His Ser Arg
  145          150          155          160
His Arg Arg Cys Asp Arg Ile Ser Gly Gly Cys Pro Trp Ser Leu Pro
          165          170          175
Val Gly His Thr Leu Ala Ser Val Ala Leu
          180          185

```

<210> 247

<211> 1805

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (360).. (1739)

<400> 247

```

ggcacgaggg actttggtgc gggcccctgg gagacgcggg gggcagcact gtgtcggggt 60
gggccgttcc cggtcacctg cccgcgggcg gagcgcgcgc ccaggcgacc cccgcctccc 120
gtcttgctcc cgccccggga ggaagcgagg ggcgcggtgt aaacagagcg gcggccgtga 180
tgtcagccgg tcacatggag cctcttatgg ctcgggatgg ctctcggcgg gcgggcagct 240
gcggcagctg ctgctgtggc tcgggcggcg gcggcaagag ggggctccgg ggtcggacgg 300
tcggctctcc ctgcgtcttc cgcaccgagg cgtaaaggat gtattttgtg atcgcagcg 359
atg aaa gct caa att gaa att att cca tgc aag atc tgt gga gac aaa 407
Met Lys Ala Gln Ile Glu Ile Ile Pro Cys Lys Ile Cys Gly Asp Lys
      1           5           10           15
tcg tca gga atc cat tat ggt gtc att acg tgt gaa ggc tgc aag ggc 455
Ser Ser Gly Ile His Tyr Gly Val Ile Thr Cys Glu Gly Cys Lys Gly
           20           25           30
ttt ttc agg aga agt cag cag agc aat gcc acc tac tcc tgt cct cgt 503
Phe Phe Arg Arg Ser Gln Gln Ser Asn Ala Thr Tyr Ser Cys Pro Arg
           35           40           45
cag aag aac tgt ttg att gat cgg acc agc aga aac cgc tgc cag cat 551
Gln Lys Asn Cys Leu Ile Asp Arg Thr Ser Arg Asn Arg Cys Gln His
           50           55           60
tgt cgg ctg cag aaa tgc ctg gcc gtg ggg atg tct cga gat gct gtc 599
Cys Arg Leu Gln Lys Cys Leu Ala Val Gly Met Ser Arg Asp Ala Val

```

65	70	75	80	
aag ttt ggt cgg atg tcc aag aag cag aga gac agc ttg tac gcc gag	647			
Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp Ser Leu Tyr Ala Glu				
85	90	95		
gtg cag aag cgc cga atg cag cag cag cag cga gac cac cag cag cag	695			
Val Gln Lys Arg Arg Met Gln Gln Gln Gln Arg Asp His Gln Gln Gln				
100	105	110		
cct ggg gag gcg acg ctg acg ccc acc tac aac atc tca gcc aat gga	743			
Pro Gly Glu Ala Thr Leu Thr Pro Thr Tyr Asn Ile Ser Ala Asn Gly				
115	120	125		
tcg gcg gaa ctg cat gat gac ctc agc acc tat atg gat ggg cac acc	791			
Ser Ala Glu Leu His Asp Asp Leu Ser Thr Tyr Met Asp Gly His Thr				
130	135	140		
ccc gag ggc agc aag gcg gac tca gcc gtc agc agc ttc tac ctg gac	839			
Pro Glu Gly Ser Lys Ala Asp Ser Ala Val Ser Ser Phe Tyr Leu Asp				
145	150	155	160	
atc cag ccc tcc cca gac cag tcg gga ttg gac atc aat ggg atc aaa	887			
Ile Gln Pro Ser Pro Asp Gln Ser Gly Leu Asp Ile Asn Gly Ile Lys				
165	170	175		
ccc gaa ccc ata tgt gac tac aca cca gca tct ggc ttc ttc ccc tac	935			
Pro Glu Pro Ile Cys Asp Tyr Thr Pro Ala Ser Gly Phe Phe Pro Tyr				
180	185	190		
tgt tcc ttc acc aac gga gag act tcc cca acc gtg tcc atg gca gaa	983			
Cys Ser Phe Thr Asn Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu				
195	200	205		
cta gaa cac ctt gcc cag aac ata tcc aaa tcc cac ctg gaa acc tgc	1031			
Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys				
210	215	220		
cag tac ttg cgg gaa gag ctc cag cag ata acg tgg cag acc ttc tgg	1079			

Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Trp
 225 230 235 240
 cag gag gag att gaa aac tac cag aac aag cag aga gag gtg atg tgg 1127
 Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp
 245 250 255
 cag ctg tgt gcc atc aag att aca gaa gct atc cag tat gtg gtg gag 1175
 Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu
 260 265 270
 ttt gcc aaa cgc att gat gga ttt atg gag ctg tgt caa aat gat caa 1223
 Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln
 275 280 285
 att gtg ctt cta aaa gca ggc tgc cta gga gtg gtg ttt att agg atg 1271
 Ile Val Leu Leu Lys Ala Gly Ser Leu Gly Val Val Phe Ile Arg Met
 290 295 300
 tgc cgt gcc ttt gac tct cag aac aac acc gtg tac ttt gac ggg aag 1319
 Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys
 305 310 315 320
 tat gcg agc ccc gat gtc ttc aag tcc cta ggt tgt gaa gac ttc atc 1367
 Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile
 325 330 335
 agc ttt gtg ttt gaa ttt ggg aag agt ttg tgt tct atg cac ctg acc 1415
 Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr
 340 345 350
 gaa gac gaa atc gcg tta ttt tct gca ttc gta ctg atg tca gcg gat 1463
 Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp
 355 360 365
 ccg tcg tgg ctt cag gaa aag gta aaa ata gaa aag ctg caa cag aaa 1511
 Pro Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys
 370 375 380

att cac atg gcc ctt cag cac gtc cta cag aag aac cac cga gaa gat 1559
 Ile His Met Ala Leu Gln His Val Leu Gln Lys Asn His Arg Glu Asp
 385 390 395 400
 gga att cta acc aag cta ata tgc aag gtg tct acg tta aga gcc cta 1607
 Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu
 405 410 415
 tgt gga cga cat acg gaa aag cta atg gca ttt aaa gca ata tac cca 1655
 Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro
 420 425 430
 gac att gtg cga ctc cat ttt cct cca tta tac aag gaa ttg ttc act 1703
 Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr
 435 440 445
 tca gaa ttt gag cca gcc atg caa atc gat ggg taa atgtcgcgcc 1749
 Ser Glu Phe Glu Pro Ala Met Gln Ile Asp Gly
 450 455 460
 cgagcacttc tagaacaatct ggagtacaac atgaaagtaa gagagaaatt ttaaaa 1805

<210> 248

<211> 459

<212> PRT

<213> Mus musculus

<400> 248

Met Lys Ala Gln Ile Glu Ile Ile Pro Cys Lys Ile Cys Gly Asp Lys.
 1 5 10 15
 Ser Ser Gly Ile His Tyr Gly Val Ile Thr Cys Glu Gly Cys Lys Gly
 20 25 30
 Phe Phe Arg Arg Ser Gln Gln Ser Asn Ala Thr Tyr Ser Cys Pro Arg
 35 40 45

Gln Lys Asn Cys Leu Ile Asp Arg Thr Ser Arg Asn Arg Cys Gln His
 50 55 60
 Cys Arg Leu Gln Lys Cys Leu Ala Val Gly Met Ser Arg Asp Ala Val
 65 70 75 80
 Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp Ser Leu Tyr Ala Glu
 85 90 95
 Val Gln Lys Arg Arg Met Gln Gln Gln Gln Arg Asp His Gln Gln Gln
 100 105 110
 Pro Gly Glu Ala Thr Leu Thr Pro Thr Tyr Asn Ile Ser Ala Asn Gly
 115 120 125
 Ser Ala Glu Leu His Asp Asp Leu Ser Thr Tyr Met Asp Gly His Thr
 130 135 140
 Pro Glu Gly Ser Lys Ala Asp Ser Ala Val Ser Ser Phe Tyr Leu Asp
 145 150 155 160
 Ile Gln Pro Ser Pro Asp Gln Ser Gly Leu Asp Ile Asn Gly Ile Lys
 165 170 175
 Pro Glu Pro Ile Cys Asp Tyr Thr Pro Ala Ser Gly Phe Phe Pro Tyr
 180 185 190
 Cys Ser Phe Thr Asn Gly Glu Thr Ser Pro Thr Val Ser Met Ala Glu
 195 200 205
 Leu Glu His Leu Ala Gln Asn Ile Ser Lys Ser His Leu Glu Thr Cys
 210 215 220
 Gln Tyr Leu Arg Glu Glu Leu Gln Gln Ile Thr Trp Gln Thr Phe Trp
 225 230 235 240
 Gln Glu Glu Ile Glu Asn Tyr Gln Asn Lys Gln Arg Glu Val Met Trp
 245 250 255
 Gln Leu Cys Ala Ile Lys Ile Thr Glu Ala Ile Gln Tyr Val Val Glu
 260 265 270
 Phe Ala Lys Arg Ile Asp Gly Phe Met Glu Leu Cys Gln Asn Asp Gln

275	280	285
Ile Val Leu Leu Lys Ala Gly Ser Leu Gly Val Val Phe Ile Arg Met		
290	295	300
Cys Arg Ala Phe Asp Ser Gln Asn Asn Thr Val Tyr Phe Asp Gly Lys		
305	310	315
Tyr Ala Ser Pro Asp Val Phe Lys Ser Leu Gly Cys Glu Asp Phe Ile		
	325	330
Ser Phe Val Phe Glu Phe Gly Lys Ser Leu Cys Ser Met His Leu Thr		335
	340	345
Glu Asp Glu Ile Ala Leu Phe Ser Ala Phe Val Leu Met Ser Ala Asp		
	355	360
Pro Ser Trp Leu Gln Glu Lys Val Lys Ile Glu Lys Leu Gln Gln Lys		
370	375	380
Ile His Met Ala Leu Gln His Val Leu Gln Lys Asn His Arg Glu Asp		
385	390	395
Gly Ile Leu Thr Lys Leu Ile Cys Lys Val Ser Thr Leu Arg Ala Leu		
	405	410
Cys Gly Arg His Thr Glu Lys Leu Met Ala Phe Lys Ala Ile Tyr Pro		
	420	425
Asp Ile Val Arg Leu His Phe Pro Pro Leu Tyr Lys Glu Leu Phe Thr		430
	435	440
Ser Glu Phe Glu Pro Ala Met Gln Ile Asp Gly		445
450	455	

<210> 249

<211> 6863

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1243).. (3771)

<400> 249

```

gcactgccct tccctgcgca gaacgacctg agcatcatgc acagtcacct ggccctccgaa 60
cccaagcttc tcttctccgt gcgcaatgac tccccgggag aaatggctgt ggtggacgac 120
tagagaacac ggagctaccc tatttgtgtt ggagatctca gggaatacag aagacatccc 180
cctgggtgcgc tggaggcagc aatggctgga gaatggcact ttactctttc atattcacca 240
ccaagatggg gctccaagtc tccctggaca agaccaact gaagaacccc aacatgaatc 300
agcagaggaa gagctgagga tccctgcacat ctacgtcatg ggtggcatga tcgctctgtt 360
gctatccatc ttgtgccctg tgaatgatct gtacactcgc aggcgctggg gcaaacgtcg 420
cggttcccca gccccagaag agtgccagtg cagaggcagc aaatgagatt cactacatcc 480
catctgtgtt gattggaggc catgggcggg aaacgttgcg caatgcccgt gtgcagggcc 540
acaactccag tggcactctg agcattcggg agacacccat cctggatggc tatgagtatg 600
acatcacaga cctgcgtcac cacctgcaaa gggagtgtat gaatggaggg gaggactttg 660
ccagtcaggt cacacgcact ttggactcct acagggatgc aatgagaagt ctgggatgga 720
tctaaccaca gggagtgcac atgccaagct tccccgatg aacaagtata aagacaatat 780
catagccaca agccccgtgg attctaacca ccagcaagcc actctgctct cccacacctc 840
cagcagccag agaaagagga tcaacaataa agccagagct ggttctgcct tcttgaacct 900
tgaaggggac tccagcacag aggccgaaa tgaccacag ctgaccttct acacagacct 960
ctctcggagc ctggcgcagt cgagtgggtt cccccgaag tccctgtgaat aagaccacct 1020
tgacctgat cagtgtcacc agctgcgtga ttggcctcgt gtgctcttct catgtcagct 1080
gccctcttgt tgtcaagatc accctacacg tccctgagca cttgatcgtt gatgggagcc 1140
gcttcatcct gctggagggg agccagctgg atcgacgtga cctggctgaa cctgcccga 1200
gtggttctct tctctcagca gaactccagc gggccctggg cc atg gac ctg tgt 1254

```

Met Asp Leu Cys

1

```

gcc cgg cgg ctg acc ctt gtg aac acc aat gtg acc ccg aaa ctg 1302

```

Ala Arg Arg Leu Leu Thr Leu Val Asn Thr Asn Val Thr Pro Lys Leu	
5 10 15 20	
gta ggc ggg agc acc ggg cag acg ggg gaa tgc ctg tgc tat gaa ggc	1350
Val Gly Gly Ser Thr Gly Gln Thr Gly Glu Cys Leu Cys Tyr Glu Gly	
25 30 35	
tac atg aag gat cct gtc cac aag cac ctt tgc att cgg aat gaa tgg	1398
Tyr Met Lys Asp Pro Val His Lys His Leu Cys Ile Arg Asn Glu Trp	
40 45 50	
ggg acc aac cag ggg cct tgg cct tac acg ata ttt cag cga ggc ttt	1446
Gly Thr Asn Gln Gly Pro Trp Pro Tyr Thr Ile Phe Gln Arg Gly Phe	
55 60 65	
gac ctg gtt ttg gga gag caa ccc tct gat aag ata ttc aga ttc acc	1494
Asp Leu Val Leu Gly Glu Gln Pro Ser Asp Lys Ile Phe Arg Phe Thr	
70 75 80	
tat acc ctc ggg gaa ggc atg tgg tta ccc ctc agt aag agc ttt gtg	1542
Tyr Thr Leu Gly Glu Gly Met Trp Leu Pro Leu Ser Lys Ser Phe Val	
85 90 95 100	
atc cca cca gct gaa cta gcc atc aat cca tca gca aag tgt aag acg	1590
Ile Pro Pro Ala Glu Leu Ala Ile Asn Pro Ser Ala Lys Cys Lys Thr	
105 110 115	
gat atg act gtg atg gaa gat gct gta gag gtc aga gag gag ctg atg	1638
Asp Met Thr Val Met Glu Asp Ala Val Glu Val Arg Glu Glu Leu Met	
120 125 130	
aca tca tca tcc ttt gac agc ctg gag gtc cta tta gac tcc ttt ggg	1686
Thr Ser Ser Ser Phe Asp Ser Leu Glu Val Leu Leu Asp Ser Phe Gly	
135 140 145	
cca gtg cgt gat tgc agc aaa gat aac gga ggc tgc agt aag aat ttt	1734
Pro Val Arg Asp Cys Ser Lys Asp Asn Gly Gly Cys Ser Lys Asn Phe	
150 155 160	

cgc tgc att tca gat cgc aag ttg gac tct act ggt tgt gtg tgt cct 1782
 Arg Cys Ile Ser Asp Arg Lys Leu Asp Ser Thr Gly Cys Val Cys Pro
 165 170 175 180
 tca gga ctc agc cct atg aag gac agc tca ggc tgc tat gat cgc cat 1830
 Ser Gly Leu Ser Pro Met Lys Asp Ser Ser Gly Cys Tyr Asp Arg His
 185 190 195
 atc gga gtg gac tgc tca gat ggt ttc aac ggc ggc tgc gaa cag ctg 1878
 Ile Gly Val Asp Cys Ser Asp Gly Phe Asn Gly Gly Cys Glu Gln Leu
 200 205 210
 tgt ctc cag cag atg gcg ccg ttc cca gag gac ccc acc ttg tac aac 1926
 Cys Leu Gln Gln Met Ala Pro Phe Pro Glu Asp Pro Thr Leu Tyr Asn
 215 220 225
 atc ctt atg ttc tgc ggg tgt atc gaa gac tac aag ctt ggt gtg gat 1974
 Ile Leu Met Phe Cys Gly Cys Ile Glu Asp Tyr Lys Leu Gly Val Asp
 230 235 240
 gga cgc tct tgc caa ctt gtc act gag acc tgc cca gag gga ggt gac 2022
 Gly Arg Ser Cys Gln Leu Val Thr Glu Thr Cys Pro Glu Gly Gly Asp
 245 250 255 260
 tgt ggg gaa agc aga gag gtt ccc atg aac cag act ctc ttt gga gaa 2070
 Cys Gly Glu Ser Arg Glu Val Pro Met Asn Gln Thr Leu Phe Gly Glu
 265 270 275
 atg ttc ttt ggc tac aac aac cag tcc aag gaa gta gcc act gga cag 2118
 Met Phe Phe Gly Tyr Asn Asn Gln Ser Lys Glu Val Ala Thr Gly Gln
 280 285 290
 gtg cta aaa gga aca ttc aga cag aac aac ttt gct cgt ggt tta gac 2166
 Val Leu Lys Gly Thr Phe Arg Gln Asn Asn Phe Ala Arg Gly Leu Asp
 295 300 305
 cag caa ctg ccg gat ggt ctt gtg gtt gcc tct gtc cca ctg gag aat 2214
 Gln Gln Leu Pro Asp Gly Leu Val Val Ala Ser Val Pro Leu Glu Asn

310	315	320	
cag tgc cta gag gaa atc tca gag ccc acc cca gac cct gac ttc ttg			2262
Gln Cys Leu Glu Glu Ile Ser Glu Pro Thr Pro Asp Pro Asp Phe Leu			
325	330	335	340
act ggg atg gtg aac ttc agt gaa gtg tct gga tac ccg gtg ctg cag			2310
Thr Gly Met Val Asn Phe Ser Glu Val Ser Gly Tyr Pro Val Leu Gln			
	345	350	355
cac tgg aag gtt cgg tct gtg atg tac cac atc aaa ctc aac caa gca			2358
His Trp Lys Val Arg Ser Val Met Tyr His Ile Lys Leu Asn Gln Ala			
	360	365	370
gcc atc tcg cag gcc ttc agc aat gct ctt cac tcc ttg gat ggg gct			2406
Ala Ile Ser Gln Ala Phe Ser Asn Ala Leu His Ser Leu Asp Gly Ala			
	375	380	385
aca tct cgt gca gat ttt gtg gct ttg ttg gat cag ttt gga aac cat			2454
Thr Ser Arg Ala Asp Phe Val Ala Leu Leu Asp Gln Phe Gly Asn His			
	390	395	400
tac atc cag gaa gct gtc tac ggc ttt gag gaa tcc tgt tct ata tgg			2502
Tyr Ile Gln Glu Ala Val Tyr Gly Phe Glu Glu Ser Cys Ser Ile Trp			
405	410	415	420
tac cca aac aag caa gtc cag cgg aga ctc tgg ctg gaa tat gaa gac			2550
Tyr Pro Asn Lys Gln Val Gln Arg Arg Leu Trp Leu Glu Tyr Glu Asp			
	425	430	435
atc agt aaa ggc aac tct cca tct gat gag tcg gag gag cgg gaa agg			2598
Ile Ser Lys Gly Asn Ser Pro Ser Asp Glu Ser Glu Glu Arg Glu Arg			
	440	445	450
gat ccc aag gtg ctg aca ttc cca gaa tac atc gct agc ctg tca gac			2646
Asp Pro Lys Val Leu Thr Phe Pro Glu Tyr Ile Ala Ser Leu Ser Asp			
	455	460	465
tct ggc acc aag cga atg gca gct gga gtc cgg atg gag tgc cag agc			2694

Ser Gly Thr Lys Arg Met Ala Ala Gly Val Arg Met Glu Cys Gln Ser
 470 475 480
 aag gga cgg tgt cct tca tcc tgt cct tta tgt cat gtg aca tcc agc 2742
 Lys Gly Arg Cys Pro Ser Ser Cys Pro Leu Cys His Val Thr Ser Ser
 485 490 495 500
 cct gaa acc cct gct gag cca gtt cta ctg gaa gtg acc aga gca tcc 2790
 Pro Glu Thr Pro Ala Glu Pro Val Leu Leu Glu Val Thr Arg Ala Ser
 505 510 515
 ccc atc tat gaa ctg gtg acc aat aac cag acc cag agg ctc tta cag 2838
 Pro Ile Tyr Glu Leu Val Thr Asn Asn Gln Thr Gln Arg Leu Leu Gln
 520 525 530
 gaa gcc acc atg agc tct ctc tgg tgt tca ggg acc gga gat gtc att 2886
 Glu Ala Thr Met Ser Ser Leu Trp Cys Ser Gly Thr Gly Asp Val Ile
 535 540 545
 gag gac tgg tgc cga tgc gac tgc act gct ttt gga gca gat gga ctt 2934
 Glu Asp Trp Cys Arg Cys Asp Ser Thr Ala Phe Gly Ala Asp Gly Leu
 550 555 560
 cct acc tgt gca ccc ctc cca cag cct gtg ctg aga ctt tcc aca gta 2982
 Pro Thr Cys Ala Pro Leu Pro Gln Pro Val Leu Arg Leu Ser Thr Val
 565 570 575 580
 cac gag ccc agc agt aac ctc gtg gtc ctg gag tgg gaa cat tca gag 3030
 His Glu Pro Ser Ser Asn Leu Val Val Leu Glu Trp Glu His Ser Glu
 585 590 595
 ccg cca att ggg gtg cag att gta gac tac ctg tac cgg caa gag aaa 3078
 Pro Pro Ile Gly Val Gln Ile Val Asp Tyr Leu Tyr Arg Gln Glu Lys
 600 605 610
 gtc act gac cgg atg gac cac tcc aaa gta gag acg gaa aca gtg ctg 3126
 Val Thr Asp Arg Met Asp His Ser Lys Val Glu Thr Glu Thr Val Leu
 615 620 625

agc ttt gta gac gac atc atc tct gga gca aag gct cca tgt gcc atg 3174
 Ser Phe Val Asp Asp Ile Ile Ser Gly Ala Lys Ala Pro Cys Ala Met
 630 635 640
 ccg tct cag gtg cca gac aaa cag ctc acc acg att tct ctc atc atc 3222
 Pro Ser Gln Val Pro Asp Lys Gln Leu Thr Thr Ile Ser Leu Ile Ile
 645 650 655 660
 cga tgc ctg gaa cct gac acc att tac atg ttc acc ctc tgg gga gta 3270
 Arg Cys Leu Glu Pro Asp Thr Ile Tyr Met Phe Thr Leu Trp Gly Val
 665 670 675
 gat aac aca ggg cga cgt tcc agg cca agt gat gtg att gtg aag acc 3318
 Asp Asn Thr Gly Arg Arg Ser Arg Pro Ser Asp Val Ile Val Lys Thr
 680 685 690
 cca tgt cct gtg gtg gat gat gtc aaa gcc caa gaa ata gca gac aag 3366
 Pro Cys Pro Val Val Asp Asp Val Lys Ala Gln Glu Ile Ala Asp Lys
 695 700 705
 atc tac aat ctc ttc aat ggc tac acc agt gga aag gag caa cag act 3414
 Ile Tyr Asn Leu Phe Asn Gly Tyr Thr Ser Gly Lys Glu Gln Gln Thr
 710 715 720
 gcc tac aac acc ctt ctg gat ctg ggt tct ccc act ttg cac cga gtc 3462
 Ala Tyr Asn Thr Leu Leu Asp Leu Gly Ser Pro Thr Leu His Arg Val
 725 730 735 740
 ctc tac cac tat aac cag cac tat gag agt ttt ggg gaa ttc tgg cgg 3510
 Leu Tyr His Tyr Asn Gln His Tyr Glu Ser Phe Gly Glu Phe Trp Arg
 745 750 755
 tgt gaa gat gag tta gga ccc agg aaa gca ggc ctc atc ctt tcc cag 3558
 Cys Glu Asp Glu Leu Gly Pro Arg Lys Ala Gly Leu Ile Leu Ser Gln
 760 765 770
 ctt gga gat ctg agc agc tgg tgc aat gga ctc ctt cag gag ccc aag 3606
 Leu Gly Asp Leu Ser Ser Trp Cys Asn Gly Leu Leu Gln Glu Pro Lys

775	780	785	
ata agc ttg agg cgt ggt tca ctc aag tac ctg gct ggc cgc tac agt	3654		
Ile Ser Leu Arg Arg Gly Ser Leu Lys Tyr Leu Ala Gly Arg Tyr Ser			
790	795	800	
gag atc aaa ccc tat gga ctg gac tgg tca gag ctc agt cgg gac ctc	3702		
Glu Ile Lys Pro Tyr Gly Leu Asp Trp Ser Glu Leu Ser Arg Asp Leu			
805	810	815	820
agg aag aca tgt gaa gaa cag acc ctg agt gtc ccc tac aat gac tac	3750		
Arg Lys Thr Cys Glu Glu Gln Thr Leu Ser Val Pro Tyr Asn Asp Tyr			
	825	830	835
ggg gac agc aaa gac atc tag catcatggga ccaggaaata actgcagaaa	3801		
Gly Asp Ser Lys Asp Ile			
840			
taaagcaggg gagaagaggg caacatctgg gttaggtttgt ggattccttag acatttttta	3861		
atggaacacc caaagctcta caagtccctt ctaccagg aagagggiag acctttgctc	3921		
cctgcaagat ttgtccagtg tgatattctc caccigcatg accagtcaac ccgccagcca	3981		
gtagcttcat gcagcactgt tcgtttttgt ttttgttttt gtttttgitt ttgttttttt	4041		
cttagaagat taccttgaaa ctacatttgg tatccattgg ttttgttcac ttttcgcct	4101		
tcagtcaacc catcaggatt ctcaagagca ctatcctgca tcctacagca ggtctaattgt	4161		
ggaggctctt ctgcctaattg ggttcccaag tctatgacac ctggggacag aagtgagggc	4221		
ataaagcttc tgctgcctca tgcctttgct caggcatitc ttaggaagca tcagaatggt	4281		
gggagcaagg catgtactga agaagataat aaatgacca tgccttttc tcatgggttt	4341		
tccccagac tctctcctgt tactgtttcc acacctcaga ggtaaaccta agctctgita	4401		
caggactgtt ggacataaca gagatttagg tctctcttcc cccattttaa accaggactc	4461		
caagttctcg ttgatttctg tcctttcttc taaacaacct gatctttgag aggcagtgag	4521		
ataatacctg ttaaataatgg ctccagagag ggctacctgc aagattatit agtagccttc	4581		
actgtaggaa ataagtggag tttattttaa aaaaaaaca gttgtacatg tctagagtat	4641		
catcagagtc ctaagagcct tgattctgct tgggtcccagg cttttttccc tggacagaaa	4701		
ggacttggct gttgtttgct ttagtccagg aatgagatta tttcttgica gtgttttagt	4761		

gaactaaagc tcttatcaat ctgaaaagta cttctgtccg cactgccctc actaaatttt 4821
cttaattata ttgtaaattt tgacagccta ttctctgatg aaaatcatca gtactctgtc 4881
attgtcactg cctgcccacc caactctgcc agttactgaa gagcaacaga gcctctggag 4941
agacctgaac atctgatgat tgcacataag gactgaggct ccatttgac acactgccc 5001
aggatgatga tacggtgaac tagctactag gaagcctagc ctgttagaaa caacctcatg 5061
ggaccagaat gactaacaat gacccaatgt acattcagcc agcttgccctt gactggaatt 5121
cttcatgttg aaacacagcc ttcatgttga aggctctata attcagccac tgagccctat 5181
tcatactttc caattaggaa taatgacaga tgacatctga ggtgtgatgt gtgctactat 5241
aataacagga atctcacagg aataatgaca gatgacatct gaggtgtgat gtgtgctact 5301
ataaataaca ggaatctcac agaacccta aagaaagttc tattcctatt cactattctt 5361
ttagtaatga ggaaaacaag gaagtgaggt gacttgccat tccccaggtc cctcatacac 5421
tatataccct gagctgcagt gcctctagaa cacaggagtt taactactct gtgttgccct 5481
aagcatatga ctgttgaagc tctaagctct actgggaaca tgcccagaga acttcacctt 5541
cctaagggac cgtgtacaaa tatacaatga gtcaaagtac acccatagcc tttggagica 5601
gggcaccttt ggtatgctca acactgtggc acactagctt cccactgatg aataggaagg 5661
aaattcagtt gcaggctggt cttatttctc tctttgcttc tttgcagaga aatattggaa 5721
aacttgccctt gtactttttg gcctcagaga taccatcact tttagaacaa aacacagcag 5781
aaaacttagc tggctttcct ctggccagca tagggatttc agtaaaagtg catccgaagg 5841
aagcttgttc actattgcca gagaagagga tgctatggga cagtgtggca gtgtggacag 5901
catcccttta ctgccgttct ttttccactc ttctgttcaa tcctatgaag aaaagagtgt 5961
cttcttttga acagaatgat agtgagactg tggatgcctt ccagccctgt tggagatagg 6021
aacttatggg ctccaggagg aggacaggag tgatataatg atcactactg ttaccacccc 6081
catcttttat tccagacata ctctctcct ctcttttacc tttatgcccc attttccaaa 6141
gatttttcac ctctcacaca catatctcct ttatctcca tctttcccc cgcttcccat 6201
cgactgcctt attctttcag tgtgctcttg tgtttctct tcagatgtgt gtgtgtctat 6261
acacacactc actcccaagc accacgtaca tagctcctat tattggagca atgtactttt 6321
gagttaaaaa ctccaacatg aatggatttg gggtcgtctg gagatggtc tacatgttgc 6381
tggaggactt ttaccctcag agagatcata tcacacctg ccaatgattc tcagtttttg 6441
cctggaggaa ctgtctagaa aggctaattgt aatgaagcca gtattaacca cctcatttct 6501

aagctgccaa acaggtctta agggagccac ttctgtccac ctaaccacct ccagctctgt 6561
gtccagctga gatctctatt gtttcctctt gaatgtccac gaaccactgt aatagcatca 6621
gacccttaaa tgagtgtgca attgtttctc ttgaagtttg gtccattcgt tatitttaat 6681
taactgcact tcttgatatt caaatgttct attaaaaata attgtgaaaa acactccact 6741
actgtagaag aaagaggtag tacaatgtga ccaacttcaa ctacaacagt gttgtttaag 6801
agatttattg tacgattatg aaaaatgaag taatcgacta aataataaac aaagctgtca 6861
gt 6863

<210> 250

<211> 842

<212> PRT

<213> Mus musculus

<400> 250

Met Asp Leu Cys Ala Arg Arg Leu Leu Thr Leu Val Asn Thr Asn Val
1 5 10 15
Thr Pro Lys Leu Val Gly Gly Ser Thr Gly Gln Thr Gly Glu Cys Leu
20 25 30
Cys Tyr Glu Gly Tyr Met Lys Asp Pro Val His Lys His Leu Cys Ile
35 40 45
Arg Asn Glu Trp Gly Thr Asn Gln Gly Pro Trp Pro Tyr Thr Ile Phe
50 55 60
Gln Arg Gly Phe Asp Leu Val Leu Gly Glu Gln Pro Ser Asp Lys Ile
65 70 75 80
Phe Arg Phe Thr Tyr Thr Leu Gly Glu Gly Met Trp Leu Pro Leu Ser
85 90 95
Lys Ser Phe Val Ile Pro Pro Ala Glu Leu Ala Ile Asn Pro Ser Ala
100 105 110
Lys Cys Lys Thr Asp Met Thr Val Met Glu Asp Ala Val Glu Val Arg

115	120	125
Glu Glu Leu Met Thr Ser Ser Ser Phe Asp Ser Leu Glu Val Leu Leu		
130	135	140
Asp Ser Phe Gly Pro Val Arg Asp Cys Ser Lys Asp Asn Gly Gly Cys		
145	150	155
Ser Lys Asn Phe Arg Cys Ile Ser Asp Arg Lys Leu Asp Ser Thr Gly		
165	170	175
Cys Val Cys Pro Ser Gly Leu Ser Pro Met Lys Asp Ser Ser Gly Cys		
180	185	190
Tyr Asp Arg His Ile Gly Val Asp Cys Ser Asp Gly Phe Asn Gly Gly		
195	200	205
Cys Glu Gln Leu Cys Leu Gln Gln Met Ala Pro Phe Pro Glu Asp Pro		
210	215	220
Thr Leu Tyr Asn Ile Leu Met Phe Cys Gly Cys Ile Glu Asp Tyr Lys		
225	230	235
Leu Gly Val Asp Gly Arg Ser Cys Gln Leu Val Thr Glu Thr Cys Pro		
245	250	255
Glu Gly Gly Asp Cys Gly Glu Ser Arg Glu Val Pro Met Asn Gln Thr		
260	265	270
Leu Phe Gly Glu Met Phe Phe Gly Tyr Asn Asn Gln Ser Lys Glu Val		
275	280	285
Ala Thr Gly Gln Val Leu Lys Gly Thr Phe Arg Gln Asn Asn Phe Ala		
290	295	300
Arg Gly Leu Asp Gln Gln Leu Pro Asp Gly Leu Val Val Ala Ser Val		
305	310	315
Pro Leu Glu Asn Gln Cys Leu Glu Glu Ile Ser Glu Pro Thr Pro Asp		
325	330	335
Pro Asp Phe Leu Thr Gly Met Val Asn Phe Ser Glu Val Ser Gly Tyr		
340	345	350

Pro Val Leu Gln His Trp Lys Val Arg Ser Val Met Tyr His Ile Lys
 355 360 365
 Leu Asn Gln Ala Ala Ile Ser Gln Ala Phe Ser Asn Ala Leu His Ser
 370 375 380
 Leu Asp Gly Ala Thr Ser Arg Ala Asp Phe Val Ala Leu Leu Asp Gln
 385 390 395 400
 Phe Gly Asn His Tyr Ile Gln Glu Ala Val Tyr Gly Phe Glu Glu Ser
 405 410 415
 Cys Ser Ile Trp Tyr Pro Asn Lys Gln Val Gln Arg Arg Leu Trp Leu
 420 425 430
 Glu Tyr Glu Asp Ile Ser Lys Gly Asn Ser Pro Ser Asp Glu Ser Glu
 435 440 445
 Glu Arg Glu Arg Asp Pro Lys Val Leu Thr Phe Pro Glu Tyr Ile Ala
 450 455 460
 Ser Leu Ser Asp Ser Gly Thr Lys Arg Met Ala Ala Gly Val Arg Met
 465 470 475 480
 Glu Cys Gln Ser Lys Gly Arg Cys Pro Ser Ser Cys Pro Leu Cys His
 485 490 495
 Val Thr Ser Ser Pro Glu Thr Pro Ala Glu Pro Val Leu Leu Glu Val
 500 505 510
 Thr Arg Ala Ser Pro Ile Tyr Glu Leu Val Thr Asn Asn Gln Thr Gln
 515 520 525
 Arg Leu Leu Gln Glu Ala Thr Met Ser Ser Leu Trp Cys Ser Gly Thr
 530 535 540
 Gly Asp Val Ile Glu Asp Trp Cys Arg Cys Asp Ser Thr Ala Phe Gly
 545 550 555 560
 Ala Asp Gly Leu Pro Thr Cys Ala Pro Leu Pro Gln Pro Val Leu Arg
 565 570 575
 Leu Ser Thr Val His Glu Pro Ser Ser Asn Leu Val Val Leu Glu Trp

580	585	590
Glu His Ser Glu Pro Pro Ile Gly Val Gln Ile Val Asp Tyr Leu Tyr		
595	600	605
Arg Gln Glu Lys Val Thr Asp Arg Met Asp His Ser Lys Val Glu Thr		
610	615	620
Glu Thr Val Leu Ser Phe Val Asp Asp Ile Ile Ser Gly Ala Lys Ala		
625	630	635
Pro Cys Ala Met Pro Ser Gln Val Pro Asp Lys Gln Leu Thr Thr Ile		
645	650	655
Ser Leu Ile Ile Arg Cys Leu Glu Pro Asp Thr Ile Tyr Met Phe Thr		
660	665	670
Leu Trp Gly Val Asp Asn Thr Gly Arg Arg Ser Arg Pro Ser Asp Val		
675	680	685
Ile Val Lys Thr Pro Cys Pro Val Val Asp Asp Val Lys Ala Gln Glu		
690	695	700
Ile Ala Asp Lys Ile Tyr Asn Leu Phe Asn Gly Tyr Thr Ser Gly Lys		
705	710	715
Glu Gln Gln Thr Ala Tyr Asn Thr Leu Leu Asp Leu Gly Ser Pro Thr		
725	730	735
Leu His Arg Val Leu Tyr His Tyr Asn Gln His Tyr Glu Ser Phe Gly		
740	745	750
Glu Phe Trp Arg Cys Glu Asp Glu Leu Gly Pro Arg Lys Ala Gly Leu		
755	760	765
Ile Leu Ser Gln Leu Gly Asp Leu Ser Ser Trp Cys Asn Gly Leu Leu		
770	775	780
Gln Glu Pro Lys Ile Ser Leu Arg Arg Gly Ser Leu Lys Tyr Leu Ala		
785	790	795
Gly Arg Tyr Ser Glu Ile Lys Pro Tyr Gly Leu Asp Trp Ser Glu Leu		
805	810	815

Ser Arg Asp Leu Arg Lys Thr Cys Glu Glu Gln Thr Leu Ser Val Pro

820

825

830

Tyr Asn Asp Tyr Gly Asp Ser Lys Asp Ile

835

840

<210> 251

<211> 516

<212> DNA

<213> Mus musculus

<400> 251

```

cgcggtcga agtcccagg agtgaggct cgcgcgcgcg ccccgccct ggccccagcg 60
cccaccggt cggccccggc cagccatgat caaggccatc ctcatcttca acaaccacgg 120
gaagccgchg ctctccaagt tctaccagcc ctatagttaa gacacgcaac agcaaatcat 180
caggagagact ttccatttgg tgtctaagcg cgatgagaac gtttgtaatt tcctagaagg 240
aggattatta attggaggct ctgacaacaa gctcatttac agacattatg caacactata 300
ttttgtcttc tgtgtggact cctcagaaag tgaacttggc attttagatc taattcaagt 360
atttgtggaa acattagaca aatgttttga aaatgtttgt gaactggatt taatattcca 420
tgtagacaag gatcataata ttcttgcaga aatggtgatg gggggaatgg tattggagac 480
caacatgaat gagattgtca cacaattga tgcaca 516

```

<210> 252

<211> 2300

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (607).. (1926)

<400> 252

tatattccgg gggctctgcgc ggccgaggac ccctgggtgc gctgctctca gctgccgggt 60
 ccgactcgcc tcactcagct cccctcctgc ctctgaagg gcagcttcgc cgacgcttgg 120
 cgggaaaaag aaggaggggg agggatcctg agtcgcagta taaaagaagc ttttcgggcg 180
 ttttttctg actcgtctga gtaattccag cgagagacag agggagtgag cggacggttg 240
 gaagagccgt gtgtgcagag ccgcgctccg gggcgacctt agaaggcagc tctggagtga 300
 gaggggcttt gcctccgagc ctgccgccca ctctcccaa ccttcgact gacccaacat 360
 cagcggccgc aacctcgcc gccgctggga aactttgcc attgcagcgg gcagacactt 420
 ctactggaa cttacaatct gcgagccagg acaggactcc ccaggctccg gggagggaa 480
 tttgtctat ttggggacag tgttctctgc ctctgccgc gatcagctct cctgaaaaga 540
 gctcctcgag ctgtttgaag gctggatttc ctittggcgt tggaaacccc gcagacagcc 600
 acgacg atg ccc ctc aac gtg aac ttc acc aac agg aac tat gac ctc 648

Met Pro Leu Asn Val Asn Phe Thr Asn Arg Asn Tyr Asp Leu

1

5

10

gac tac gac tcc gta cag ccc tat ttc atc tgc gac gag gaa gag aat 696
 Asp Tyr Asp Ser Val Gln Pro Tyr Phe Ile Cys Asp Glu Glu Glu Asn

15

20

25

30

ttc tat cac cag caa cag cag agc gag ctg cag ccg ccc gcg ccc agt 744
 Phe Tyr His Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser

35

40

45

gag gat atc tgg aag aaa ttc gag ctg ctt ccc acc ccg ccc ctg tcc 792
 Glu Asp Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser

50

55

60

ccg agc cgc cgc tcc ggg ctc tgc tct cca tcc tat gtt gcg gtc gct 840
 Pro Ser Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Ala

65

70

75

acg tcc ttc tcc cca agg gaa gac gat gac ggc ggc ggt ggc aac ttc 888
 Thr Ser Phe Ser Pro Arg Glu Asp Asp Asp Gly Gly Gly Gly Asn Phe

80	85	90	
tcc acc gcc gat cag ctg gag atg atg acc gag tta ctt gga gga gac	936		
Ser Thr Ala Asp Gln Leu Glu Met Met Thr Glu Leu Leu Gly Gly Asp			
95	100	105	110
atg gtg aac cag agc ttc atc tgc gat cct gac gac gag acc ttc atc	984		
Met Val Asn Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile			
	115	120	125
aag aac atc atc atc cag gac tgt atg tgg agc ggt ttc tca gcc gct	1032		
Lys Asn Ile Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala			
	130	135	140
gcc aag ctg gtc tcg gag aag ctg gcc tcc tac cag gct gcg cgc aaa	1080		
Ala Lys Leu Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys			
	145	150	155
gac agc acc agc ctg agc ccc gcc cgc ggg cac agc gtc tgc tcc acc	1128		
Asp Ser Thr Ser Leu Ser Pro Ala Arg Gly His Ser Val Cys Ser Thr			
	160	165	170
tcc agc ctg tac ctg cag gac ctc acc gcc gcc gcg tcc gag tgc att	1176		
Ser Ser Leu Tyr Leu Gln Asp Leu Thr Ala Ala Ala Ser Glu Cys Ile			
175	180	185	190
gac ccc tca gtg gtc ttt ccc tac ccg ctc aac gac agc agc tcg ccc	1224		
Asp Pro Ser Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro			
	195	200	205
aaa tcc tgt acc tcg tcc gat tcc acg gcc ttc tct cct tcc tcg gac	1272		
Lys Ser Cys Thr Ser Ser Asp Ser Thr Ala Phe Ser Pro Ser Ser Asp			
	210	215	220
tcg ctg ctg tcc tcc gag tcc tcc cca cgg gcc agc cct gag ccc cta	1320		
Ser Leu Leu Ser Ser Glu Ser Ser Pro Arg Ala Ser Pro Glu Pro Leu			
	225	230	235
gtg ctg cat gag gag aca ccg ccc acc acc agc agc gac tct gaa gaa	1368		

Val	Leu	His	Glu	Glu	Thr	Pro	Pro	Thr	Thr	Ser	Ser	Asp	Ser	Glu	Glu		
240						245						250					
gag caa gaa gat gag gaa gaa att gat gtg gtg tct gtg gag aag agg																1416	
Glu	Gln	Glu	Asp	Glu	Glu	Glu	Ile	Asp	Val	Val	Ser	Val	Glu	Lys	Arg		
255					260					265				270			
caa acc cct gcc aag agg tcg gag tcg ggc tca tct cca tcc cga ggc																1464	
Gln	Thr	Pro	Ala	Lys	Arg	Ser	Glu	Ser	Gly	Ser	Ser	Pro	Ser	Arg	Gly		
					275				280					285			
cac agc aaa cct ccg cac agc cca ctg gtc ctc aag agg tgc cac gtc																1512	
His	Ser	Lys	Pro	Pro	His	Ser	Pro	Leu	Val	Leu	Lys	Arg	Cys	His	Val		
					290				295					300			
tcc act cac cag cac aac tac gcc gca ccc ccc tcc aca agg aag gac																1560	
Ser	Thr	His	Gln	His	Asn	Tyr	Ala	Ala	Pro	Pro	Ser	Thr	Arg	Lys	Asp		
					305				310					315			
tat cca gct gcc aag agg gcc aag ttg gac agt ggc agg gtc ctg aag																1608	
Tyr	Pro	Ala	Ala	Lys	Arg	Ala	Lys	Leu	Asp	Ser	Gly	Arg	Val	Leu	Lys		
					320				325					330			
cag atc agc aac aac cgc aag tgc tcc agc ccc agg tcc tca gac acg																1656	
Gln	Ile	Ser	Asn	Asn	Arg	Lys	Cys	Ser	Ser	Pro	Arg	Ser	Ser	Asp	Thr		
335					340					345				350			
gag gaa aac gac aag agg cgg aca cac aac gtc ttg gaa cgt cag agg																1704	
Glu	Glu	Asn	Asp	Lys	Arg	Arg	Thr	His	Asn	Val	Leu	Glu	Arg	Gln	Arg		
					355					360				365			
agg aac gag ctg aag cgc agc ttt ttt gcc ctg cgt gac cag atc cct																1752	
Arg	Asn	Glu	Leu	Lys	Arg	Ser	Phe	Phe	Ala	Leu	Arg	Asp	Gln	Ile	Pro		
					370					375				380			
gaa ttg gaa aac aac gaa aag gcc ccc aag gta gtg atc ctc aaa aaa																1800	
Glu	Leu	Glu	Asn	Asn	Glu	Lys	Ala	Pro	Lys	Val	Val	Ile	Leu	Lys	Lys		
					385					390				395			

gcc acc gcc tac atc ctg tcc att caa gca gac gag cac aag ctc acc 1848
 Ala Thr Ala Tyr Ile Leu Ser Ile Gln Ala Asp Glu His Lys Leu Thr
 400 405 410
 tct gaa aag gac tta ttg agg aaa cga cga gaa cag ttg aaa cac aaa 1896
 Ser Glu Lys Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys
 415 420 425 430
 ctc gaa cag ctt cga aac tct ggt gca taa actgacctaa ctgaggagg 1946
 Leu Glu Gln Leu Arg Asn Ser Gly Ala
 435 440
 agctggaatc tctcgtgaga gtaaggagaa cggttccttc tgacagaact gatgcgctgg 2006
 aattaaaaatg catgctcaaa gcctaaccctc acaacccttg ctggggccttt gggactgtaa 2066
 gcttcagcca taattttaac tgcctcaaac ttaaataagta taaaagaact ttttttatgc 2126
 ttcccatctt ttttcttttt ccttttaaca gatttgtatt taattgtttt tttaaaaaaa 2186
 tcttaaaatc tatccaattt tcccatgtaa atagggcctt gaaatgtaaa taactttaat 2246
 aaaacgttta taacagttac aaaagatttt aagacatgta ccataatttt tttt 2300

 <210> 253
 <211> 439
 <212> PRT
 <213> Mus musculus

 <400> 253
 Met Pro Leu Asn Val Asn Phe Thr Asn Arg Asn Tyr Asp Leu Asp Tyr
 1 5 10 15
 Asp Ser Val Gln Pro Tyr Phe Ile Cys Asp Glu Glu Glu Asn Phe Tyr
 20 25 30
 His Gln Gln Gln Gln Ser Glu Leu Gln Pro Pro Ala Pro Ser Glu Asp
 35 40 45
 Ile Trp Lys Lys Phe Glu Leu Leu Pro Thr Pro Pro Leu Ser Pro Ser

50	55	60
Arg Arg Ser Gly Leu Cys Ser Pro Ser Tyr Val Ala Val Ala Thr Ser		
65	70	75
Phe Ser Pro Arg Glu Asp Asp Asp Gly Gly Gly Gly Asn Phe Ser Thr		80
85	90	95
Ala Asp Gln Leu Glu Met Met Thr Glu Leu Leu Gly Gly Asp Met Val		
100	105	110
Asn Gln Ser Phe Ile Cys Asp Pro Asp Asp Glu Thr Phe Ile Lys Asn		
115	120	125
Ile Ile Ile Gln Asp Cys Met Trp Ser Gly Phe Ser Ala Ala Ala Lys		
130	135	140
Leu Val Ser Glu Lys Leu Ala Ser Tyr Gln Ala Ala Arg Lys Asp Ser		
145	150	155
Thr Ser Leu Ser Pro Ala Arg Gly His Ser Val Cys Ser Thr Ser Ser		
165	170	175
Leu Tyr Leu Gln Asp Leu Thr Ala Ala Ala Ser Glu Cys Ile Asp Pro		
180	185	190
Ser Val Val Phe Pro Tyr Pro Leu Asn Asp Ser Ser Ser Pro Lys Ser		
195	200	205
Cys Thr Ser Ser Asp Ser Thr Ala Phe Ser Pro Ser Ser Asp Ser Leu		
210	215	220
Leu Ser Ser Glu Ser Ser Pro Arg Ala Ser Pro Glu Pro Leu Val Leu		
225	230	235
His Glu Glu Thr Pro Pro Thr Thr Ser Ser Asp Ser Glu Glu Glu Gln		
245	250	255
Glu Asp Glu Glu Glu Ile Asp Val Val Ser Val Glu Lys Arg Gln Thr		
260	265	270
Pro Ala Lys Arg Ser Glu Ser Gly Ser Ser Pro Ser Arg Gly His Ser		
275	280	285

Lys Pro Pro His Ser Pro Leu Val Leu Lys Arg Cys His Val Ser Thr
 290 295 300
 His Gln His Asn Tyr Ala Ala Pro Pro Ser Thr Arg Lys Asp Tyr Pro
 305 310 315 320
 Ala Ala Lys Arg Ala Lys Leu Asp Ser Gly Arg Val Leu Lys Gln Ile
 325 330 335
 Ser Asn Asn Arg Lys Cys Ser Ser Pro Arg Ser Ser Asp Thr Glu Glu
 340 345 350
 Asn Asp Lys Arg Arg Thr His Asn Val Leu Glu Arg Gln Arg Arg Asn
 355 360 365
 Glu Leu Lys Arg Ser Phe Phe Ala Leu Arg Asp Gln Ile Pro Glu Leu
 370 375 380
 Glu Asn Asn Glu Lys Ala Pro Lys Val Val Ile Leu Lys Lys Ala Thr
 385 390 395 400
 Ala Tyr Ile Leu Ser Ile Gln Ala Asp Glu His Lys Leu Thr Ser Glu
 405 410 415
 Lys Asp Leu Leu Arg Lys Arg Arg Glu Gln Leu Lys His Lys Leu Glu
 420 425 430
 Gln Leu Arg Asn Ser Gly Ala
 435

<210> 254

<211> 3586

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (80).. (2080)

<400> 254

gaattcctcg ttcttgcaac ctcgccccg cgcgccgcag acttgctctc actgccgctg 60
 ccgccgccgc ccccggggc atg gcc tgt ctg atg gcc gct ttc tgc gtc ggc 112

Met Ala Cys Leu Met Ala Ala Phe Ser Val Gly

1

5

10

acc gcc atg aat gcc agc agc tac tct gcc gca atg acg gag ccc aag 160
 Thr Ala Met Asn Ala Ser Ser Tyr Ser Ala Ala Met Thr Glu Pro Lys

15

20

25

tcc gtg tgc gtg tca gtg gac gag gtc gtg tcc agc aac gtg gat gag 208
 Ser Val Cys Val Ser Val Asp Glu Val Val Ser Ser Asn Val Asp Glu

30

35

40

gtt gag aca gac ctg ctc aat ggg cac ctg aag aag gtg gac aac aac 256
 Val Glu Thr Asp Leu Leu Asn Gly His Leu Lys Lys Val Asp Asn Asn

45

50

55

ttc aca gag gcc cag cgc ttt tcc tcc ctt ccg cgg agg gcg gcc gtg 304
 Phe Thr Glu Ala Gln Arg Phe Ser Ser Leu Pro Arg Arg Ala Ala Val

60

65

70

75

aac atc gaa ttc aag gac ctt tcc tac tct gta ccc gag ggg ccc tgg 352
 Asn Ile Glu Phe Lys Asp Leu Ser Tyr Ser Val Pro Glu Gly Pro Trp

80

85

90

tgg aag aag aaa gga tac aag acc ctt ttg aaa ggg atc tct ggg aaa 400
 Trp Lys Lys Lys Gly Tyr Lys Thr Leu Leu Lys Gly Ile Ser Gly Lys

95

100

105

ttc aac agt gga gag ctg gtg gcc atc atg ggt cct tct gga gct ggg 448
 Phe Asn Ser Gly Glu Leu Val Ala Ile Met Gly Pro Ser Gly Ala Gly

110

115

120

aag tcc aca ctc atg aat att ctg gca gga tac agg gag act ggc atg 496
 Lys Ser Thr Leu Met Asn Ile Leu Ala Gly Tyr Arg Glu Thr Gly Met

125	130	135	
aaa ggg gca gtc ctt atc aat gga atg ccc cgg gac ctg cgc tgc ttc			544
Lys Gly Ala Val Leu Ile Asn Gly Met Pro Arg Asp Leu Arg Cys Phe			
140	145	150	155
cgg aag gtc tcc tgc tac atc atg cag gac gac atg ctg ctg cct cac			592
Arg Lys Val Ser Cys Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His			
160	165	170	
ctc act gtt cag gag gcc atg atg gtg tcc gcg cat ctg aag ctg cag			640
Leu Thr Val Gln Glu Ala Met Met Val Ser Ala His Leu Lys Leu Gln			
175	180	185	
gag aag gat gaa ggc aga cgg gag atg gtc aaa gag atc ctg aca gcc			688
Glu Lys Asp Glu Gly Arg Arg Glu Met Val Lys Glu Ile Leu Thr Ala			
190	195	200	
ctg ggc ttg ctg ccc tgt gcc aac aca cgc acg ggg agc ctc tca ggc			736
Leu Gly Leu Leu Pro Cys Ala Asn Thr Arg Thr Gly Ser Leu Ser Gly			
205	210	215	
ggc cag cgg aaa cgc ctg gcc att gcc ctg gag ctg gtc aac aac ccg			784
Gly Gln Arg Lys Arg Leu Ala Ile Ala Leu Glu Leu Val Asn Asn Pro			
220	225	230	235
cct gtc atg ttc ttt gat gag ccc acc agt ggc ctg gac agc gcc tcc			832
Pro Val Met Phe Phe Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser			
240	245	250	
tgc ttc caa gtg gtg tct ctg atg aaa gga ctg gcc cag ggt ggc cgc			880
Cys Phe Gln Val Val Ser Leu Met Lys Gly Leu Ala Gln Gly Gly Arg			
255	260	265	
tcc atc gtc tgt acc atc cac cag ccc agt gcc aag ctc ttt gag ctc			928
Ser Ile Val Cys Thr Ile His Gln Pro Ser Ala Lys Leu Phe Glu Leu			
270	275	280	
ttt gac cag ctt tat gtc cta agt caa gga caa tgc gta tac agg gga			976

Phe Asp Gln Leu Tyr Val Leu Ser Gln Gly Gln Cys Val Tyr Arg Gly
 285 290 295
 aag gtc tcc aat ctc gtg ccg tat ctg agg gat ctg ggt ctg aac tgc 1024
 Lys Val Ser Asn Leu Val Pro Tyr Leu Arg Asp Leu Gly Leu Asn Cys
 300 305 310 315
 cct acc tac cac aac cca gca gac ttt gtc atg gaa gtg gca tca ggg 1072
 Pro Thr Tyr His Asn Pro Ala Asp Phe Val Met Glu Val Ala Ser Gly
 320 325 330
 gag tac ggg gat cag aac agt cgc ctg gtg aga gcc gtg cga gag ggc 1120
 Glu Tyr Gly Asp Gln Asn Ser Arg Leu Val Arg Ala Val Arg Glu Gly
 335 340 345
 atg tgt gac gct gac tat aag aga gac ctc ggg ggc gac acc gat gtg 1168
 Met Cys Asp Ala Asp Tyr Lys Arg Asp Leu Gly Gly Asp Thr Asp Val
 350 355 360
 aac ccg ttt ctt tgg cac cgg cct gct gaa gag gac tcc gcc tcc atg 1216
 Asn Pro Phe Leu Trp His Arg Pro Ala Glu Glu Asp Ser Ala Ser Met
 365 370 375
 gaa ggt tgc cat agc ttc tcg gcc agc tgc ctc acc cag ttc tgc atc 1264
 Glu Gly Cys His Ser Phe Ser Ala Ser Cys Leu Thr Gln Phe Cys Ile
 380 385 390 395
 ctc ttc aag agg acc ttc ctc agc atc atg cgg gac tcg gtc ctg aca 1312
 Leu Phe Lys Arg Thr Phe Leu Ser Ile Met Arg Asp Ser Val Leu Thr
 400 405 410
 cat ctg cga atc acc tcg cac att ggg atc ggc ctg ctc att ggc ctg 1360
 His Leu Arg Ile Thr Ser His Ile Gly Ile Gly Leu Leu Ile Gly Leu
 415 420 425
 ctg tac ctg ggg att ggg aat gaa gcc aag aag gtc ctt agc aac tcc 1408
 Leu Tyr Leu Gly Ile Gly Asn Glu Ala Lys Lys Val Leu Ser Asn Ser
 430 435 440

ggc ttc ctg ttc ttc tcc atg ctg ttc ctc atg ttt gct gcc ctc atg 1456
 Gly Phe Leu Phe Phe Ser Met Leu Phe Leu Met Phe Ala Ala Leu Met
 445 450 455
 ccc act gtt ctg acc ttt ccc ctg gag atg agt gtc ttc ctc cgg gag 1504
 Pro Thr Val Leu Thr Phe Pro Leu Glu Met Ser Val Phe Leu Arg Glu
 460 465 470 475
 cac ctg aac tac tgg tac agc ctg aag gcc tac tac ctg gca aag acc 1552
 His Leu Asn Tyr Trp Tyr Ser Leu Lys Ala Tyr Tyr Leu Ala Lys Thr
 480 485 490
 atg gcc gat gtc ccc ttt cag atc atg ttc cct gtg gcc tac tgc agt 1600
 Met Ala Asp Val Pro Phe Gln Ile Met Phe Pro Val Ala Tyr Cys Ser
 495 500 505
 atc gta tac tgg atg acg tcc cag ccg tgc gac gct gtg cgt ttt gtg 1648
 Ile Val Tyr Trp Met Thr Ser Gln Pro Ser Asp Ala Val Arg Phe Val
 510 515 520
 ctg ttc gct gct ctg ggt acc atg aca tgc ctg gtg gcc cag tcc tta 1696
 Leu Phe Ala Ala Leu Gly Thr Met Thr Ser Leu Val Ala Gln Ser Leu
 525 530 535
 gga cta ctg att gga gct gca tcc aca tcc ctg cag gtt gcg aca ttt 1744
 Gly Leu Leu Ile Gly Ala Ala Ser Thr Ser Leu Gln Val Ala Thr Phe
 540 545 550 555
 gtg ggt ccc gtg aca gcc atc ccc gtc ctg ctc ttc tcc gga ttc ttt 1792
 Val Gly Pro Val Thr Ala Ile Pro Val Leu Leu Phe Ser Gly Phe Phe
 560 565 570
 gtc agc ttt gac acc atc cca gcc tac ctg cag tgg atg tcc tac atc 1840
 Val Ser Phe Asp Thr Ile Pro Ala Tyr Leu Gln Trp Met Ser Tyr Ile
 575 580 585
 tcc tat gtc aga tac ggc ttt gag ggg gtc atc ctg tcc atc tac ggc 1888
 Ser Tyr Val Arg Tyr Gly Phe Glu Gly Val Ile Leu Ser Ile Tyr Gly

590	595	600	
ttg gac cga gaa gac ctg cac tgc gac atc gcg gag aca tgc cac ttc			1936
Leu Asp Arg Glu Asp Leu His Cys Asp Ile Ala Glu Thr Cys His Phe			
605	610	615	
cag aag tca gag gcc atc ctg agg gag ctg gac gtg gag aat gcg aag			1984
Gln Lys Ser Glu Ala Ile Leu Arg Glu Leu Asp Val Glu Asn Ala Lys			
620	625	630	635
ctg tac ctg gat ttc atc gtc ctg ggc atc ttc ttc atc tcc ctg cgg			2032
Leu Tyr Leu Asp Phe Ile Val Leu Gly Ile Phe Phe Ile Ser Leu Arg			
640	645	650	
ctc atc gcc tat ttc gtc ctc aga tac aaa atc cgg gct gag agg taa			2080
Leu Ile Ala Tyr Phe Val Leu Arg Tyr Lys Ile Arg Ala Glu Arg			
655	660	665	
aaaccgcctc caagccagca acgaggcaaa gcagacattg tgaccaaggg cactgctggg			2140
aggtagcagc cgacctgctc ctggtgacac agactctccc aacccaacct ggaggccacg			2200
caagtctgac gatgaccagt gttagcgcc tctgcccgcc gggttgaaac tgttcgtttc			2260
ctttictaac taggaagatg taggacggtt gggttttttt ttttcttttt tttttttttt			2320
ttagatgtgg gattcaaaat acaactggca tagaatgcca tcctgtgctc cagctgggga			2380
cagtggcttc ctcccgaggt ccaggacaca ctggccccgg atgaggagtg ttagccgagt			2440
tggtccccag agaggtggat atcttgggga gaaggccac acctagcggg cacagaggcc			2500
acctgaggac catcttctct taaggctcga gccttctaaa gticctctca tttctgatga			2560
agtcactttc cgagccaaag tcgataaatt tcattcactt cgagagattg tatcttttta			2620
gtacttcttg aggacttat tcagggtaaa agatgtgttt tgcttagaaa cagaagagtc			2680
caaccgagtc accaaggagg cctcacaaat aaaaccagag aaggtaaat gcaggctccg			2740
ggtgagggag acaccacacc agctgcgctg gggcagcagg gactaacgca acgcaatgca			2800
acgcaatgca gacagtgtg gggctacttg caggctcctc ccagacttcc tttctcatgt			2860
gcttcttagc ttaaaactct tcctagtttt ccagccactt tcattttgcc caagaaatac			2920
tcgatccacc ttgtgatgtt taaagaccca tttccctttt ctcatgaat cacattaact			2980
acctccaccg agcctgggaa gccggcctgg ggacatatcg ggtgtatccc tccaacttga			3040

ggggagccgt ggggtgtcaa ggaaggcag gccggctgag tggaagggga ggtgccatgg 3100
 atgtccccgt taagaaaatg cagctgctcg cctcttcag agcaccacca tctaaggta 3160
 gcctcc taca aaagtctcta ttttgaggg taggtcagtt taaccctgt gagctcagt 3220
 tccccacct gtaagtaatt gcactagatc atgtcttgac aggtcctgag attcctcggc 3280
 tgtggccttg atgctttcgt atcttatctg tagagaatga taagggtccg aattttactt 3340
 accgcatgga taatgtgctt tggaactctt tagagattct tttattttt tacactccta 3400
 gatctttttt atagagaaca cacaattgaa atgcatatta tgatgtaatt ttcggtttgc 3460
 ttgttctata caaacacggc ctgcttct agactcagct tttaccagg gacacgattc 3520
 gcctttataa aaaaaaaaaag tcttcattaa aaaagaaac accaaaaaaaa aaaaaaaaaa 3580
 aaaaaa 3586

<210> 255

<211> 666

<212> PRT

<213> Mus musculus

<400> 255

Met	Ala	Cys	Leu	Met	Ala	Ala	Phe	Ser	Val	Gly	Thr	Ala	Met	Asn	Ala
1				5						10				15	
Ser	Ser	Tyr	Ser	Ala	Ala	Met	Thr	Glu	Pro	Lys	Ser	Val	Cys	Val	Ser
				20						25				30	
Val	Asp	Glu	Val	Val	Ser	Ser	Asn	Val	Asp	Glu	Val	Glu	Thr	Asp	Leu
				35						40				45	
Leu	Asn	Gly	His	Leu	Lys	Lys	Val	Asp	Asn	Asn	Phe	Thr	Glu	Ala	Gln
				50						55				60	
Arg	Phe	Ser	Ser	Leu	Pro	Arg	Arg	Ala	Ala	Val	Asn	Ile	Glu	Phe	Lys
				65						70				75	
Asp	Leu	Ser	Tyr	Ser	Val	Pro	Glu	Gly	Pro	Trp	Trp	Lys	Lys	Lys	Gly
				85						90				95	

Tyr Lys Thr Leu Leu Lys Gly Ile Ser Gly Lys Phe Asn Ser Gly Glu
 100 105 110
 Leu Val Ala Ile Met Gly Pro Ser Gly Ala Gly Lys Ser Thr Leu Met
 115 120 125
 Asn Ile Leu Ala Gly Tyr Arg Glu Thr Gly Met Lys Gly Ala Val Leu
 130 135 140
 Ile Asn Gly Met Pro Arg Asp Leu Arg Cys Phe Arg Lys Val Ser Cys
 145 150 155 160
 Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His Leu Thr Val Gln Glu
 165 170 175
 Ala Met Met Val Ser Ala His Leu Lys Leu Gln Glu Lys Asp Glu Gly
 180 185 190
 Arg Arg Glu Met Val Lys Glu Ile Leu Thr Ala Leu Gly Leu Leu Pro
 195 200 205
 Cys Ala Asn Thr Arg Thr Gly Ser Leu Ser Gly Gly Gln Arg Lys Arg
 210 215 220
 Leu Ala Ile Ala Leu Glu Leu Val Asn Asn Pro Pro Val Met Phe Phe
 225 230 235 240
 Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser Cys Phe Gln Val Val
 245 250 255
 Ser Leu Met Lys Gly Leu Ala Gln Gly Gly Arg Ser Ile Val Cys Thr
 260 265 270
 Ile His Gln Pro Ser Ala Lys Leu Phe Glu Leu Phe Asp Gln Leu Tyr
 275 280 285
 Val Leu Ser Gln Gly Gln Cys Val Tyr Arg Gly Lys Val Ser Asn Leu
 290 295 300
 Val Pro Tyr Leu Arg Asp Leu Gly Leu Asn Cys Pro Thr Tyr His Asn
 305 310 315 320
 Pro Ala Asp Phe Val Met Glu Val Ala Ser Gly Glu Tyr Gly Asp Gln

	325		330		335
Asn Ser Arg Leu Val Arg Ala Val Arg Glu Gly Met Cys Asp Ala Asp					
	340		345		350
Tyr Lys Arg Asp Leu Gly Gly Asp Thr Asp Val Asn Pro Phe Leu Trp					
	355		360		365
His Arg Pro Ala Glu Glu Asp Ser Ala Ser Met Glu Gly Cys His Ser					
	370		375		380
Phe Ser Ala Ser Cys Leu Thr Gln Phe Cys Ile Leu Phe Lys Arg Thr					
385		390		395	400
Phe Leu Ser Ile Met Arg Asp Ser Val Leu Thr His Leu Arg Ile Thr					
	405		410		415
Ser His Ile Gly Ile Gly Leu Leu Ile Gly Leu Leu Tyr Leu Gly Ile					
	420		425		430
Gly Asn Glu Ala Lys Lys Val Leu Ser Asn Ser Gly Phe Leu Phe Phe					
	435		440		445
Ser Met Leu Phe Leu Met Phe Ala Ala Leu Met Pro Thr Val Leu Thr					
	450		455		460
Phe Pro Leu Glu Met Ser Val Phe Leu Arg Glu His Leu Asn Tyr Trp					
465		470		475	480
Tyr Ser Leu Lys Ala Tyr Tyr Leu Ala Lys Thr Met Ala Asp Val Pro					
	485		490		495
Phe Gln Ile Met Phe Pro Val Ala Tyr Cys Ser Ile Val Tyr Trp Met					
	500		505		510
Thr Ser Gln Pro Ser Asp Ala Val Arg Phe Val Leu Phe Ala Ala Leu					
	515		520		525
Gly Thr Met Thr Ser Leu Val Ala Gln Ser Leu Gly Leu Leu Ile Gly					
	530		535		540
Ala Ala Ser Thr Ser Leu Gln Val Ala Thr Phe Val Gly Pro Val Thr					
545		550		555	560

Ala Ile Pro Val Leu Leu Phe Ser Gly Phe Phe Val Ser Phe Asp Thr

565

570

575

Ile Pro Ala Tyr Leu Gln Trp Met Ser Tyr Ile Ser Tyr Val Arg Tyr

580

585

590

Gly Phe Glu Gly Val Ile Leu Ser Ile Tyr Gly Leu Asp Arg Glu Asp

595

600

605

Leu His Cys Asp Ile Ala Glu Thr Cys His Phe Gln Lys Ser Glu Ala

610

615

620

Ile Leu Arg Glu Leu Asp Val Glu Asn Ala Lys Leu Tyr Leu Asp Phe

625

630

635

640

Ile Val Leu Gly Ile Phe Phe Ile Ser Leu Arg Leu Ile Ala Tyr Phe

645

650

655

Val Leu Arg Tyr Lys Ile Arg Ala Glu Arg

660

665

<210> 256

<211> 2755

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (58).. (1242)

<400> 256

ggcagcagca acaatgtgct ccagctgctg gatatccaag catctcagct gcggagg 57

atg gag tca tcc atc aat cac atc tca cag act gtg gat att cat aaa 105

Met Glu Ser Ser Ile Asn His Ile Ser Gln Thr Val Asp Ile His Lys

1

5

10

15

gaa aaa gtg gct cga aga gag att ggt att ttg aca aca aat aag aat 153
 Glu Lys Val Ala Arg Arg Glu Ile Gly Ile Leu Thr Thr Asn Lys Asn
 20 25 30
 aca tca aga act cac aaa ata atc gca ccc gca aat atg gag cgt cct 201
 Thr Ser Arg Thr His Lys Ile Ile Ala Pro Ala Asn Met Glu Arg Pro
 35 40 45
 gtc agg tat att cgg aaa cct atc gac tat aca gtt ctg gat gat gtg 249
 Val Arg Tyr Ile Arg Lys Pro Ile Asp Tyr Thr Val Leu Asp Asp Val
 50 55 60
 ggc cat gga gtt aag cac gga aat aac cag cct gca aga act ggc aca 297
 Gly His Gly Val Lys His Gly Asn Asn Gln Pro Ala Arg Thr Gly Thr
 65 70 75 80
 ttg tcg aga aca aac cct ccc acg cag aaa cca cca agc cct ccc gtg 345
 Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro Val
 85 90 95
 tcg ggc cga ggg act ttg gga cgg aat acc cct tac aaa acc cta gag 393
 Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu
 100 105 110
 cct gtt aag cct cca aca gtt ccc aat gac tac atg act agt cct gcg 441
 Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr Met Thr Ser Pro Ala
 115 120 125
 agg ctt gga agc cag cat agt cca ggc agg aca gct tct tta atc aga 489
 Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr Ala Ser Leu Ile Arg
 130 135 140
 gac caa gga cgc att agt gga agt agt gga gga agc gga agc cga gag 537
 Asp Gln Gly Arg Ile Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu
 145 150 155 160
 aac agt ggg agc agc agc att ggc att cct att gct gtg cct acg ccc 585
 Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile Ala Val Pro Thr Pro

	165	170	175	
tca ccg ccc act gcg ggc cca gcc cct ggc gca gct cct ggt tcc cag	633			
Ser Pro Pro Thr Ala Gly Pro Ala Pro Gly Ala Ala Pro Gly Ser Gln				
	180	185	190	
tat ggc aca atg acc agg cag att tct cga cac aac tct acc act tct	681			
Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His Asn Ser Thr Thr Ser				
	195	200	205	
tcg aca tct tct ggt gga tat aga cga act cct tct gtg gcc gcc caa	729			
Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro Ser Val Ala Ala Gln				
	210	215	220	
ttc tct gct cag cct cat gtt aat gga ggt cca ctt tta ttc tca aaa	777			
Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro Leu Leu Phe Ser Lys				
225	230	235	240	
ttc aat ttc ttg ttg gcc ctc ctc ctc ccc cca tgg cct cag ttg act	825			
Phe Asn Phe Leu Leu Ala Leu Leu Leu Pro Pro Trp Pro Gln Leu Thr				
	245	250	255	
cca cag atc cct ctc aca ggg ttc ggg ggc agg gtg caa gga aac att	873			
Pro Gln Ile Pro Leu Thr Gly Phe Gly Gly Arg Val Gln Gly Asn Ile				
	260	265	270	
gct gat agg ggg caa act cca cca cca ccc cct cca cca gat gac att	921			
Ala Asp Arg Gly Gln Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile				
	275	280	285	
ccc atg ttt gat gac tct ccg cct cct ccg cca cct cct cct gtg gac	969			
Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp				
	290	295	300	
tat gaa gat gag gaa gct gca gta gtt cag tat agt gac cca tat gca	1017			
Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Ser Asp Pro Tyr Ala				
305	310	315	320	
gat ggg gac cct gca tgg gct tcc cca aga act ata ttg aga aag ttg	1065			

Asp Gly Asp Pro Ala Trp Ala Ser Pro Arg Thr Ile Leu Arg Lys Leu
 325 330 335
 ttg caa tat atg att ata tac caa aag aca agg atg atg agc tgt cct 1113
 Leu Gln Tyr Met Ile Ile Tyr Gln Lys Thr Arg Met Met Ser Cys Pro
 340 345 350
 tta aaa gag ggt gca atc atc tat gtt ata aag aag aat gat gat ggc 1161
 Leu Lys Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly
 355 360 365
 tgg ttt gaa gga gtt tgc aat cga gtg act gga ctc ttc cct ggg aac 1209
 Trp Phe Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn
 370 375 380
 tat gtt gaa tca atc atg cac tat act gat tag tttttctttt ttcttttcat 1262
 Tyr Val Glu Ser Ile Met His Tyr Thr Asp
 385 390 395
 gtaggttatt actccgtcat actgtgggat tataatggta acagaatigt tttaatgtta 1322
 aaaatgtgcc catattttca aggacatgtt ttattggat atttggatgt ctacctgtaa 1382
 gcataaattt tggaggcagt tccaaacatt gctgagcagc agttaaatat gccataaact 1442
 tgattatgca atatgtactc acaccttgct aagtttatga ccagcctaaa acttctgggg 1502
 attgggtatt atgtttaaca aatcatgggt cagaatgcac cattacatgt ttcagtgcag 1562
 catggtcact aacatttgtt cagactaata ggaaaaaaca gaaaacgtca atgctgggtgc 1622
 tggtcatact ttggtttca attctcattt ttaaaaaaat actgtgttta aagcatgcat 1682
 aaatttttat gtattgaaat atacttaaca attcaagatg ctccaattt gtgtaacgat 1742
 tatctggagt actcactatt gagtctccta agctctccat gtgaaatgaa agactatctg 1802
 taatgttgta atttgtatct aagtttttta atgagtgaaa ttgcattat aaatttttcc 1862
 attcataaat acataagtga accaaaggat ttggccctct cttttactgg ttgtctttta 1922
 attatgtatg ctagtgcata tgcattgcaca cctcccacc cttttaagaa agatttattg 1982
 cagaattatg gttctatttt ctcaatgcat cagttttgaa aatattttta gcttaatctt 2042
 aatgtgtcca aacagtcaat gtgacagaat ttgacagatt ttggagctag actgtgtcag 2102
 agtaagcaca tgataattctg ggggcaacat ctgaaggagg gagtgcacaca ccggtcctgt 2162

ggattttaat gaaactgaat ttacattgac tcagtgaaag gaaaatcctt tacatatttg 2222
 taaagatgga tgcaagtcca ttgtggata ggcatattta atcccttccc tggcacttag 2282
 aaacataaaa ttgtatcgat aagtttgaaa gaaactaggc catgtattaa tctgtaaaca 2342
 ggtaataagc aggtttgtat tgtaactttg atgcaacaca tgcactttgt gtgtctcctt 2402
 gattcaaggg aggggtgtgag ggatacttct ctgtatata agactgtact gcttaggata 2462
 ttaaagtaga tcacacaagt gtgggtttct atgtactgag ggttgcagat ttatgacagc 2522
 atagtgatga gagcagagca aaatatttct gaaaattaaa gaccattgtt cctaccaaatt 2582
 caatgattcc atatTTTTT tcaccttcg ttattttgga gtactatgtc attagcacc 2642
 agatagcttt ttattatgca tticcttttt gaagcaaaat gttttcttca ttigttaaata 2702
 acctgtgtc taaattttat ctagtctttt ataataaact atgtctctat atg 2755

<210> 257

<211> 394

<212> PRT

<213> Mus musculus

<400> 257

Met	Glu	Ser	Ser	Ile	Asn	His	Ile	Ser	Gln	Thr	Val	Asp	Ile	His	Lys
1				5				10				15			
Glu	Lys	Val	Ala	Arg	Arg	Glu	Ile	Gly	Ile	Leu	Thr	Thr	Asn	Lys	Asn
				20				25				30			
Thr	Ser	Arg	Thr	His	Lys	Ile	Ile	Ala	Pro	Ala	Asn	Met	Glu	Arg	Pro
				35				40				45			
Val	Arg	Tyr	Ile	Arg	Lys	Pro	Ile	Asp	Tyr	Thr	Val	Leu	Asp	Asp	Val
				50				55				60			
Gly	His	Gly	Val	Lys	His	Gly	Asn	Asn	Gln	Pro	Ala	Arg	Thr	Gly	Thr
				65				70				75			80
Leu	Ser	Arg	Thr	Asn	Pro	Pro	Thr	Gln	Lys	Pro	Pro	Ser	Pro	Pro	Val
				85				90				95			

Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu Glu
 100 105 110
 Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr Met Thr Ser Pro Ala
 115 120 125
 Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr Ala Ser Leu Ile Arg
 130 135 140
 Asp Gln Gly Arg Ile Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg Glu
 145 150 155 160
 Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile Ala Val Pro Thr Pro
 165 170 175
 Ser Pro Pro Thr Ala Gly Pro Ala Pro Gly Ala Ala Pro Gly Ser Gln
 180 185 190
 Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His Asn Ser Thr Thr Ser
 195 200 205
 Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro Ser Val Ala Ala Gln
 210 215 220
 Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro Leu Leu Phe Ser Lys
 225 230 235 240
 Phe Asn Phe Leu Leu Ala Leu Leu Leu Pro Pro Trp Pro Gln Leu Thr
 245 250 255
 Pro Gln Ile Pro Leu Thr Gly Phe Gly Gly Arg Val Gln Gly Asn Ile
 260 265 270
 Ala Asp Arg Gly Gln Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile
 275 280 285
 Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Val Asp
 290 295 300
 Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Ser Asp Pro Tyr Ala
 305 310 315 320
 Asp Gly Asp Pro Ala Trp Ala Ser Pro Arg Thr Ile Leu Arg Lys Leu

	325		330		335										
Leu	Gln	Tyr	Met	Ile	Ile	Tyr	Gln	Lys	Thr	Arg	Met	Met	Ser	Cys	Pro
	340		345		350										
Leu	Lys	Glu	Gly	Ala	Ile	Ile	Tyr	Val	Ile	Lys	Lys	Asn	Asp	Asp	Gly
	355		360		365										
Trp	Phe	Glu	Gly	Val	Cys	Asn	Arg	Val	Thr	Gly	Leu	Phe	Pro	Gly	Asn
	370		375		380										
Tyr	Val	Glu	Ser	Ile	Met	His	Tyr	Thr	Asp						
385			390												

<210> 258

<211> 1825

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (124).. (1392)

<400> 258

```

tggctgtgga gcggacccgg ccgctgcgac gctctggcgg cccgagcgcg cctagtcggt 60
gtgagcccgg cgcgaggicc cgggccccgg ggcgctcgct caggtaaata ttccataac 120
ctt atg gag aga aag gac ttt gag aca tgg ctt gat aac att tct gtt 168
Met Glu Arg Lys Asp Phe Glu Thr Trp Leu Asp Asn Ile Ser Val
      1             5             10             15
aca ttt ctt tct ctg atg gac ttg cag aaa aat gaa act ctg gac cac 216
Thr Phe Leu Ser Leu Met Asp Leu Gln Lys Asn Glu Thr Leu Asp His
      20             25             30
ctg att agt ctg agt ggg gca gtc cag ctc agg cat ctc tcc aat aac 264

```

Leu Ile Ser Leu Ser Gly Ala Val Gln Leu Arg His Leu Ser Asn Asn	
35 40 45	
ctg gag act ctc ctc aag cgg gac ttc ctc aaa ctc ctt ccc ctg gag	312
Leu Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu	
50 55 60	
ctc agt ttt tat ttg tta aaa tgg ctc gat cct cag act tta ctc aca	360
Leu Ser Phe Tyr Leu Leu Lys Trp Leu Asp Pro Gln Thr Leu Leu Thr	
65 70 75	
tgc tgc ctg gtc tct aag cag cgg aat aag gtg ata agt gcc tgt aca	408
Cys Cys Leu Val Ser Lys Gln Arg Asn Lys Val Ile Ser Ala Cys Thr	
80 85 90 95	
gag gtg tgg cag act gca tgt aaa aat ttg ggc tgg cag ata gat gat	456
Glu Val Trp Gln Thr Ala Cys Lys Asn Leu Gly Trp Gln Ile Asp Asp	
100 105 110	
tct gtt cag gac tca ttg cac tgg aag aag gtt tat ttg aag gct att	504
Ser Val Gln Asp Ser Leu His Trp Lys Lys Val Tyr Leu Lys Ala Ile	
115 120 125	
ttg agg atg aag caa ctg gag gac cat gaa gcc ttt gag acc tct tcg	552
Leu Arg Met Lys Gln Leu Glu Asp His Glu Ala Phe Glu Thr Ser Ser	
130 135 140	
tta att gga cat agt gcc aga gtg tat gca ctt tac tac aaa gat gga	600
Leu Ile Gly His Ser Ala Arg Val Tyr Ala Leu Tyr Tyr Lys Asp Gly	
145 150 155	
ctt ctc tgt aca ggg tca gat gac ttg tct gca aag ctg tgg gat gta	648
Leu Leu Cys Thr Gly Ser Asp Asp Leu Ser Ala Lys Leu Trp Asp Val	
160 165 170 175	
agc aca ggg cag tgt gtt tac ggc atc cag acc cac act tgt gca gct	696
Ser Thr Gly Gln Cys Val Tyr Gly Ile Gln Thr His Thr Cys Ala Ala	
180 185 190	

gtg aag ttc gat gaa cag aag ctt gtg aca ggc tcc ttt gac aac act	744
Val Lys Phe Asp Glu Gln Lys Leu Val Thr Gly Ser Phe Asp Asn Thr	
195 200 205	
gtg gcc tgc tgg gag tgg agt tcc gga gcc agg acc cag cac ttc cgg	792
Val Ala Cys Trp Glu Trp Ser Ser Gly Ala Arg Thr Gln His Phe Arg	
210 215 220	
ggg cac acg ggg gcg gtg ttc agt gtg gac tac agt gat gaa ctg gat	840
Gly His Thr Gly Ala Val Phe Ser Val Asp Tyr Ser Asp Glu Leu Asp	
225 230 235	
att ttg gtg agt ggc tct gcg gac ttc gct gtg aaa gta tgg gct tta	888
Ile Leu Val Ser Gly Ser Ala Asp Phe Ala Val Lys Val Trp Ala Leu	
240 245 250 255	
tct gct ggg aca tgc ctg aat aca ctc act ggg cat act gaa tgg gtc	936
Ser Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val	
260 265 270	
acc aag gtg gtt ttg cag aag tgc aaa gtc aag tct ctc ttg cac agc	984
Thr Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser	
275 280 285	
cct gga gac tac atc ctc tta agt gca gac aaa tat gag atc aag att	1032
Pro Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile	
290 295 300	
tgg cca att ggg aga gaa atc aac tgt aag tgc ttg aag aca ctg tct	1080
Trp Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser	
305 310 315	
gtc tct gag gat aga agt atc tgc ctg cag cca aga ctt cat ttt gat	1128
Val Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp	
320 325 330 335	
gga aaa tac att gtc tgt agt tca gcc ctg ggt ctg tac cag tgg gac	1176
Gly Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp	

340 345 350
 ttt gcc agt tat gat att ctc agg gtc atc aag aca cct gag gta gca 1224
 Phe Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Val Ala
 355 360 365
 aac ttg gcc ttg ctt ggc ttt gga gat gtc ttc gcc ctg ctg ttt gac 1272
 Asn Leu Ala Leu Leu Gly Phe Gly Asp Val Phe Ala Leu Leu Phe Asp
 370 375 380
 aac cac tac cta tat atc atg gac ttg agg aca gag agc cta att agc 1320
 Asn His Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser
 385 390 395
 cgc tgg cct ctg cca gag tac agg aaa tca aag aga ggc acc agc ttc 1368
 Arg Trp Pro Leu Pro Glu Tyr Arg Lys Ser Lys Arg Gly Thr Ser Phe
 400 405 410 415
 ctg gca ggc gaa cgt cct ggt tga atggattgga tgggcacaat gacacgggct 1422
 Leu Ala Gly Glu Arg Pro Gly
 420
 tagtctttgc caccagcatg cctgaccaca gtattcacct ggtgttatgg aaggagcatt 1482
 gctgacacca ggagctacca ccgctgactg actttgggtg ccagggctgc gggttttggg 1542
 tgcaatgtct atggcagcca actgcatgaa ccaaagttct cacctaaagg tatcatcacg 1602
 cagtgcacaa tcattttatct gtttgccagg gciggggcgg ggagggcttg tttactgaca 1662
 tacaccgcag catgctaattg ggatacacca ttgacttcat ttgatcttag ttaagtgtgt 1722
 cagtgtgaaga gaggttgcat ttttgattt atctttctga gtggaatatt gagtaaagaa 1782
 agttaaatga ttcactaatc tgcctaattg gttgcccata aaa 1825

<210> 259

<211> 422

<212> PRT

<213> Mus musculus

<400> 259

Met	Glu	Arg	Lys	Asp	Phe	Glu	Thr	Trp	Leu	Asp	Asn	Ile	Ser	Val	Thr
1				5					10					15	
Phe	Leu	Ser	Leu	Met	Asp	Leu	Gln	Lys	Asn	Glu	Thr	Leu	Asp	His	Leu
			20					25						30	
Ile	Ser	Leu	Ser	Gly	Ala	Val	Gln	Leu	Arg	His	Leu	Ser	Asn	Asn	Leu
		35					40						45		
Glu	Thr	Leu	Leu	Lys	Arg	Asp	Phe	Leu	Lys	Leu	Leu	Pro	Leu	Glu	Leu
	50					55					60				
Ser	Phe	Tyr	Leu	Leu	Lys	Trp	Leu	Asp	Pro	Gln	Thr	Leu	Leu	Thr	Cys
65					70					75				80	
Cys	Leu	Val	Ser	Lys	Gln	Arg	Asn	Lys	Val	Ile	Ser	Ala	Cys	Thr	Glu
				85					90					95	
Val	Trp	Gln	Thr	Ala	Cys	Lys	Asn	Leu	Gly	Trp	Gln	Ile	Asp	Asp	Ser
		100						105						110	
Val	Gln	Asp	Ser	Leu	His	Trp	Lys	Lys	Val	Tyr	Leu	Lys	Ala	Ile	Leu
		115					120						125		
Arg	Met	Lys	Gln	Leu	Glu	Asp	His	Glu	Ala	Phe	Glu	Thr	Ser	Ser	Leu
	130					135						140			
Ile	Gly	His	Ser	Ala	Arg	Val	Tyr	Ala	Leu	Tyr	Tyr	Lys	Asp	Gly	Leu
145				150						155				160	
Leu	Cys	Thr	Gly	Ser	Asp	Asp	Leu	Ser	Ala	Lys	Leu	Trp	Asp	Val	Ser
			165						170					175	
Thr	Gly	Gln	Cys	Val	Tyr	Gly	Ile	Gln	Thr	His	Thr	Cys	Ala	Ala	Val
		180						185					190		
Lys	Phe	Asp	Glu	Gln	Lys	Leu	Val	Thr	Gly	Ser	Phe	Asp	Asn	Thr	Val
		195					200						205		
Ala	Cys	Trp	Glu	Trp	Ser	Ser	Gly	Ala	Arg	Thr	Gln	His	Phe	Arg	Gly
	210						215						220		

His Thr Gly Ala Val Phe Ser Val Asp Tyr Ser Asp Glu Leu Asp Ile
 225 230 235 240
 Leu Val Ser Gly Ser Ala Asp Phe Ala Val Lys Val Trp Ala Leu Ser
 245 250 255
 Ala Gly Thr Cys Leu Asn Thr Leu Thr Gly His Thr Glu Trp Val Thr
 260 265 270
 Lys Val Val Leu Gln Lys Cys Lys Val Lys Ser Leu Leu His Ser Pro
 275 280 285
 Gly Asp Tyr Ile Leu Leu Ser Ala Asp Lys Tyr Glu Ile Lys Ile Trp
 290 295 300
 Pro Ile Gly Arg Glu Ile Asn Cys Lys Cys Leu Lys Thr Leu Ser Val
 305 310 315 320
 Ser Glu Asp Arg Ser Ile Cys Leu Gln Pro Arg Leu His Phe Asp Gly
 325 330 335
 Lys Tyr Ile Val Cys Ser Ser Ala Leu Gly Leu Tyr Gln Trp Asp Phe
 340 345 350
 Ala Ser Tyr Asp Ile Leu Arg Val Ile Lys Thr Pro Glu Val Ala Asn
 355 360 365
 Leu Ala Leu Leu Gly Phe Gly Asp Val Phe Ala Leu Leu Phe Asp Asn
 370 375 380
 His Tyr Leu Tyr Ile Met Asp Leu Arg Thr Glu Ser Leu Ile Ser Arg
 385 390 395 400
 Trp Pro Leu Pro Glu Tyr Arg Lys Ser Lys Arg Gly Thr Ser Phe Leu
 405 410 415
 Ala Gly Glu Arg Pro Gly
 420

<210> 260

<211> 1861

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (110).. (1708)

<400> 260

ctctgctagc ctcacggcca cgggacgcct ctctgaacgg ggatccaggc aggattagag 60
 ctgcctcatt gactacaggc cgtgtcgtgt caccgtttct gcaggcacc atg agc cag 118

Met Ser Gln

1

gac acc gaa gtg gac atg aaa gat gtg gag ctg aac gag cta gaa ccg 166
 Asp Thr Glu Val Asp Met Lys Asp Val Glu Leu Asn Glu Leu Glu Pro

5

10

15

gag aag cag ccc atg aat gca gcg gac ggg gcg gcg atg tcc ctg gcc 214
 Glu Lys Gln Pro Met Asn Ala Ala Asp Gly Ala Ala Met Ser Leu Ala

20

25

30

35

ggg gcc gag aag aac ggt ctg gtg aag atc aag gtg gcg gag gac gag 262
 Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala Glu Asp Glu

40

45

50

acg gag gcc ggg gtc gcg gct aag ttc acc ggc tta tcc aag gag gag 310
 Thr Glu Ala Gly Val Ala Ala Lys Phe Thr Gly Leu Ser Lys Glu Glu

55

60

65

cta ctg aag gta gcg ggc agc cct ggc tgg gtg cgc acc cgc tgg gcg 358
 Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr Arg Trp Ala

70

75

80

ctg ctg ctg ctc ttc tgg ctc ggt tgg ctg ggc atg ctg gcg ggc gcc 406
 Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu Ala Gly Ala

85	90	95	
gtg gtt atc atc gtt cgg gcg ccg cgc tgc cgt gag ctg cct gta cag	454		
Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu Pro Val Gln			
100	105	110	115
agg tgg tgg cac aag ggc gcc ctc tac cgc atc ggc gac ctt cag gcc	502		
Arg Trp Trp His Lys Gly Ala Leu Tyr Arg Ile Gly Asp Leu Gln Ala			
120	125	130	
ttt gta ggc cgg gat gcg gga ggc ata gct ggt ctg aag agc cat ctg	550		
Phe Val Gly Arg Asp Ala Gly Gly Ile Ala Gly Leu Lys Ser His Leu			
135	140	145	
gag tac ttg agc acc ctg aag gtg aag ggc ctg gtg tta ggc cca att	598		
Glu Tyr Leu Ser Thr Leu Lys Val Lys Gly Leu Val Leu Gly Pro Ile			
150	155	160	
cac aag aac cag aag gat gaa atc aat gaa acc gac ctg aaa cag att	646		
His Lys Asn Gln Lys Asp Glu Ile Asn Glu Thr Asp Leu Lys Gln Ile			
165	170	175	
aat ccc act ttg ggc tcc cag gaa gat ttt aaa gac ctt cta caa agt	694		
Asn Pro Thr Leu Gly Ser Gln Glu Asp Phe Lys Asp Leu Leu Gln Ser			
180	185	190	195
gcc aag aaa aag agc att cac atc att ttg gac ctc act ccc aac tac	742		
Ala Lys Lys Lys Ser Ile His Ile Ile Leu Asp Leu Thr Pro Asn Tyr			
200	205	210	
cag ggc cag aat gcg tgg ttc ctc cct gct cag gct gac att gta gcc	790		
Gln Gly Gln Asn Ala Trp Phe Leu Pro Ala Gln Ala Asp Ile Val Ala			
215	220	225	
acc aaa atg aag gaa gct ctg agt tct tgg ttg cag gac ggt gtg gat	838		
Thr Lys Met Lys Glu Ala Leu Ser Ser Trp Leu Gln Asp Gly Val Asp			
230	235	240	
ggc ttc caa ttc cgg gat gtg gga aag ctg atg aat gca ccc ttg tac	886		

Gly Phe Gln Phe Arg Asp Val Gly Lys Leu Met Asn Ala Pro Leu Tyr	
245	250
255	
ttg gct gag tgg cag aat atc acc aag aac tta agt gag gac agg ctt	934
Leu Ala Glu Trp Gln Asn Ile Thr Lys Asn Leu Ser Glu Asp Arg Leu	
260	265
270	275
gtg att gca ggg act gag tcc tct gac ctg cag caa att gtc aac ata	982
Val Ile Ala Gly Thr Glu Ser Ser Asp Leu Gln Gln Ile Val Asn Ile	
280	285
290	
ctt gac tcc acc agc gac ctg ctg ttg acc agc tcc tac ctg tca aat	1030
Leu Asp Ser Thr Ser Asp Leu Leu Leu Thr Ser Ser Tyr Leu Ser Asn	
295	300
305	
tcc act cac act ggg gag cgt act gaa tcc cta gac act agg ttg gtg	1078
Ser Thr His Thr Gly Glu Arg Thr Glu Ser Leu Asp Thr Arg Leu Val	
310	315
320	
agt gcc act ggc agc cat tgg tgc agc tgg agt gtg tgc caa gca gct	1126
Ser Ala Thr Gly Ser His Trp Cys Ser Trp Ser Val Ser Gln Ala Ala	
325	330
335	
ctc ctc gca gac ttt ata ccg gac cat ctt ctc cga ctc tac cag ctg	1174
Leu Leu Ala Asp Phe Ile Pro Asp His Leu Leu Arg Leu Tyr Gln Leu	
340	345
350	355
ctg ctc ttc act ctg cca ggg act cct gtt ttt agc tac ggg gat gag	1222
Leu Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr Gly Asp Glu	
360	365
370	
ctt ggc ctt cag ggt gcc ctt cct gga cag cct gcg aag gcc cca ctc	1270
Leu Gly Leu Gln Gly Ala Leu Pro Gly Gln Pro Ala Lys Ala Pro Leu	
375	380
385	
atg ccg tgg aat gag tcc agt atc ttt cac atc cca aga cct gta agc	1318
Met Pro Trp Asn Glu Ser Ser Ile Phe His Ile Pro Arg Pro Val Ser	
390	395
400	

ctc aac atg aca gtg aag ggc cag aat gaa gac cct ggc tcc ctc ctt 1366
 Leu Asn Met Thr Val Lys Gly Gln Asn Glu Asp Pro Gly Ser Leu Leu
 405 410 415
 acc cag ttc cgg cgg ctg agt gac ctt cgg ggt aag gag cgc tct ctg 1414
 Thr Gln Phe Arg Arg Leu Ser Asp Leu Arg Gly Lys Glu Arg Ser Leu
 420 425 430 435
 ttg cac ggt gac ttc cat gca ctg tct tcc aca cct gac ctc ttc tcc 1462
 Leu His Gly Asp Phe His Ala Leu Ser Ser Thr Pro Asp Leu Phe Ser
 440 445 450
 tac ata cga cac tgg gac cag aat gag cgt tac ctg gtg gtg ctc aac 1510
 Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val Val Leu Asn
 455 460 465
 ttc cga gat tcg ggc cgg tca gcc agg cta ggg gcc tcc aac ctc cct 1558
 Phe Arg Asp Ser Gly Arg Ser Ala Arg Leu Gly Ala Ser Asn Leu Pro
 470 475 480
 gct ggt ata agc ctg cca gcc agc gct aaa ctt ttg ctt agt acc gac 1606
 Ala Gly Ile Ser Leu Pro Ala Ser Ala Lys Leu Leu Leu Ser Thr Asp
 485 490 495
 agt gcc cgg caa agc cgt gag gag gac acc tcc ctg aag ctg gaa aac 1654
 Ser Ala Arg Gln Ser Arg Glu Glu Asp Thr Ser Leu Lys Leu Glu Asn
 500 505 510 515
 ctg agc ctg aat cct tat gag ggc ttg ctg tta cag ttc ccc ttt gtg 1702
 Leu Ser Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe Pro Phe Val
 520 525 530
 gcc tga tccttctat gcagaacctt ccacctcct ttgttctccc caggccttgg 1758
 Ala
 gggattctag tcttctctc ctgttttta aacttgggga gattacatac gaattcttat 1818
 actgggtgtt tgggtctaca aataaaaaca tcacccttgc ctc 1861

<210> 261

<211> 532

<212> PRT

<213> Mus musculus

<400> 261

Met Ser Gln Asp Thr Glu Val Asp Met Lys Asp Val Glu Leu Asn Glu
 1 5 10 15
 Leu Glu Pro Glu Lys Gln Pro Met Asn Ala Ala Asp Gly Ala Ala Met
 20 25 30
 Ser Leu Ala Gly Ala Glu Lys Asn Gly Leu Val Lys Ile Lys Val Ala
 35 40 45
 Glu Asp Glu Thr Glu Ala Gly Val Ala Ala Lys Phe Thr Gly Leu Ser
 50 55 60
 Lys Glu Glu Leu Leu Lys Val Ala Gly Ser Pro Gly Trp Val Arg Thr
 65 70 75 80
 Arg Trp Ala Leu Leu Leu Leu Phe Trp Leu Gly Trp Leu Gly Met Leu
 85 90 95
 Ala Gly Ala Val Val Ile Ile Val Arg Ala Pro Arg Cys Arg Glu Leu
 100 105 110
 Pro Val Gln Arg Trp Trp His Lys Gly Ala Leu Tyr Arg Ile Gly Asp
 115 120 125
 Leu Gln Ala Phe Val Gly Arg Asp Ala Gly Gly Ile Ala Gly Leu Lys
 130 135 140
 Ser His Leu Glu Tyr Leu Ser Thr Leu Lys Val Lys Gly Leu Val Leu
 145 150 155 160
 Gly Pro Ile His Lys Asn Gln Lys Asp Glu Ile Asn Glu Thr Asp Leu
 165 170 175
 Lys Gln Ile Asn Pro Thr Leu Gly Ser Gln Glu Asp Phe Lys Asp Leu

180	185	190
Leu Gln Ser Ala Lys Lys Lys Ser Ile His Ile Ile Leu Asp Leu Thr		
195	200	205
Pro Asn Tyr Gln Gly Gln Asn Ala Trp Phe Leu Pro Ala Gln Ala Asp		
210	215	220
Ile Val Ala Thr Lys Met Lys Glu Ala Leu Ser Ser Trp Leu Gln Asp		
225	230	235
Gly Val Asp Gly Phe Gln Phe Arg Asp Val Gly Lys Leu Met Asn Ala		
245	250	255
Pro Leu Tyr Leu Ala Glu Trp Gln Asn Ile Thr Lys Asn Leu Ser Glu		
260	265	270
Asp Arg Leu Val Ile Ala Gly Thr Glu Ser Ser Asp Leu Gln Gln Ile		
275	280	285
Val Asn Ile Leu Asp Ser Thr Ser Asp Leu Leu Leu Thr Ser Ser Tyr		
290	295	300
Leu Ser Asn Ser Thr His Thr Gly Glu Arg Thr Glu Ser Leu Asp Thr		
305	310	315
Arg Leu Val Ser Ala Thr Gly Ser His Trp Cys Ser Trp Ser Val Ser		
325	330	335
Gln Ala Ala Leu Leu Ala Asp Phe Ile Pro Asp His Leu Leu Arg Leu		
340	345	350
Tyr Gln Leu Leu Leu Phe Thr Leu Pro Gly Thr Pro Val Phe Ser Tyr		
355	360	365
Gly Asp Glu Leu Gly Leu Gln Gly Ala Leu Pro Gly Gln Pro Ala Lys		
370	375	380
Ala Pro Leu Met Pro Trp Asn Glu Ser Ser Ile Phe His Ile Pro Arg		
385	390	395
Pro Val Ser Leu Asn Met Thr Val Lys Gly Gln Asn Glu Asp Pro Gly		
405	410	415

Ser Leu Leu Thr Gln Phe Arg Arg Leu Ser Asp Leu Arg Gly Lys Glu
 420 425 430
 Arg Ser Leu Leu His Gly Asp Phe His Ala Leu Ser Ser Thr Pro Asp
 435 440 445
 Leu Phe Ser Tyr Ile Arg His Trp Asp Gln Asn Glu Arg Tyr Leu Val
 450 455 460
 Val Leu Asn Phe Arg Asp Ser Gly Arg Ser Ala Arg Leu Gly Ala Ser
 465 470 475 480
 Asn Leu Pro Ala Gly Ile Ser Leu Pro Ala Ser Ala Lys Leu Leu Leu
 485 490 495
 Ser Thr Asp Ser Ala Arg Gln Ser Arg Glu Glu Asp Thr Ser Leu Lys
 500 505 510
 Leu Glu Asn Leu Ser Leu Asn Pro Tyr Glu Gly Leu Leu Leu Gln Phe
 515 520 525
 Pro Phe Val Ala
 530

<210> 262

<211> 1094

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (74).. (1027)

<400> 262

ctctcgccag gcgtcctcgt tggagtgaca tcgtctttaa accccgcgtg gcaatccctg 60
 acgcaccgcc gtg atg ccc agg gaa gac agg gcg acc tgg aag tcc aac 109

Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn

1 5 10

tac ttc ctc aag atc atc caa ctt ttg gat gat tat cca aaa tgc ttc 157

Tyr Phe Leu Lys Ile Ile Gln Leu Leu Asp Asp Tyr Pro Lys Cys Phe

15 20 25

att gtg gga gca gac aac gtg ggc tcc aag cag atg cag cag atc cgc 205

Ile Val Gly Ala Asp Asn Val Gly Ser Lys Gln Met Gln Gln Ile Arg

30 35 40

atg tcg ctc cga ggg aag gcc gtg gtg ctg atg ggc aag aac acc atg 253

Met Ser Leu Arg Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met

45 50 55 60

atg cgc aag gct atc agg ggc cac ctg gag aac aac cca gct ctg gag 301

Met Arg Lys Ala Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu

65 70 75

aaa ctg ctg cct cac atc cgg ggg aac gtg ggc ttc gtg ttc acc aag 349

Lys Leu Leu Pro His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys

80 85 90

gag gac ctc act gag att cgg gat atg ctg ttg gcc aat aag gtg cca 397

Glu Asp Leu Thr Glu Ile Arg Asp Met Leu Leu Ala Asn Lys Val Pro

95 100 105

gct gct gct cgg gct ggt gcc atc gcc cgg tgt gag gtc act gtg cca 445

Ala Ala Ala Arg Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro

110 115 120

gct cag aac act ggt cta gga ccc gag aag acc tcc ttc ttc cag gct 493

Ala Gln Asn Thr Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala

125 130 135 140

ttg ggc atc acc acg aaa atc tcc aga ggc acc att gaa att ctg agt 541

Leu Gly Ile Thr Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser

145 150 155

gat gtg cag ctg ata aag act gga gac aag gtg gga gcc agc gag gcc 589
 Asp Val Gln Leu Ile Lys Thr Gly Asp Lys Val Gly Ala Ser Glu Ala
 160 165 170
 aca ctg ctg aac atg ctg aac atc tcc ccc ttc tcc ttc ggg ctg atc 637
 Thr Leu Leu Asn Met Leu Asn Ile Ser Pro Phe Ser Phe Gly Leu Ile
 175 180 185
 atc cag cag gtg ttt gac aac ggc agc att tat aac cct gaa gtg ctc 685
 Ile Gln Gln Val Phe Asp Asn Gly Ser Ile Tyr Asn Pro Glu Val Leu
 190 195 200
 gac atc aca gag cag gcc ctg cac tct cgc ttt ctg gag ggt gtc cgc 733
 Asp Ile Thr Glu Gln Ala Leu His Ser Arg Phe Leu Glu Gly Val Arg
 205 210 215 220
 aac gtg gcc agt gtg tgt ctg cag atc ggg tac cca act gtt gcc tcg 781
 Asn Val Ala Ser Val Cys Leu Gln Ile Gly Tyr Pro Thr Val Ala Ser
 225 230 235
 gtg cca cac tcc atc atc aat ggg tac aag cgc gtc ctg gca ttg tct 829
 Val Pro His Ser Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Leu Ser
 240 245 250
 gtg gag act gag tac acc ttc cca ctt act gaa aag gtc aag gcc ttc 877
 Val Glu Thr Glu Tyr Thr Phe Pro Leu Thr Glu Lys Val Lys Ala Phe
 255 260 265
 ctg gct gat cca tct gca ttt gcg gct gct gcc cct gca gct gct gcc 925
 Leu Ala Asp Pro Ser Ala Phe Ala Ala Ala Ala Pro Ala Ala Ala Ala
 270 275 280
 acc act gct gcc cct gcg gct gct gca gcc cct gcc aaa gct gaa gca 973
 Thr Thr Ala Ala Pro Ala Ala Ala Ala Ala Pro Ala Lys Ala Glu Ala
 285 290 295 300
 aag gaa gag tcg gag gaa tca gat gag gat atg gga ttc ggt ctc ttc 1021
 Lys Glu Glu Ser Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe

305 310 315
gac taa tcccgccaaa gcaaccaagt cagcctgctt aatttgagaa agatggaaat 1077
Asp
aaaggcttac tttctctt 1094

<210> 263

<211> 317

<212> PRT

<213> Mus musculus

<400> 263

Met Pro Arg Glu Asp Arg Ala Thr Trp Lys Ser Asn Tyr Phe Leu Lys
1 5 10 15
Ile Ile Gln Leu Leu Asp Asp Tyr Pro Lys Cys Phe Ile Val Gly Ala
20 25 30
Asp Asn Val Gly Ser Lys Gln Met Gln Gln Ile Arg Met Ser Leu Arg
35 40 45
Gly Lys Ala Val Val Leu Met Gly Lys Asn Thr Met Met Arg Lys Ala
50 55 60
Ile Arg Gly His Leu Glu Asn Asn Pro Ala Leu Glu Lys Leu Leu Pro
65 70 75 80
His Ile Arg Gly Asn Val Gly Phe Val Phe Thr Lys Glu Asp Leu Thr
85 90 95
Glu Ile Arg Asp Met Leu Leu Ala Asn Lys Val Pro Ala Ala Ala Arg
100 105 110
Ala Gly Ala Ile Ala Pro Cys Glu Val Thr Val Pro Ala Gln Asn Thr
115 120 125
Gly Leu Gly Pro Glu Lys Thr Ser Phe Phe Gln Ala Leu Gly Ile Thr
130 135 140

Thr Lys Ile Ser Arg Gly Thr Ile Glu Ile Leu Ser Asp Val Gln Leu
 145 150 155 160
 Ile Lys Thr Gly Asp Lys Val Gly Ala Ser Glu Ala Thr Leu Leu Asn
 165 170 175
 Met Leu Asn Ile Ser Pro Phe Ser Phe Gly Leu Ile Ile Gln Gln Val
 180 185 190
 Phe Asp Asn Gly Ser Ile Tyr Asn Pro Glu Val Leu Asp Ile Thr Glu
 195 200 205
 Gln Ala Leu His Ser Arg Phe Leu Glu Gly Val Arg Asn Val Ala Ser
 210 215 220
 Val Cys Leu Gln Ile Gly Tyr Pro Thr Val Ala Ser Val Pro His Ser
 225 230 235 240
 Ile Ile Asn Gly Tyr Lys Arg Val Leu Ala Leu Ser Val Glu Thr Glu
 245 250 255
 Tyr Thr Phe Pro Leu Thr Glu Lys Val Lys Ala Phe Leu Ala Asp Pro
 260 265 270
 Ser Ala Phe Ala Ala Ala Ala Pro Ala Ala Ala Ala Thr Thr Ala Ala
 275 280 285
 Pro Ala Ala Ala Ala Ala Pro Ala Lys Ala Glu Ala Lys Glu Glu Ser
 290 295 300
 Glu Glu Ser Asp Glu Asp Met Gly Phe Gly Leu Phe Asp
 305 310 315

<210> 264

<211> 1584

<212> DNA

<213> Mus musculus

<400> 264

cttaggttagga aggcctcttt tttttttttt tttccttccc ccccccgagt ccgcgcctttt 60
 cgicgtcgcc gccgccgcca tgtcgggagg tgggtgtgac cgtaggcccgg cggggaacaa 120
 cgactgccgc atctacgtgg gtaacctacc tccggatata cgaaccaagg acatcgagga 180
 cgtgtttttac aaatacggcg ccateccgca catcgacctg aagaaccgcc gcgggggacc 240
 gcccttcgcc ttcgttgagt tgcaggaccc gcgagacgcg gaagatgcgg tgtacggtcg 300
 cgacggctac gactacgacg gctaccggct gcgggtagag tttccccgaa gcggccgcgg 360
 gaccggccga ggccggcgcg ggggtggagg cggcggcgcc ccgagaggcc gctatggccc 420
 gccgtccagg cggctccgaga acagagtggg tgtctctgga ctgcctccga gtggaagctg 480
 gcaggactta aaggatcaca tgcgtgaggc aggtgatgta tgttacgctg atgtttaccg 540
 agatggcact ggtgtcgtgg agtttgtacg gaaagaagat atgacgtatg cagttcgaaa 600
 actggataac actaagttta gatctcacga ggtaggttat acacttattc ttttttttgg 660
 ccagaatttg atacagtttt cttaacagtg gaatttgaag gtaaggatac aggcaagggt 720
 gttcacgtaa attaccagag cctgatctg tctttgtatt cgttcagctt gcttgaagac 780
 aggtgaaagc ttagatcttt caatggaaag ttctgtctat ccaataggga gaaactgcct 840
 acatccgggt taaagttgat gggcccagaa gtccaagtta tggaagatct cgatctcgaa 900
 gccgtagtcg tagcagaagc cgtagcagaa gcaacagcag gagtcgcagt tactccccaa 960
 ggagaagcag aggatcacca cgctattctc cccgtcatag cagatctcgc tctcgtacat 1020
 aagatgattg gtgacacttt ttgtagaacc catgttgtat acagttttcc tttactcagt 1080
 acaatctttt cattttttta attcaagctg ttttgttcag aatgggctaa agtgttgaat 1140
 tgcattcttg tgtaatatcc ctttctctta acatctacat tcccccatg tctttggtaa 1200
 cttgtatttt aagtgatgtc atagacagga ttgtttaaat ttagttaatt tccatgctct 1260
 tcagactgtg atatttgtta aatgtctatt ctgctctggt ttgtgtgaaa tgggattgtg 1320
 ggggtgtttg tggttatctt acttggggaa gttcttatgt ttatcttgct tttcatgtgt 1380
 ctttctgtag acatatctga agagatggat taagaatgct ttggattaag gattgtggag 1440
 cacatttcaa tcattttagg attgtcaaaa ggaggattga ggaggatcag atcaataatg 1500
 gaggcaatgg tatgactcca agtgctattg tcacagatga aattggcagt attgacctta 1560
 tactagaagg cgaggggtta aaaa 1584

<211> 927

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (78).. (827)

<400> 265

```

gtcttcccca gagcagctgc cttgatgttt actttgacaa gtagtgactg aaaaagttcc 60
accagggtgag aagagtg atg acc atc ctt ttc ctt act atg gtt att tca 110
      Met Thr Ile Leu Phe Leu Thr Met Val Ile Ser
              1              5              10
tac ttc ggt tgc atg aaa gcg gcg ccc atg aaa gaa gta aac gtc cac 158
Tyr Phe Gly Cys Met Lys Ala Ala Pro Met Lys Glu Val Asn Val His
              15              20              25
gga caa ggc aac ttg gcc tac cca ggt gtg cgg acc cat ggg act ctg 206
Gly Gln Gly Asn Leu Ala Tyr Pro Gly Val Arg Thr His Gly Thr Leu
              30              35              40
gag agc gtg aat ggg ccc agg gca ggt tcg aga ggt ctg acg acg aca 254
Glu Ser Val Asn Gly Pro Arg Ala Gly Ser Arg Gly Leu Thr Thr Thr
              45              50              55
tca ctg gct gac act ttt gag cac gtc atc gaa gag ctg ctg gat gag 302
Ser Leu Ala Asp Thr Phe Glu His Val Ile Glu Glu Leu Leu Asp Glu
              60              65              70              75
gac cag aag gtt cgg ccc aac gaa gaa aac cat aag gac gcg gac ttg 350
Asp Gln Lys Val Arg Pro Asn Glu Glu Asn His Lys Asp Ala Asp Leu
              80              85              90
tac act tcc cgg gtg atg ctc agc agt caa gtg cct ttg gag cct cct 398

```


Tyr Thr Ser Arg Val Met Leu Ser Ser Gln Val Pro Leu Glu Pro Pro	
95 100 105	
cta ctc ttt ctg ctg gag gaa tac aaa aat tac ctg gat gcc gca aac	446
Leu Leu Phe Leu Leu Glu Glu Tyr Lys Asn Tyr Leu Asp Ala Ala Asn	
110 115 120	
atg tct atg agg gtt cgg cgc cac tcc gac cct gcc cgc cgt ggg gag	494
Met Ser Met Arg Val Arg Arg His Ser Asp Pro Ala Arg Arg Gly Glu	
125 130 135	
ctg agc gtg tgt gac agt att agc gag tgg gtc aca gcg gca gat aaa	542
Leu Ser Val Cys Asp Ser Ile Ser Glu Trp Val Thr Ala Ala Asp Lys	
140 145 150 155	
aag act gca gtg gac atg tct ggc ggg acg gtc aca gtc cta gag aaa	590
Lys Thr Ala Val Asp Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys	
160 165 170	
gtc ccg gta tcc aaa ggc caa ctg aag cag tat ttc tac gag acc aag	638
Val Pro Val Ser Lys Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys	
175 180 185	
tgt aat ccc atg ggt tac acc aag gaa ggc tgc agg ggc ata gac aaa	686
Cys Asn Pro Met Gly Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys	
190 195 200	
agg cac tgg aac tcg caa tgc cga act acc caa tcg tat gtt cgg gcc	734
Arg His Trp Asn Ser Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala	
205 210 215	
ctt act atg gat agc aaa aag aga att ggc tgg cga ttc ata agg ata	782
Leu Thr Met Asp Ser Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile	
220 225 230 235	
gac act tcc tgt gta tgt aca ctg acc att aaa agg gga aga tag	827
Asp Thr Ser Cys Val Cys Thr Leu Thr Ile Lys Arg Gly Arg	
240 245 250	

tggatttaag ttgtatagat tatattgaga caaaattatc tatttgtata tatacataac 887
aggataaatt attcagittaa gaaaaaataa ttttatgaac 927

<210> 266

<211> 249

<212> PRT

<213> Mus musculus

<400> 266

Met	Thr	Ile	Leu	Phe	Leu	Thr	Met	Val	Ile	Ser	Tyr	Phe	Gly	Cys	Met
1					5				10					15	
Lys	Ala	Ala	Pro	Met	Lys	Glu	Val	Asn	Val	His	Gly	Gln	Gly	Asn	Leu
					20				25					30	
Ala	Tyr	Pro	Gly	Val	Arg	Thr	His	Gly	Thr	Leu	Glu	Ser	Val	Asn	Gly
					35				40					45	
Pro	Arg	Ala	Gly	Ser	Arg	Gly	Leu	Thr	Thr	Thr	Ser	Leu	Ala	Asp	Thr
					50				55					60	
Phe	Glu	His	Val	Ile	Glu	Glu	Leu	Leu	Asp	Glu	Asp	Gln	Lys	Val	Arg
					65				70					75	
Pro	Asn	Glu	Glu	Asn	His	Lys	Asp	Ala	Asp	Leu	Tyr	Thr	Ser	Arg	Val
					85				90					95	
Met	Leu	Ser	Ser	Gln	Val	Pro	Leu	Glu	Pro	Pro	Leu	Leu	Phe	Leu	Leu
					100				105					110	
Glu	Glu	Tyr	Lys	Asn	Tyr	Leu	Asp	Ala	Ala	Asn	Met	Ser	Met	Arg	Val
					115				120					125	
Arg	Arg	His	Ser	Asp	Pro	Ala	Arg	Arg	Gly	Glu	Leu	Ser	Val	Cys	Asp
					130				135					140	
Ser	Ile	Ser	Glu	Trp	Val	Thr	Ala	Ala	Asp	Lys	Lys	Thr	Ala	Val	Asp
					145				150					155	
															160

Met Ser Gly Gly Thr Val Thr Val Leu Glu Lys Val Pro Val Ser Lys

165

170

175

Gly Gln Leu Lys Gln Tyr Phe Tyr Glu Thr Lys Cys Asn Pro Met Gly

180

185

190

Tyr Thr Lys Glu Gly Cys Arg Gly Ile Asp Lys Arg His Trp Asn Ser

195

200

205

Gln Cys Arg Thr Thr Gln Ser Tyr Val Arg Ala Leu Thr Met Asp Ser

210

215

220

Lys Lys Arg Ile Gly Trp Arg Phe Ile Arg Ile Asp Thr Ser Cys Val

225

230

235

240

Cys Thr Leu Thr Ile Lys Arg Gly Arg

245

<210> 267

<211> 547

<212> DNA

<213> Mus musculus

<400> 267

acctttatit ccacatagga atagacittta agatcaaaac agtggaacta caaggaaaga 60
 agatcaagct acagatatgg gacacagcag gccaggagcg atttcacacc atcacaacct 120
 cctactacag aggagcaatg ggcatcatgc tagtgtatga catcaccaac ggtaaaagct 180
 ttgagaacat cagcaagtgg cttagaaaca tagatgagca tgccaatgaa gatgtggaaa 240
 gaatgttact agggaacaag tgtgacatgg acgacaagag agttgtaccg aaaggcaaag 300
 gagaacagat tgcaagggag catggtatta ggTTTTTTga gactagtgc aaagcaaata 360
 taaacatcga aaaggcggtc ctcacattag ctgaagacat cctccgaaag acccctgtaa 420
 aagaacccaa cagtgaaaac gtagatatca gcagtggagg aggcgtgacg ggctggaaga 480
 gcaagtgcig ctgagtgcic tccgtgccat ctgctgccat ccaccatccg gtctcttct 540
 tgctgca 547

<210> 268

<211> 825

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (21).. (800)

<400> 268

agggtagttc agccaccagc atg tcc aag cac aaa ctt att ata cta aga cat 53

Met Ser Lys His Lys Leu Ile Ile Leu Arg His

1 5 10

gga gag ggc caa tgg aat aag gag aac cga ttc tgt agt tgg gtg gac 101

Gly Glu Gly Gln Trp Asn Lys Glu Asn Arg Phe Cys Ser Trp Val Asp

15 20 25

cag aaa ctt aac aac gac gga ctg gag gag gct cgg aac tgt ggg agg 149

Gln Lys Leu Asn Asn Asp Gly Leu Glu Glu Ala Arg Asn Cys Gly Arg

30 35 40

cag ctc aaa gct ctc aac ttc gag ttt gat ctt gtc ttc aca tcc atc 197

Gln Leu Lys Ala Leu Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Ile

45 50 55

ctt aac agg tcc att cac aca gcc tgg ctg atc ctg gaa gag ctg ggg 245

Leu Asn Arg Ser Ile His Thr Ala Trp Leu Ile Leu Glu Glu Leu Gly

60 65 70 75

cag gag tgg gtg cct gtg gag agc tcc tgg cgt ttg aat gag cgt cac 293

Gln Glu Trp Val Pro Val Glu Ser Ser Trp Arg Leu Asn Glu Arg His

80 85 90

tat gga gcc ttg att ggc ctc aac agg gag aaa atg gct ttg aat cat	341
Tyr Gly Ala Leu Ile Gly Leu Asn Arg Glu Lys Met Ala Leu Asn His	
95 100 105	
ggt gaa gag cag gta agg ctc tgg agg aga agc tac aac gtg acc cca	389
Gly Glu Glu Gln Val Arg Leu Trp Arg Arg Ser Tyr Asn Val Thr Pro	
110 115 120	
cct cct ata gag gag tct cat ccc tac ttc cac gag atc tac agt gac	437
Pro Pro Ile Glu Glu Ser His Pro Tyr Phe His Glu Ile Tyr Ser Asp	
125 130 135	
cgg agg tac aaa gtg tgc gat gtg ccc ttg gat caa ctg cca cgt tca	485
Arg Arg Tyr Lys Val Cys Asp Val Pro Leu Asp Gln Leu Pro Arg Ser	
140 145 150 155	
gaa agc ttg aag gat gtt ctg gag aga ctt ctt ccc tac tgg aag gaa	533
Glu Ser Leu Lys Asp Val Leu Glu Arg Leu Leu Pro Tyr Trp Lys Glu	
160 165 170	
agg att gct ccg gaa atc tta aag ggc aaa agc att ctg ata tct gct	581
Arg Ile Ala Pro Glu Ile Leu Lys Gly Lys Ser Ile Leu Ile Ser Ala	
175 180 185	
cac ggg aat agc agt aga gct ctc ctg aaa cat ctg gaa ggt atc tca	629
His Gly Asn Ser Ser Arg Ala Leu Leu Lys His Leu Glu Gly Ile Ser	
190 195 200	
gac gag gat att atc aac atc act ctg ccc act gga gtt ccg att ctg	677
Asp Glu Asp Ile Ile Asn Ile Thr Leu Pro Thr Gly Val Pro Ile Leu	
205 210 215	
ctg gag ttg gat gaa aac ctg cgt gcc gtt ggg cct cac cag ttc ctg	725
Leu Glu Leu Asp Glu Asn Leu Arg Ala Val Gly Pro His Gln Phe Leu	
220 225 230 235	
ggc aac cag gag gcc atc cag gca gcc att aag aaa gtg gat gat caa	773
Gly Asn Gln Glu Ala Ile Gln Ala Ala Ile Lys Lys Val Asp Asp Gln	

240 245 250
 ggg aaa gtg aaa caa ggc aaa caa taa agtgtggcca ggaacgagtt tgggg 825
 Gly Lys Val Lys Gln Gly Lys Gln

255 260

<210> 269

<211> 259

<212> PRT

<213> Mus musculus

<400> 269

Met Ser Lys His Lys Leu Ile Ile Leu Arg His Gly Glu Gly Gln Trp

1 5 10 15

Asn Lys Glu Asn Arg Phe Cys Ser Trp Val Asp Gln Lys Leu Asn Asn

20 25 30

Asp Gly Leu Glu Glu Ala Arg Asn Cys Gly Arg Gln Leu Lys Ala Leu

35 40 45

Asn Phe Glu Phe Asp Leu Val Phe Thr Ser Ile Leu Asn Arg Ser Ile

50 55 60

His Thr Ala Trp Leu Ile Leu Glu Glu Leu Gly Gln Glu Trp Val Pro

65 70 75 80

Val Glu Ser Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu Ile

85 90 95

Gly Leu Asn Arg Glu Lys Met Ala Leu Asn His Gly Glu Glu Gln Val

100 105 110

Arg Leu Trp Arg Arg Ser Tyr Asn Val Thr Pro Pro Pro Ile Glu Glu

115 120 125

Ser His Pro Tyr Phe His Glu Ile Tyr Ser Asp Arg Arg Tyr Lys Val

130 135 140

Cys Asp Val Pro Leu Asp Gln Leu Pro Arg Ser Glu Ser Leu Lys Asp
 145 150 155 160
 Val Leu Glu Arg Leu Leu Pro Tyr Trp Lys Glu Arg Ile Ala Pro Glu
 165 170 175
 Ile Leu Lys Gly Lys Ser Ile Leu Ile Ser Ala His Gly Asn Ser Ser
 180 185 190
 Arg Ala Leu Leu Lys His Leu Glu Gly Ile Ser Asp Glu Asp Ile Ile
 195 200 205
 Asn Ile Thr Leu Pro Thr Gly Val Pro Ile Leu Leu Glu Leu Asp Glu
 210 215 220
 Asn Leu Arg Ala Val Gly Pro His Gln Phe Leu Gly Asn Gln Glu Ala
 225 230 235 240
 Ile Gln Ala Ala Ile Lys Lys Val Asp Asp Gln Gly Lys Val Lys Gln
 245 250 255
 Gly Lys Gln

<210> 270

<211> 1912

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (58)..(1665)

<400> 270

ggcttcccg ggcggattgt gaggggttct ctccctctacg cggaatccgt cggaacc 57
 atg gct tcc ctt tcc ctc gca cct gtt aat atc ttc aag gct gga gct 105
 Met Ala Ser Leu Ser Leu Ala Pro Val Asn Ile Phe Lys Ala Gly Ala

1	5	10	15	
gat gaa gag agg gcc gag ata gct cgc ctg tgc tgc ttt atc ggt gcc				153
Asp Glu Glu Arg Ala Glu Ile Ala Arg Leu Ser Ser Phe Ile Gly Ala				
20	25	30		
atc gcc att gga gac ttg gtg aag agc act ttg gga ccg aag ggc atg				201
Ile Ala Ile Gly Asp Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met				
35	40	45		
gac aaa att ctc cta agc agt gga cga gac gcc gct ctg atg gtg acc				249
Asp Lys Ile Leu Leu Ser Ser Gly Arg Asp Ala Ala Leu Met Val Thr				
50	55	60		
aac gac ggt gct acc att ctc aag aac att ggt gtg gac aac ccc gca				297
Asn Asp Gly Ala Thr Ile Leu Lys Asn Ile Gly Val Asp Asn Pro Ala				
65	70	75	80	
gca aag gtt cta gtt gat atg tca agg gtt caa gat gat gaa gtt ggt				345
Ala Lys Val Leu Val Asp Met Ser Arg Val Gln Asp Asp Glu Val Gly				
85	90	95		
gat ggc act acc tct gtt act gtc tta gcc gca gag ctg ctc cgg gaa				393
Asp Gly Thr Thr Ser Val Thr Val Leu Ala Ala Glu Leu Leu Arg Glu				
100	105	110		
gca gaa tct tta att gca aaa aag ata cat cca cag acc atc atc tca				441
Ala Glu Ser Leu Ile Ala Lys Lys Ile His Pro Gln Thr Ile Ile Ser				
115	120	125		
ggt tgg aga gaa gcc aca aag gca gca aga gag gcc ctg ctg agc tcc				489
Gly Trp Arg Glu Ala Thr Lys Ala Ala Arg Glu Ala Leu Leu Ser Ser				
130	135	140		
gct gtg gat cat ggt tct gat gaa gcc aga ttc tgg cag gac tta atg				537
Ala Val Asp His Gly Ser Asp Glu Ala Arg Phe Trp Gln Asp Leu Met				
145	150	155	160	
aac att gca gga acg aca ttg tcc tca aag ctc ctt act cac cac aag				585

Asn Ile Ala Gly Thr Thr Leu Ser Ser Lys Leu Leu Thr His His Lys	
165 170 175	
gac cac ttt act aaa ctg gcc gtg gaa gcg ggt ctc aga ctg aaa ggc	633
Asp His Phe Thr Lys Leu Ala Val Glu Ala Gly Leu Arg Leu Lys Gly	
180 185 190	
tct ggc aac ctg gag gcg att cat gtc atc aag aaa cta ggt ggg agt	681
Ser Gly Asn Leu Glu Ala Ile His Val Ile Lys Lys Leu Gly Gly Ser	
195 200 205	
ctg gca gac tcc tat cta gat gaa ggt ttt ctt ttg gat aaa aaa att	729
Leu Ala Asp Ser Tyr Leu Asp Glu Gly Phe Leu Leu Asp Lys Lys Ile	
210 215 220	
gga gta aat caa cca aag aga att gaa aat gct aaa att ctt att gca	777
Gly Val Asn Gln Pro Lys Arg Ile Glu Asn Ala Lys Ile Leu Ile Ala	
225 230 235 240	
aat act ggg atg gat aca gac aaa ata aag ata ttt ggc tct cgg gta	825
Asn Thr Gly Met Asp Thr Asp Lys Ile Lys Ile Phe Gly Ser Arg Val	
245 250 255	
aga gtt gat tcc aca gca aag gtt gca gag ata gaa cat gca gaa aag	873
Arg Val Asp Ser Thr Ala Lys Val Ala Glu Ile Glu His Ala Glu Lys	
260 265 270	
gag aag atg aag gag aaa gtt gaa cgt att ctt aag cat gga ata aat	921
Glu Lys Met Lys Glu Lys Val Glu Arg Ile Leu Lys His Gly Ile Asn	
275 280 285	
tgc ttt att aac aga cag tta att tat aat tac cct gaa caa ctc ttc	969
Cys Phe Ile Asn Arg Gln Leu Ile Tyr Asn Tyr Pro Glu Gln Leu Phe	
290 295 300	
ggc gct gct ggc gtc atg gct att gag cat gcg gat ttc gca ggt gtg	1017
Gly Ala Ala Gly Val Met Ala Ile Glu His Ala Asp Phe Ala Gly Val	
305 310 315 320	

gag cgc ctc gct ctt gtc aca ggt ggt gag att gcc tct acc ttt gat	1065
Glu Arg Leu Ala Leu Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp	
325 330 335	
cac cca gaa ctt gtg aag ctt gga agt tgc aaa ctt att gaa gaa gtt	1113
His Pro Glu Leu Val Lys Leu Gly Ser Cys Lys Leu Ile Glu Glu Val	
340 345 350	
atg atc ggg gaa gat aaa ctc att cac ttt tct ggg gtt gcc ctt ggt	1161
Met Ile Gly Glu Asp Lys Leu Ile His Phe Ser Gly Val Ala Leu Gly	
355 360 365	
gag gca tgc acc att gtg ctt cgt ggt gcc act cag caa att ctg gat	1209
Glu Ala Cys Thr Ile Val Leu Arg Gly Ala Thr Gln Gln Ile Leu Asp	
370 375 380	
gaa gct gaa cga tct ctg cat gat gct ctt tgt gtt ctt gct cag act	1257
Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu Ala Gln Thr	
385 390 395 400	
gta aaa gat cct aga aca gtt tac ggg gga ggc tgc tct gag atg ctg	1305
Val Lys Asp Pro Arg Thr Val Tyr Gly Gly Gly Cys Ser Glu Met Leu	
405 410 415	
atg gcc cat gct gtg aca cag ctt gcc aac aga acc cca gga aaa gaa	1353
Met Ala His Ala Val Thr Gln Leu Ala Asn Arg Thr Pro Gly Lys Glu	
420 425 430	
gct gta gca atg gag tcg ttt gca aaa gcc ctg aga atg ttg ccg acc	1401
Ala Val Ala Met Glu Ser Phe Ala Lys Ala Leu Arg Met Leu Pro Thr	
435 440 445	
atc ata gcc gac aat gcg ggc tat gac agt gca gat ctg gtg gca cag	1449
Ile Ile Ala Asp Asn Ala Gly Tyr Asp Ser Ala Asp Leu Val Ala Gln	
450 455 460	
ctc cga gct gct cac agt gaa ggc cat ata act gct gga ctg gat atg	1497
Leu Arg Ala Ala His Ser Glu Gly His Ile Thr Ala Gly Leu Asp Met	

465 470 475 480
 aag gaa ggt acc atc ggc gat atg gca gta ctg ggt ata aca gag agt 1545
 Lys Glu Gly Thr Ile Gly Asp Met Ala Val Leu Gly Ile Thr Glu Ser
 485 490 495
 ttt caa gtg aag cga cag gtt ctt ctg agt gcg gct gaa gca gca gag 1593
 Phe Gln Val Lys Arg Gln Val Leu Leu Ser Ala Ala Glu Ala Ala Glu
 500 505 510
 gtg atc ctg cga gtg gac aac att atc aaa gca gca cca agg aaa cgt 1641
 Val Ile Leu Arg Val Asp Asn Ile Ile Lys Ala Ala Pro Arg Lys Arg
 515 520 525
 gtc ccc gat cac cac ccc tgt taa gcattcccat ttgctgatga actctgggcc 1695
 Val Pro Asp His His Pro Cys
 530 535
 agttcatagc aaagttgtac ttggaagact tcaaccttta aagaagactg gtggaattga 1755
 cctgtccatg atagccttaa gtttgaacat tagctgacct tctgtgttaa acatgggtct 1815
 aatttatatta ctgtttcatt ticcatacaa ttcagttgat ttacaagttc atttctcata 1875
 ctgtgtatta aaataaaaat ccagttactt agccctt 1912

<210> 271

<211> 535

<212> PRT

<213> Mus musculus

<400> 271

Met Ala Ser Leu Ser Leu Ala Pro Val Asn Ile Phe Lys Ala Gly Ala
 1 5 10 15
 Asp Glu Glu Arg Ala Glu Ile Ala Arg Leu Ser Ser Phe Ile Gly Ala
 20 25 30
 Ile Ala Ile Gly Asp Leu Val Lys Ser Thr Leu Gly Pro Lys Gly Met

35	40	45
Asp Lys Ile Leu Leu Ser Ser Gly Arg Asp Ala Ala Leu Met Val Thr		
50	55	60
Asn Asp Gly Ala Thr Ile Leu Lys Asn Ile Gly Val Asp Asn Pro Ala		
65	70	75
Ala Lys Val Leu Val Asp Met Ser Arg Val Gln Asp Asp Glu Val Gly		
85	90	95
Asp Gly Thr Thr Ser Val Thr Val Leu Ala Ala Glu Leu Leu Arg Glu		
100	105	110
Ala Glu Ser Leu Ile Ala Lys Lys Ile His Pro Gln Thr Ile Ile Ser		
115	120	125
Gly Trp Arg Glu Ala Thr Lys Ala Ala Arg Glu Ala Leu Leu Ser Ser		
130	135	140
Ala Val Asp His Gly Ser Asp Glu Ala Arg Phe Trp Gln Asp Leu Met		
145	150	155
Asn Ile Ala Gly Thr Thr Leu Ser Ser Lys Leu Leu Thr His His Lys		
165	170	175
Asp His Phe Thr Lys Leu Ala Val Glu Ala Gly Leu Arg Leu Lys Gly		
180	185	190
Ser Gly Asn Leu Glu Ala Ile His Val Ile Lys Lys Leu Gly Gly Ser		
195	200	205
Leu Ala Asp Ser Tyr Leu Asp Glu Gly Phe Leu Leu Asp Lys Lys Ile		
210	215	220
Gly Val Asn Gln Pro Lys Arg Ile Glu Asn Ala Lys Ile Leu Ile Ala		
225	230	235
Asn Thr Gly Met Asp Thr Asp Lys Ile Lys Ile Phe Gly Ser Arg Val		
245	250	255
Arg Val Asp Ser Thr Ala Lys Val Ala Glu Ile Glu His Ala Glu Lys		
260	265	270

Glu Lys Met Lys Glu Lys Val Glu Arg Ile Leu Lys His Gly Ile Asn
 275 280 285
 Cys Phe Ile Asn Arg Gln Leu Ile Tyr Asn Tyr Pro Glu Gln Leu Phe
 290 295 300
 Gly Ala Ala Gly Val Met Ala Ile Glu His Ala Asp Phe Ala Gly Val
 305 310 315 320
 Glu Arg Leu Ala Leu Val Thr Gly Gly Glu Ile Ala Ser Thr Phe Asp
 325 330 335
 His Pro Glu Leu Val Lys Leu Gly Ser Cys Lys Leu Ile Glu Glu Val
 340 345 350
 Met Ile Gly Glu Asp Lys Leu Ile His Phe Ser Gly Val Ala Leu Gly
 355 360 365
 Glu Ala Cys Thr Ile Val Leu Arg Gly Ala Thr Gln Gln Ile Leu Asp
 370 375 380
 Glu Ala Glu Arg Ser Leu His Asp Ala Leu Cys Val Leu Ala Gln Thr
 385 390 395 400
 Val Lys Asp Pro Arg Thr Val Tyr Gly Gly Gly Cys Ser Glu Met Leu
 405 410 415
 Met Ala His Ala Val Thr Gln Leu Ala Asn Arg Thr Pro Gly Lys Glu
 420 425 430
 Ala Val Ala Met Glu Ser Phe Ala Lys Ala Leu Arg Met Leu Pro Thr
 435 440 445
 Ile Ile Ala Asp Asn Ala Gly Tyr Asp Ser Ala Asp Leu Val Ala Gln
 450 455 460
 Leu Arg Ala Ala His Ser Glu Gly His Ile Thr Ala Gly Leu Asp Met
 465 470 475 480
 Lys Glu Gly Thr Ile Gly Asp Met Ala Val Leu Gly Ile Thr Glu Ser
 485 490 495
 Phe Gln Val Lys Arg Gln Val Leu Leu Ser Ala Ala Glu Ala Ala Glu

500	505	510
Val Ile Leu Arg Val Asp Asn Ile Ile Lys Ala Ala Pro Arg Lys Arg		
515	520	525
Val Pro Asp His His Pro Cys		
530	535	

<210> 272

<211> 1734

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (3).. (1637)

<400> 272

ag atg atg ccc aca cca gtt atc ctg ttg aaa gag ggt act gat agc	47
Met Met Pro Thr Pro Val Ile Leu Leu Lys Glu Gly Thr Asp Ser	
1 5 10 15	
tcc cag ggc atc cct cag ctc gtg agt aac atc agt gcc tgc caa gtg	95
Ser Gln Gly Ile Pro Gln Leu Val Ser Asn Ile Ser Ala Cys Gln Val	
20 25 30	
att gct gag gct gta aga acc acc ctg ggt ccc cgt ggc atg gac aaa	143
Ile Ala Glu Ala Val Arg Thr Thr Leu Gly Pro Arg Gly Met Asp Lys	
35 40 45	
ctt att gtg gat ggc cga ggc aaa gca aca ata tct aat gat ggg gcc	191
Leu Ile Val Asp Gly Arg Gly Lys Ala Thr Ile Ser Asn Asp Gly Ala	
50 55 60	
aca att ctg aaa ctc ctc gat gtt gtc cat cct gca gca aag act tta	239

Thr Ile Leu Lys Leu Leu Asp Val Val His Pro Ala Ala Lys Thr Leu
 65 70 75
 gtg gac ata gcc aag tcc cag gat gct gag gtt ggt gat ggc acc acc 287
 Val Asp Ile Ala Lys Ser Gln Asp Ala Glu Val Gly Asp Gly Thr Thr
 80 85 90 95
 tca gtg acc ctg ctg gct gcg gag ttt ctg aag cag gtg aag ccc tac 335
 Ser Val Thr Leu Leu Ala Ala Glu Phe Leu Lys Gln Val Lys Pro Tyr
 100 105 110
 gtg gaa gaa ggt tta cac cct cag atc atc atc cga gct ttc cgc aca 383
 Val Glu Glu Gly Leu His Pro Gln Ile Ile Ile Arg Ala Phe Arg Thr
 115 120 125
 gcc acc caa ttg gct gtt aac aaa atc aaa gag ata gct gtg act gtg 431
 Ala Thr Gln Leu Ala Val Asn Lys Ile Lys Glu Ile Ala Val Thr Val
 130 135 140
 aag aag caa gat aaa gta gag cag agg aag atg ctg gag aag tgt gcg 479
 Lys Lys Gln Asp Lys Val Glu Gln Arg Lys Met Leu Glu Lys Cys Ala
 145 150 155
 atg aca gcc ctg agc tcc aag ctg atc tcc cag cag aag gtc ttc ttc 527
 Met Thr Ala Leu Ser Ser Lys Leu Ile Ser Gln Gln Lys Val Phe Phe
 160 165 170 175
 gcc aag atg gtg gtt gat gcc gtg atg atg ctt gac gag ctg ctg cag 575
 Ala Lys Met Val Val Asp Ala Val Met Met Leu Asp Glu Leu Leu Gln
 180 185 190
 ctt aaa atg att ggc atc aag aag gtg cag ggg gga gcc ctg gag gag 623
 Leu Lys Met Ile Gly Ile Lys Lys Val Gln Gly Gly Ala Leu Glu Glu
 195 200 205
 tct cag cta gtt gct ggt gtt gcg ttc aag aag act ttc tct tat gct 671
 Ser Gln Leu Val Ala Gly Val Ala Phe Lys Lys Thr Phe Ser Tyr Ala
 210 215 220

ggg ttt gaa atg cag ccc aag aag tat aag aac ccc aag att gcc ctc 719
 Gly Phe Glu Met Gln Pro Lys Lys Tyr Lys Asn Pro Lys Ile Ala Leu
 225 230 235
 tta aat gtt gag ctt gag ctg aaa gca gag aaa gat aat gct gaa atc 767
 Leu Asn Val Glu Leu Glu Leu Lys Ala Glu Lys Asp Asn Ala Glu Ile
 240 245 250 255
 aga gtc cac aca gtg gag gat tac cag gca att gtt gat gcc gag tgg 815
 Arg Val His Thr Val Glu Asp Tyr Gln Ala Ile Val Asp Ala Glu Trp
 260 265 270
 aat att ctc tat gac aag tta gag aag atc cat cag tct gga gcc aaa 863
 Asn Ile Leu Tyr Asp Lys Leu Glu Lys Ile His Gln Ser Gly Ala Lys
 275 280 285
 gtc atc ttg tct aaa ctc cct att ggg gat gtg gcc acc cag tac ttt 911
 Val Ile Leu Ser Lys Leu Pro Ile Gly Asp Val Ala Thr Gln Tyr Phe
 290 295 300
 gct gat agg gac atg ttc tgt gct ggc cga gtg cct gag gag gat ctg 959
 Ala Asp Arg Asp Met Phe Cys Ala Gly Arg Val Pro Glu Glu Asp Leu
 305 310 315
 aag agg acg atg atg gct tgt gga ggc tca atc cag acc agt gtg aat 1007
 Lys Arg Thr Met Met Ala Cys Gly Gly Ser Ile Gln Thr Ser Val Asn
 320 325 330 335
 gct ctg gtt cca gat gtg ctg ggc cac tgc caa gtg ttt gaa gag acc 1055
 Ala Leu Val Pro Asp Val Leu Gly His Cys Gln Val Phe Glu Glu Thr
 340 345 350
 caa att gga gga gag agg tac aat ttc ttc act ggc tgc cct aag gcc 1103
 Gln Ile Gly Gly Glu Arg Tyr Asn Phe Phe Thr Gly Cys Pro Lys Ala
 355 360 365
 aag aca tgt acc atc atc ctc cgt ggt ggc gct gag cag ttt atg gaa 1151
 Lys Thr Cys Thr Ile Ile Leu Arg Gly Gly Ala Glu Gln Phe Met Glu

370	375	380	
gag aca gag agg tcc cta cat gat gcc atc atg att gtg agg agg gcc			1199
Glu Thr Glu Arg Ser Leu His Asp Ala Ile Met Ile Val Arg Arg Ala			
385	390	395	
atc aag aat gac tct gtg gtg gct ggt ggt gga gcc atc gag atg gaa			1247
Ile Lys Asn Asp Ser Val Val Ala Gly Gly Gly Ala Ile Glu Met Glu			
400	405	410	415
ctt tcc aaa tac ctg cgg gat tac tcg agg acc att cct ggg aag cag			1295
Leu Ser Lys Tyr Leu Arg Asp Tyr Ser Arg Thr Ile Pro Gly Lys Gln			
420	425	430	
cag ctg ttg att ggg gca tat gcc aag gcc ctg gag att att cca cga			1343
Gln Leu Leu Ile Gly Ala Tyr Ala Lys Ala Leu Glu Ile Ile Pro Arg			
435	440	445	
cag cta tgt gac aac gct ggc ttt gat gcc aca aac atc ctc aac aag			1391
Gln Leu Cys Asp Asn Ala Gly Phe Asp Ala Thr Asn Ile Leu Asn Lys			
450	455	460	
ctg cgg gct cga cac gca cag gga ggt atg tgg tat ggg gtg gac atc			1439
Leu Arg Ala Arg His Ala Gln Gly Gly Met Trp Tyr Gly Val Asp Ile			
465	470	475	
aac aat gag aac atc gcc gac aac ttc cag gca ttt gtg tgg gag cca			1487
Asn Asn Glu Asn Ile Ala Asp Asn Phe Gln Ala Phe Val Trp Glu Pro			
480	485	490	495
gcc atg gtg cgc atc aac gct ctg aca gca gct tct gag gct gca tgc			1535
Ala Met Val Arg Ile Asn Ala Leu Thr Ala Ala Ser Glu Ala Ala Cys			
500	505	510	
ctt att gtg tcc gtg gat gag act atc aag aac ccc cgc tcc act gtg			1583
Leu Ile Val Ser Val Asp Glu Thr Ile Lys Asn Pro Arg Ser Thr Val			
515	520	525	
gat cct cca gct cca tca gct ggc cgt ggc aga ggc caa gcc cgc ttc			1631

Asp Pro Pro Ala Pro Ser Ala Gly Arg Gly Arg Gly Gln Ala Arg Phe
 530 535 540
 cac tga gaggcgaggc ggtctgcacc tccttgtgag gtgagggggt ggatgagaag 1687
 His
 545
 atggttgctg gtcctgctggg ttctcactga ggattatttaa ataaagc 1734

<210> 273

<211> 544

<212> PRT

<213> Mus musculus

<400> 273

Met Met Pro Thr Pro Val Ile Leu Leu Lys Glu Gly Thr Asp Ser Ser
 1 5 10 15
 Gln Gly Ile Pro Gln Leu Val Ser Asn Ile Ser Ala Cys Gln Val Ile
 20 25 30
 Ala Glu Ala Val Arg Thr Thr Leu Gly Pro Arg Gly Met Asp Lys Leu
 35 40 45
 Ile Val Asp Gly Arg Gly Lys Ala Thr Ile Ser Asn Asp Gly Ala Thr
 50 55 60
 Ile Leu Lys Leu Leu Asp Val Val His Pro Ala Ala Lys Thr Leu Val
 65 70 75 80
 Asp Ile Ala Lys Ser Gln Asp Ala Glu Val Gly Asp Gly Thr Thr Ser
 85 90 95
 Val Thr Leu Leu Ala Ala Glu Phe Leu Lys Gln Val Lys Pro Tyr Val
 100 105 110
 Glu Glu Gly Leu His Pro Gln Ile Ile Ile Arg Ala Phe Arg Thr Ala
 115 120 125

Thr Gln Leu Ala Val Asn Lys Ile Lys Glu Ile Ala Val Thr Val Lys
 130 135 140
 Lys Gln Asp Lys Val Glu Gln Arg Lys Met Leu Glu Lys Cys Ala Met
 145 150 155 160
 Thr Ala Leu Ser Ser Lys Leu Ile Ser Gln Gln Lys Val Phe Phe Ala
 165 170 175
 Lys Met Val Val Asp Ala Val Met Met Leu Asp Glu Leu Leu Gln Leu
 180 185 190
 Lys Met Ile Gly Ile Lys Lys Val Gln Gly Gly Ala Leu Glu Glu Ser
 195 200 205
 Gln Leu Val Ala Gly Val Ala Phe Lys Lys Thr Phe Ser Tyr Ala Gly
 210 215 220
 Phe Glu Met Gln Pro Lys Lys Tyr Lys Asn Pro Lys Ile Ala Leu Leu
 225 230 235 240
 Asn Val Glu Leu Glu Leu Lys Ala Glu Lys Asp Asn Ala Glu Ile Arg
 245 250 255
 Val His Thr Val Glu Asp Tyr Gln Ala Ile Val Asp Ala Glu Trp Asn
 260 265 270
 Ile Leu Tyr Asp Lys Leu Glu Lys Ile His Gln Ser Gly Ala Lys Val
 275 280 285
 Ile Leu Ser Lys Leu Pro Ile Gly Asp Val Ala Thr Gln Tyr Phe Ala
 290 295 300
 Asp Arg Asp Met Phe Cys Ala Gly Arg Val Pro Glu Glu Asp Leu Lys
 305 310 315 320
 Arg Thr Met Met Ala Cys Gly Gly Ser Ile Gln Thr Ser Val Asn Ala
 325 330 335
 Leu Val Pro Asp Val Leu Gly His Cys Gln Val Phe Glu Glu Thr Gln
 340 345 350
 Ile Gly Gly Glu Arg Tyr Asn Phe Phe Thr Gly Cys Pro Lys Ala Lys

355 360 365
Thr Cys Thr Ile Ile Leu Arg Gly Gly Ala Glu Gln Phe Met Glu Glu
370 375 380
Thr Glu Arg Ser Leu His Asp Ala Ile Met Ile Val Arg Arg Ala Ile
385 390 395 400
Lys Asn Asp Ser Val Val Ala Gly Gly Gly Ala Ile Glu Met Glu Leu
405 410 415
Ser Lys Tyr Leu Arg Asp Tyr Ser Arg Thr Ile Pro Gly Lys Gln Gln
420 425 430
Leu Leu Ile Gly Ala Tyr Ala Lys Ala Leu Glu Ile Ile Pro Arg Gln
435 440 445
Leu Cys Asp Asn Ala Gly Phe Asp Ala Thr Asn Ile Leu Asn Lys Leu
450 455 460
Arg Ala Arg His Ala Gln Gly Gly Met Trp Tyr Gly Val Asp Ile Asn
465 470 475 480
Asn Glu Asn Ile Ala Asp Asn Phe Gln Ala Phe Val Trp Glu Pro Ala
485 490 495
Met Val Arg Ile Asn Ala Leu Thr Ala Ala Ser Glu Ala Ala Cys Leu
500 505 510
Ile Val Ser Val Asp Glu Thr Ile Lys Asn Pro Arg Ser Thr Val Asp
515 520 525
Pro Pro Ala Pro Ser Ala Gly Arg Gly Arg Gly Gln Ala Arg Phe His
530 535 540

<210> 274

<211> 490

<212> DNA

<213> Mus musculus

<400> 274

aattcggatc catgccagca gttgtgcctg gaagccttat agaccaacca tcagggcaga 60
aaccctaatta catcaagaag ttgtcatcag gtggctgtga caacctcatt aagctatgga 120
gggaagagga ggaatggccag tggaaggagg agcagaagct agaggcacac agcgactggg 180
tccgagatgt tgcctgggcc ccttccattg gcttggccac cagcaccatt gccagctgct 240
ctcaggatgg tcgagtgttt atttggacct gtgacgatgc ctcaggcaat atgtggtcac 300
ctaaactcct acacaagttc aatgatgttg tgtggcacgt gagctgggcc atcacagcca 360
acatcctggc tgtgtcaggt ggagacaata aggtgacct gtggaaagag tcggtggacg 420
gacagtgggt gtgcatcagt gacgtcaaca agggccaggg ttctgtgtca gcctccatca 480
cagagggcca 490

<210> 275

<211> 2189

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (55).. (1650)

<400> 275

gaagaccccg cagagagcac gttgttctcg gcctctcccg gagctaggcc agcc atg 57
Met
1.
gcg gcg gla aag acc cta aat ccg aag gcc gag gtg gcc cgg gcc cag 105
Ala Ala Val Lys Thr Leu Asn Pro Lys Ala Glu Val Ala Arg Ala Gln
5 10 15
gca gcg ctg gcg gtg aac atc agc gcg gct cgg ggc ctg cag gat gtt 153
Ala Ala Leu Ala Val Asn Ile Ser Ala Ala Arg Gly Leu Gln Asp Val

20	25	30	
ctg agg acc aac ttg ggg cct aag ggc acc atg aag atg ctt gta tct	201		
Leu Arg Thr Asn Leu Gly Pro Lys Gly Thr Met Lys Met Leu Val Ser			
35	40	45	
ggt gct gga gac atc aaa ctt act aaa gat ggc aat gtg ctg ctt cat	249		
Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu His			
50	55	60	65
gaa atg caa att caa cac cca aca gcc tct ttg ata gca aaa gtg gct	297		
Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val Ala			
70	75	80	
aca gcc cag gat gac ata act ggc gat ggc act aca tcc aat gtc ctc	345		
Thr Ala Gln Asp Asp Ile Thr Gly Asp Gly Thr Thr Ser Asn Val Leu			
85	90	95	
atc atc ggg gag ctg ctc aaa cag gcg gac ctg tac att tct gaa ggt	393		
Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu Gly			
100	105	110	
ctt cac cca aga ata ata act gaa ggt ttt gaa gcg gca aaa gaa aag	441		
Leu His Pro Arg Ile Ile Thr Glu Gly Phe Glu Ala Ala Lys Glu Lys			
115	120	125	
gca ctc caa ttt ctg gaa caa gtc aaa gta agc aaa gag atg gac aga	489		
Ala Leu Gln Phe Leu Glu Gln Val Lys Val Ser Lys Glu Met Asp Arg			
130	135	140	145
gaa aca ctc atc gat gtg gcc agg aca tct ctg cgg act aaa gtt cat	537		
Glu Thr Leu Ile Asp Val Ala Arg Thr Ser Leu Arg Thr Lys Val His			
150	155	160	
gct gaa ctt gca gat gtc ttg aca gag gct gta gtg gac tcc atc ttg	585		
Ala Glu Leu Ala Asp Val Leu Thr Glu Ala Val Val Asp Ser Ile Leu			
165	170	175	
gcc att agg aaa aag gac gag ccc att gac ctc ttc atg gtt gag atc	633		

Ala Ile Arg Lys Lys Asp Glu Pro Ile Asp Leu Phe Met Val Glu Ile
 180 185 190
 atg gag atg aag cat aaa tct gag aca gat aca agc tta atc aga ggg 681
 Met Glu Met Lys His Lys Ser Glu Thr Asp Thr Ser Leu Ile Arg Gly
 195 200 205
 ctt gtt ttg gat cat gga gct cgg cat cct gat atg aag aag aga gtg 729
 Leu Val Leu Asp His Gly Ala Arg His Pro Asp Met Lys Lys Arg Val
 210 215 220 225
 gaa aat gcc tac atc ctc acg tgc aac gtg tcc tta gag tat gag aaa 777
 Glu Asn Ala Tyr Ile Leu Thr Cys Asn Val Ser Leu Glu Tyr Glu Lys
 230 235 240
 .aca gaa gtg aat tct ggg ttt ttt tac aag agt gca gaa gag aga gaa 825
 Thr Glu Val Asn Ser Gly Phe Phe Tyr Lys Ser Ala Glu Glu Arg Glu
 245 250 255
 aaa cta gta aag gct gaa aga aaa ttc att gaa gat aga gtt aaa aaa 873
 Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Lys Lys
 260 265 270
 atc ata gag ctg aaa aag aaa gtc tgt ggt gac tca gat aaa gga ttt 921
 Ile Ile Glu Leu Lys Lys Lys Val Cys Gly Asp Ser Asp Lys Gly Phe
 275 280 285
 gtc gtt att aat caa aag ggg att gac ccc ttt tcc tta gat gcc ctt 969
 Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ala Leu
 290 295 300 305
 gcg aaa gaa ggg atc gta gct ctg cgc aga gcc aag agg aga aac atg 1017
 Ala Lys Glu Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn Met
 310 315 320
 gag agg ctg aca ctt gct tgt ggt ggg ata gct ctg aat tcc ttt gat 1065
 Glu Arg Leu Thr Leu Ala Cys Gly Gly Ile Ala Leu Asn Ser Phe Asp
 325 330 335

gac ctg aat cct gac tgt ttg gga cat gca ggg ctt gtc tat gag tat 1113
 Asp Leu Asn Pro Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu Tyr
 340 345 350
 aca ctg ggt gag gag aag ttc acc ttt att gag aag tgt aac aat ccc 1161
 Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Lys Cys Asn Asn Pro
 355 360 365
 cgt tct gtc act tta ctg gtt aaa gga cca aat aag cac aca ctg act 1209
 Arg Ser Val Thr Leu Leu Val Lys Gly Pro Asn Lys His Thr Leu Thr
 370 375 380 385
 caa atc aag gat gca ata aga gat ggc ttg agg gct gtc aaa aat gct 1257
 Gln Ile Lys Asp Ala Ile Arg Asp Gly Leu Arg Ala Val Lys Asn Ala
 390 395 400
 att gat gat ggc tgt gtt gtc cca ggt gcg ggt gca gta gaa gtg gca 1305
 Ile Asp Asp Gly Cys Val Val Pro Gly Ala Gly Ala Val Glu Val Ala
 405 410 415
 ctg gca gaa gct ctg att aaa tac aag ccc agt gtg aag ggc agg gcg 1353
 Leu Ala Glu Ala Leu Ile Lys Tyr Lys Pro Ser Val Lys Gly Arg Ala
 420 425 430
 cag ctt gga gtc cag gca ttt gca gat gcc ttg ctc atc att ccc aag 1401
 Gln Leu Gly Val Gln Ala Phe Ala Asp Ala Leu Leu Ile Ile Pro Lys
 435 440 445
 gtt ctt gcg caa aac tct ggt ttt gac ctt cag gaa aca tta gtt aaa 1449
 Val Leu Ala Gln Asn Ser Gly Phe Asp Leu Gln Glu Thr Leu Val Lys
 450 455 460 465
 gtt caa gct gaa cat tca gaa tcg ggc cag ctc gta ggt gtg gat ctg 1497
 Val Gln Ala Glu His Ser Glu Ser Gly Gln Leu Val Gly Val Asp Leu
 470 475 480
 agc aca ggt gag ccg atg gtg gcc gca gag atg ggt gtg tgg gat aac 1545
 Ser Thr Gly Glu Pro Met Val Ala Ala Glu Met Gly Val Trp Asp Asn

485	490	495	
tac tgt gtg aag aag cag ctg cta cac tcc tgt act gtg atc gcc acc			1593
Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala Thr			
500	505	510	
aac att ctc ctg gtc gac gag atc atg cga gct ggg atg tcc tct ctg			1641
Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser Leu			
515	520	525	
aag ggt tga ggcctgcctg tgatactaca ggatgttggg gggaatggtt			1690
Lys Gly			
530			
atttttgtcc aagcttcaag tgatttggaa aaaaattttc tcttcctgat tggagaaaag			1750
aaacgggaca tttagacacct attcaaatta tactgtaaaa ttttatttta tttttgcctt			1810
gagtatctga agacactcaa agcagctctt tttcaacca ctgaacaaga tgttttagct			1870
acaccgatac aaaaattaca taataagata agcatgttgt ctacccttgt tccataagtg			1930
ttctttgaaa gtttgtaatg gttttctcct aaataaggca tggtagacaca tgcctgtaag			1990
cctagccctt tggaaatagt ccggaatttc tatgccaaact caggctacag gagaccccag			2050
gtcgaaagaa taatttggtg tggatgtatt tgaaattatc cagccaactc cctgttaaac			2110
atgtaagatc cttagccagtg taaaacacat ctgggtaatt tatgggttgc ataatgtcta			2170
ataaatactt aaaagagtg			2189

<210> 276

<211> 531

<212> PRT

<213> Mus musculus

<400> 276

Met Ala Ala Val Lys Thr Leu Asn Pro Lys Ala Glu Val Ala Arg Ala

1

5

10

15

Gln Ala Ala Leu Ala Val Asn Ile Ser Ala Ala Arg Gly Leu Gln Asp

20	25	30
Val Leu Arg Thr Asn Leu Gly Pro Lys Gly Thr Met Lys Met Leu Val		
35	40	45
Ser Gly Ala Gly Asp Ile Lys Leu Thr Lys Asp Gly Asn Val Leu Leu		
50	55	60
His Glu Met Gln Ile Gln His Pro Thr Ala Ser Leu Ile Ala Lys Val		
65	70	75
Ala Thr Ala Gln Asp Asp Ile Thr Gly Asp Gly Thr Thr Ser Asn Val		
85	90	95
Leu Ile Ile Gly Glu Leu Leu Lys Gln Ala Asp Leu Tyr Ile Ser Glu		
100	105	110
Gly Leu His Pro Arg Ile Ile Thr Glu Gly Phe Glu Ala Ala Lys Glu		
115	120	125
Lys Ala Leu Gln Phe Leu Glu Gln Val Lys Val Ser Lys Glu Met Asp		
130	135	140
Arg Glu Thr Leu Ile Asp Val Ala Arg Thr Ser Leu Arg Thr Lys Val		
145	150	155
His Ala Glu Leu Ala Asp Val Leu Thr Glu Ala Val Val Asp Ser Ile		
165	170	175
Leu Ala Ile Arg Lys Lys Asp Glu Pro Ile Asp Leu Phe Met Val Glu		
180	185	190
Ile Met Glu Met Lys His Lys Ser Glu Thr Asp Thr Ser Leu Ile Arg		
195	200	205
Gly Leu Val Leu Asp His Gly Ala Arg His Pro Asp Met Lys Lys Arg		
210	215	220
Val Glu Asn Ala Tyr Ile Leu Thr Cys Asn Val Ser Leu Glu Tyr Glu		
225	230	235
Lys Thr Glu Val Asn Ser Gly Phe Phe Tyr Lys Ser Ala Glu Glu Arg		
245	250	255

Glu Lys Leu Val Lys Ala Glu Arg Lys Phe Ile Glu Asp Arg Val Lys
 260 265 270
 Lys Ile Ile Glu Leu Lys Lys Lys Val Cys Gly Asp Ser Asp Lys Gly
 275 280 285
 Phe Val Val Ile Asn Gln Lys Gly Ile Asp Pro Phe Ser Leu Asp Ala
 290 295 300
 Leu Ala Lys Glu Gly Ile Val Ala Leu Arg Arg Ala Lys Arg Arg Asn
 305 310 315 320
 Met Glu Arg Leu Thr Leu Ala Cys Gly Gly Ile Ala Leu Asn Ser Phe
 325 330 335
 Asp Asp Leu Asn Pro Asp Cys Leu Gly His Ala Gly Leu Val Tyr Glu
 340 345 350
 Tyr Thr Leu Gly Glu Glu Lys Phe Thr Phe Ile Glu Lys Cys Asn Asn
 355 360 365
 Pro Arg Ser Val Thr Leu Leu Val Lys Gly Pro Asn Lys His Thr Leu
 370 375 380
 Thr Gln Ile Lys Asp Ala Ile Arg Asp Gly Leu Arg Ala Val Lys Asn
 385 390 395 400
 Ala Ile Asp Asp Gly Cys Val Val Pro Gly Ala Gly Ala Val Glu Val
 405 410 415
 Ala Leu Ala Glu Ala Leu Ile Lys Tyr Lys Pro Ser Val Lys Gly Arg
 420 425 430
 Ala Gln Leu Gly Val Gln Ala Phe Ala Asp Ala Leu Leu Ile Ile Pro
 435 440 445
 Lys Val Leu Ala Gln Asn Ser Gly Phe Asp Leu Gln Glu Thr Leu Val
 450 455 460
 Lys Val Gln Ala Glu His Ser Glu Ser Gly Gln Leu Val Gly Val Asp
 465 470 475 480
 Leu Ser Thr Gly Glu Pro Met Val Ala Ala Glu Met Gly Val Trp Asp

	485		490		495
Asn Tyr Cys Val Lys Lys Gln Leu Leu His Ser Cys Thr Val Ile Ala					
500		505		510	
Thr Asn Ile Leu Leu Val Asp Glu Ile Met Arg Ala Gly Met Ser Ser					
515		520		525	
Leu Lys Gly					
530					

<210> 277

<211> 421

<212> DNA

<213> Mus musculus

<400> 277

```

ggacctcaag acaagtagga gagcggacct gacgggtaca gtaatagaca gtggagacgg 60
atcactcatg tcattcctgt ggctgaagga tatgttatcg gcagctgtat taaacacatt 120
ccaatcgag gaagagatat aacatatttt attcagcaac tgctgcgaga ccgagaagta 180
ggaatccctc ctgagcagtc ctgggaaact gcgaaacaga tgaaggaacg ctacagttat 240
gtctgcccag atttagtaaa agagttaaac aagtatgaca ccgatgggtc aaagtggatc 300
aaacagtaca ccggagtcaa cgccatctca aagaaagagt tttctattga tgttggctat 360
gagcgattcc tgggaccgga gatcttttc catccagagt ttgctaatac agattttaca 420
c                                                                 421

```

<210> 278

<211> 1247

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (81).. (1184)

<400> 278

atttgacttc gctagtcggt gacgcggcgg ggaagggaac cgagggggac cggagcctgg 60
 aggagttgag ttaaaagaag atg gat gca cag agt tca gct aaa gtc aat tcg 113

Met Asp Ala Gln Ser Ser Ala Lys Val Asn Ser

1 5 10

agg aag agg agg aaa gag gca cct ggc cct aat gga gca aca gag gaa 161
 Arg Lys Arg Arg Lys Glu Ala Pro Gly Pro Asn Gly Ala Thr Glu Glu

15 20 25

gat gga att cct tcc aaa gtg cag cgt tgc gca gtt ggt tta cgg cag 209
 Asp Gly Ile Pro Ser Lys Val Gln Arg Cys Ala Val Gly Leu Arg Gln

30 35 40

cca gct cct ttt tct gat gaa att gaa gtt gac ttt agt aag ccc tat 257
 Pro Ala Pro Phe Ser Asp Glu Ile Glu Val Asp Phe Ser Lys Pro Tyr

45 50 55

gtc agg gtg act atg gaa gaa gcc tgc agg gga act ccg tgt gag cgg 305
 Val Arg Val Thr Met Glu Glu Ala Cys Arg Gly Thr Pro Cys Glu Arg

60 65 70 75

cct gtg aga gtt tat gcg gat gga ata ttt gac ttg ttt cac tct ggt 353
 Pro Val Arg Val Tyr Ala Asp Gly Ile Phe Asp Leu Phe His Ser Gly

80 85 90

cat gcc cgg gct ctg atg caa gca aag aac ctt ttc cct aat acg tat 401
 His Ala Arg Ala Leu Met Gln Ala Lys Asn Leu Phe Pro Asn Thr Tyr

95 100 105

cta att gtg gga gtc tgc agt gat gag cta acg cac aac ttc aag ggc 449
 Leu Ile Val Gly Val Cys Ser Asp Glu Leu Thr His Asn Phe Lys Gly

110 115 120

```

ttc act gtg atg aac gag aat gag cgc tat gac gcc gtg cag cac tgc 497
Phe Thr Val Met Asn Glu Asn Glu Arg Tyr Asp Ala Val Gln His Cys
      125              130              135
cgc tac gtg gac gag gtg gtg cgg aac gcc ccc tgg act ctg acg cct 545
Arg Tyr Val Asp Glu Val Val Arg Asn Ala Pro Trp Thr Leu Thr Pro
140              145              150              155
gag ttc ctg gca gag cac cgg att gat ttt gtc gcc cat gac gac atc 593
Glu Phe Leu Ala Glu His Arg Ile Asp Phe Val Ala His Asp Asp Ile
      160              165              170
ccc tat tct tct gca ggg agc gat gat gtg tat aag cac atc aag gac 641
Pro Tyr Ser Ser Ala Gly Ser Asp Asp Val Tyr Lys His Ile Lys Asp
      175              180              185
gca ggc atg ttt gct ccc aca cag agg aca gaa ggt atc tcc aca tca 689
Ala Gly Met Phe Ala Pro Thr Gln Arg Thr Glu Gly Ile Ser Thr Ser
      190              195              200
gac atc atc acc cgc att gtc cgt gac tat gat gtg tat gca aga cgg 737
Asp Ile Ile Thr Arg Ile Val Arg Asp Tyr Asp Val Tyr Ala Arg Arg
      205              210              215
aac cta cag agg ggc tac act gcc aag gag ctc aat gtc agc ttt atc 785
Asn Leu Gln Arg Gly Tyr Thr Ala Lys Glu Leu Asn Val Ser Phe Ile
220              225              230              235
aac gag aag aaa tac cac ttg caa gaa cga gtt gat aaa gta aag aag 833
Asn Glu Lys Lys Tyr His Leu Gln Glu Arg Val Asp Lys Val Lys Lys
      240              245              250
aaa gtg aaa gat gtg gag gaa aag tca aaa gag ttt gtg cag aag gtg 881
Lys Val Lys Asp Val Glu Glu Lys Ser Lys Glu Phe Val Gln Lys Val
      255              260              265
gaa gag aag agc atc gac ctc atc cag aag tgg gag gag aag tcc cga 929
Glu Glu Lys Ser Ile Asp Leu Ile Gln Lys Trp Glu Glu Lys Ser Arg

```

270	275	280	
gag ttc att gga agt ttc ctg gaa atg ttt ggt cca gaa gga gca ctg 977			
Glu Phe Ile Gly Ser Phe Leu Glu Met Phe Gly Pro Glu Gly Ala Leu			
285	290	295	
aag cac atg ctg aag gag gga aaa ggt cgg atg ctg cag gcc atc agt 1025			
Lys His Met Leu Lys Glu Gly Lys Gly Arg Met Leu Gln Ala Ile Ser			
300	305	310	315
ccc aag cag agc ccc agc agc agc cct act cat gag cgc tcc ccc tcc 1073			
Pro Lys Gln Ser Pro Ser Ser Ser Pro Thr His Glu Arg Ser Pro Ser			
	320	325	330
ccc tcc ttt cgg tgg ccc ttc tct ggc aag act tcc cca tct tcc tcc 1121			
Pro Ser Phe Arg Trp Pro Phe Ser Gly Lys Thr Ser Pro Ser Ser Ser			
	335	340	345
cca gca agt ctt tct agg tgc agg gct gtg acc tgt gac atc agc gag 1169			
Pro Ala Ser Leu Ser Arg Cys Arg Ala Val Thr Cys Asp Ile Ser Glu			
350	355	360	
gat gaa gag gac taa cttttcatcc ctgttcctc tctccccac tgcccatcac 1224			
Asp Glu Glu Asp			
365			
ctccagaagc tctctgtcga att 1247			

<210> 279

<211> 367

<212> PRT

<213> Mus musculus

<400> 279

Met Asp Ala Gln Ser Ser Ala Lys Val Asn Ser Arg Lys Arg Arg Lys

1

5

10

15

Glu Ala Pro Gly Pro Asn Gly Ala Thr Glu Glu Asp Gly Ile Pro Ser
 20 25 30
 Lys Val Gln Arg Cys Ala Val Gly Leu Arg Gln Pro Ala Pro Phe Ser
 35 40 45
 Asp Glu Ile Glu Val Asp Phe Ser Lys Pro Tyr Val Arg Val Thr Met
 50 55 60
 Glu Glu Ala Cys Arg Gly Thr Pro Cys Glu Arg Pro Val Arg Val Tyr
 65 70 75 80
 Ala Asp Gly Ile Phe Asp Leu Phe His Ser Gly His Ala Arg Ala Leu
 85 90 95
 Met Gln Ala Lys Asn Leu Phe Pro Asn Thr Tyr Leu Ile Val Gly Val
 100 105 110
 Cys Ser Asp Glu Leu Thr His Asn Phe Lys Gly Phe Thr Val Met Asn
 115 120 125
 Glu Asn Glu Arg Tyr Asp Ala Val Gln His Cys Arg Tyr Val Asp Glu
 130 135 140
 Val Val Arg Asn Ala Pro Trp Thr Leu Thr Pro Glu Phe Leu Ala Glu
 145 150 155 160
 His Arg Ile Asp Phe Val Ala His Asp Asp Ile Pro Tyr Ser Ser Ala
 165 170 175
 Gly Ser Asp Asp Val Tyr Lys His Ile Lys Asp Ala Gly Met Phe Ala
 180 185 190
 Pro Thr Gln Arg Thr Glu Gly Ile Ser Thr Ser Asp Ile Ile Thr Arg
 195 200 205
 Ile Val Arg Asp Tyr Asp Val Tyr Ala Arg Arg Asn Leu Gln Arg Gly
 210 215 220
 Tyr Thr Ala Lys Glu Leu Asn Val Ser Phe Ile Asn Glu Lys Lys Tyr
 225 230 235 240
 His Leu Gln Glu Arg Val Asp Lys Val Lys Lys Lys Val Lys Asp Val

245	250	255
Glu Glu Lys Ser Lys Glu Phe Val Gln Lys Val Glu Glu Lys Ser Ile		
260	265	270
Asp Leu Ile Gln Lys Trp Glu Glu Lys Ser Arg Glu Phe Ile Gly Ser		
275	280	285
Phe Leu Glu Met Phe Gly Pro Glu Gly Ala Leu Lys His Met Leu Lys		
290	295	300
Glu Gly Lys Gly Arg Met Leu Gln Ala Ile Ser Pro Lys Gln Ser Pro		
305	310	315
Ser Ser Ser Pro Thr His Glu Arg Ser Pro Ser Pro Ser Phe Arg Trp		
325	330	335
Pro Phe Ser Gly Lys Thr Ser Pro Ser Ser Ser Pro Ala Ser Leu Ser		
340	345	350
Arg Cys Arg Ala Val Thr Cys Asp Ile Ser Glu Asp Glu Glu Asp		
355	360	365

<210> 280

<211> 2633

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (2018).. (2425)

<400> 280

ggatccactc tcagctcagc aacagaccag ggcttactgt ccctactgtg tgtcaagcac 60

tacatgagac ttggcataa accatctcag gaggttcac tcagggcaca aagggaagtg 120

gctggagagg atgaaggact ttggacttgt tggggagtgg atggtggaag aaacgtttgc 180

ttagctttca agcctccaga gacccaaacc tccattccag tgaatcagga tgacaacgaa 240
gctgtgtgcc ttggctgccc ctacacaaat gtcttacact agatgatttg ggccaaagtg 300
cctgaagaag tggcttccca cacctttacc ttacacaggc ctgggacagg cagtcttgac 360
tgcccaacct gagttctgta ctaactgggg aggggacaca gggccaggat ctagataaca 420
atcggatgcc ctgagcatgc cagagcagac aaaggacaga ccaaggctgt gatgggaatc 480
caactgtggc cctcaaccag tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg tgtgtgtgtg 540
tgtgtgtgtg ttttctaacc ccagaactta aaaataatctg gagataatctt tgcagaactt 600
taggggacca ggaccagcag tgctactgaa aatcttctaa gattcatttc gataaggctg 660
aggatgagag tccctgggtg tcagcaagag agtccctgag agagtaagga gggctaaaat 720
tccaaccttt ctcccagagg acacttgccct accctgatgg tgtgcccttt agtcatttag 780
ctgggggagg catggttctg cactgagaag aaagcatacc agatctcatt ccacaggctc 840
ctaggctctg atctgttggg gggaggggga gaatttaaag aaatatattag tcittagtag 900
gtcaaaaaggt cagacactga atgtcatctc tttgtaacac acaggtagca ggtgagaagg 960
gataaaggte ttcactgcta ctgttgccaa tggcaacaag gatcagaagc cacggaacac 1020
gcccaccccc tccccacccc cctccccgac ccaggtaaat aggagctgaa gctgtataga 1080
agcttacaga aatgactggg gagtctttcc gtgcacaggt atggaaaggg ccagaatat 1140
attaactgaa aaaaaaaaaa accacaaacg taaattccag aaaaggctctg tgctttcctt 1200
tcctggaaga agacagaacc acacgatecc gcagaatagt gtcagtcac acgcgcaaaa 1260
agccttgggt ctctgaccac caccgtgcat gggttcacct ggagcgcttt ctgtccagtg 1320
catatttaat accaccaact tcgcatcatt tcctgggaga gctgtggtag ttgctctgct 1380
cttcatccct agagttaaaa catcagcttc ctaggaactg gccaggccac ggatgctgag 1440
ctttagacaa aggcctgtaa atggcctctt ccttgatgac gctagcaaac ctgaaggaga 1500
cgcgttttca acactcaaga ggcgtttgaa gaactcccag ggggtaccg gtgagaattc 1560
caggcgtttg aaggactctc aagggaagta aggaggggggt acacaaaaac taggaccaa 1620
agcaaccttt ccccttcac acctcctctt tctaggctag gaggggttgg gtgaaaagag 1680
caaatggaag gtctgaactg aaagtggcca acagcaggga caaacctggc tctgcacat 1740
cttcgcccc gccctcccc cccctgccc cgccccgccc cgatcccccc ccgtgccgcc 1800
ctctcaccct gggaggagg atcgctacaa tggaccctcc tgcgggcttg tgcactcttg 1860
gaatccagct gtcgcgcccc gcggagcccc gtgtcccccg agggcgccca tticcgggcc 1920

gtccatcacc cggagtgcac tggcagcaac cgiccgggcc gaacccacag cccgtcccg 1980
 ctcttggtg tcaggcgatc cccagtcgtt cccaaaa atg cct gtg gac ttc aac 2035

Met Pro Val Asp Phe Asn

1

5

ggg tac tgg aag atg ctg agc aat gag aat ttc gag gag tac ctg cgc 2083
 Gly Tyr Trp Lys Met Leu Ser Asn Glu Asn Phe Glu Glu Tyr Leu Arg

10

15

20

gcg ctc gac gtc aac gtg gcc tta cgc aaa atc gcc aac ttg ctg aag 2131
 Ala Leu Asp Val Asn Val Ala Leu Arg Lys Ile Ala Asn Leu Leu Lys

25

30

35

cca gac aaa gag atc gtg cag gat ggc gac cac atg atc atc cgc acg 2179
 Pro Asp Lys Glu Ile Val Gln Asp Gly Asp His Met Ile Ile Arg Thr

40

45

50

ctg agc act ttt cgg aac tat atc atg gac ttc caa gtt ggg aag gag 2227
 Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp Phe Gln Val Gly Lys Glu

55

60

65

70

ttt gag gaa gat ctg aca ggc ata gac gac cgc aag tgc atg acc act 2275
 Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp Arg Lys Cys Met Thr Thr

75

80

85

gtg agc tgg gat ggt gac aaa ctc cag tgt gtg cag aag gga gag aag 2323
 Val Ser Trp Asp Gly Asp Lys Leu Gln Cys Val Gln Lys Gly Glu Lys

90

95

100

gag gga cgt ggc tgg acg cag tgg atc gag ggt gat gaa ctt cac ctg 2371
 Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu Gly Asp Glu Leu His Leu

105

110

115

gaa atg aga gct gag ggt gtg atc tgc aag caa gtg ttt aag aaa gta 2419
 Glu Met Arg Ala Glu Gly Val Ile Cys Lys Gln Val Phe Lys Lys Val

120

125

130

cac tga gcagcccgaa cagcccgagg agataacctt ggtcttcagg aacaagtggg 2475

His

135

atgggcctgt ggtcaggagc cccctctgcc taacatgggg accgaaacgc ataccacccc 2535
 caggcttctg ccagcgaagt ctctctcttt gcctgggtctc ttttcttta cttaaaaatga 2595
 agtgacccca ataaaagtga tctctgitta aaaaaaaaa 2633

<210> 281

<211> 135

<212> PRT

<213> Mus musculus

<400> 281

Met Pro Val Asp Phe Asn Gly Tyr Trp Lys Met Leu Ser Asn Glu Asn
 1 5 10 15
 Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
 20 25 30
 Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
 35 40 45
 His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
 50 55 60
 Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
 65 70 75 80
 Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
 85 90 95
 Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
 100 105 110
 Gly Asp Glu Leu His Leu Glu Met Arg Ala Glu Gly Val Ile Cys Lys
 115 120 125
 Gln Val Phe Lys Lys Val His

130

135

<210> 282

<211> 2308

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (76).. (1368)

<400> 282

gaattcggca cgaggtggat agccagaggt tagggtgtct tctcgaatcg gggaacctct 60

gattttggag gagcc atg gcc ctc agg gtc act agg aac acg aaa att aac 111

Met Ala Leu Arg Val Thr Arg Asn Thr Lys Ile Asn

1

5

10

gca gaa aat aag gcc aag gtc agt atg gca ggc gca atg cgt gtg cct 159

Ala Glu Asn Lys Ala Lys Val Ser Met Ala Gly Ala Met Arg Val Pro

15

20

25

gtg aca gtt act gct gct tcc aag ccc ggg ctg aga ccg aga act gct 207

Val Thr Val Thr Ala Ala Ser Lys Pro Gly Leu Arg Pro Arg Thr Ala

30

35

40

ctt gga gac att ggt aat aaa gtc agc gaa gag cta cag gca aga gtg 255

Leu Gly Asp Ile Gly Asn Lys Val Ser Glu Glu Leu Gln Ala Arg Val

45

50

55

60

cct ctg aaa agg gaa gca aaa acg cta ggt act gga aaa ggt act gtt 303

Pro Leu Lys Arg Glu Ala Lys Thr Leu Gly Thr Gly Lys Gly Thr Val

65

70

75

aaa gcc cta cca aaa cct gta gag aag gtg cct gtg tgt gaa cca gag 351

Lys	Ala	Leu	Pro	Lys	Pro	Val	Glu	Lys	Val	Pro	Val	Cys	Glu	Pro	Glu		
			80						85					90			
gtg	gaa	ctt	gct	gag	cct	gag	cct	gaa	cct	gaa	ctt	gaa	cat	gtt	aga	399	
Val	Glu	Leu	Ala	Glu	Pro	Glu	Pro	Glu	Pro	Glu	Leu	Glu	His	Val	Arg		
			95						100					105			
gaa	gag	aag	ctt	tct	cct	gaa	cct	att	ttg	gtt	gat	aat	ccc	tct	cca	447	
Glu	Glu	Lys	Leu	Ser	Pro	Glu	Pro	Ile	Leu	Val	Asp	Asn	Pro	Ser	Pro		
			110						115					120			
agc	ccg	atg	gaa	aca	tct	gga	tgt	gcg	cct	gca	gaa	gag	tat	ctg	tgt	495	
Ser	Pro	Met	Glu	Thr	Ser	Gly	Cys	Ala	Pro	Ala	Glu	Glu	Tyr	Leu	Cys		
			125											130			
cag	gct	ttc	tct	gat	gta	atc	ctt	gca	gtg	agt	gac	gta	gac	gca	gat	543	
Gln	Ala	Phe	Ser	Asp	Val	Ile	Leu	Ala	Val	Ser	Asp	Val	Asp	Ala	Asp		
														145			
gat	ggg	gct	gac	cca	aac	ctc	tgt	agt	gaa	tat	gtg	aaa	gat	atc	tat	591	
Asp	Gly	Ala	Asp	Pro	Asn	Leu	Cys	Ser	Glu	Tyr	Val	Lys	Asp	Ile	Tyr		
														160			
gct	tat	ctc	cga	caa	ctg	gag	gaa	gag	cag	tca	gtt	aga	cca	aaa	tac	639	
Ala	Tyr	Leu	Arg	Gln	Leu	Glu	Glu	Glu	Gln	Ser	Val	Arg	Pro	Lys	Tyr		
														175			
cta	cag	ggt	cgt	gaa	gtg	act	gga	aac	atg	aga	gct	atc	ctc	att	gac	687	
Leu	Gln	Gly	Arg	Glu	Val	Thr	Gly	Asn	Met	Arg	Ala	Ile	Leu	Ile	Asp		
														190			
tggt	cta	ata	cag	gtt	cag	atg	aaa	ttt	agg	ctg	ctt	cag	gag	acc	atg	735	
Trp	Leu	Ile	Gln	Val	Gln	Met	Lys	Phe	Arg	Leu	Leu	Gln	Glu	Thr	Met		
														205			
tac	atg	act	gtg	tcc	att	att	gat	cgg	ttc	atg	cag	aac	agt	tgt	gtg	783	
Tyr	Met	Thr	Val	Ser	Ile	Ile	Asp	Arg	Phe	Met	Gln	Asn	Ser	Cys	Val		
														225			
														230			
														235			

```

ccc aag aag atg cta cag ctg gtc ggt gta acg gcc atg ttt att gca 831
Pro Lys Lys Met Leu Gln Leu Val Gly Val Thr Ala Met Phe Ile Ala
      240              245              250

agc aaa tat gag gag atg tac cct cca gaa ata ggt gac ttc gcc ttt 879
Ser Lys Tyr Glu Glu Met Tyr Pro Pro Glu Ile Gly Asp Phe Ala Phe
      255              260              265

gtg act aac aac acg tac act aag cac cag atc aga cag atg gag atg 927
Val Thr Asn Asn Thr Tyr Thr Lys His Gln Ile Arg Gln Met Glu Met
      270              275              280

aag att ctc aga gtt ctg aac ttc agc ctg ggt cgc cct ctg cct ctg 975
Lys Ile Leu Arg Val Leu Asn Phe Ser Leu Gly Arg Pro Leu Pro Leu
285              290              295              300

cac ttc ctc cgt aga gca tct aaa gtc gga gag gtt gac gtc gag cag 1023
His Phe Leu Arg Arg Ala Ser Lys Val Gly Glu Val Asp Val Glu Gln
      305              310              315

cac act ttg gcc aaa tac ctc atg gag ctc tcc atg ctg gac tgc gac 1071
His Thr Leu Ala Lys Tyr Leu Met Glu Leu Ser Met Leu Asp Cys Asp
      320              325              330

atg gtg cat ttt gct cct tct caa att gca gct ggg gct ttc tgc tta 1119
Met Val His Phe Ala Pro Ser Gln Ile Ala Ala Gly Ala Phe Cys Leu
      335              340              345

gcg ctg aaa att ctt gac aac ggt gaa tgg aca cca act ctg cag cac 1167
Ala Leu Lys Ile Leu Asp Asn Gly Glu Trp Thr Pro Thr Leu Gln His
      350              355              360

tac cta tcc tac agt gaa gac tcc ctg ctt cct gtt atg cag cac ctg 1215
Tyr Leu Ser Tyr Ser Glu Asp Ser Leu Leu Pro Val Met Gln His Leu
365              370              375              380

gct aag aat gta gtc atg gtg aac tgt ggc ctc aca aag cac atg act 1263
Ala Lys Asn Val Val Met Val Asn Cys Gly Leu Thr Lys His Met Thr

```

385	390	395	
gtc aag aac aag tat gca gca tct aag cat gct aag atc agc acg ctg			1311
Val Lys Asn Lys Tyr Ala Ala Ser Lys His Ala Lys Ile Ser Thr Leu			
400	405	410	
gca cag ctg aac tgt aca cta gtt cag aat ttg tct aag gcc gtg aca			1359
Ala Gln Leu Asn Cys Thr Leu Val Gln Asn Leu Ser Lys Ala Val Thr			
415	420	425	
aag gca taa ctccaataga ctgctacatc tgcagatgca gttagccatg			1408
Lys Ala			
430			
tgccgcctgt acataggata cctaccgtgt ttacttgctc ttcaataaag gttgtgactt			1468
ctcattttac atagcttaac tcatttgaat gttgttgctt ctgagtttag gctaacggaa			1528
gttgtcgaat ttaggagiat attaaaaact gcacttagtt ttaacagtgg atccaactaa			1588
tgtatatatc tgtagcciat atgtctatat acatccitca ctgtgtgicc ttatatcatc			1648
atgtcttctg cctcacteta gtttaaactc taaatctacc agctagtcct ttgttccatt			1708
ttccagtggg tgccaccttt aaccactgtc tcttggttgg tcaactttca gatctgaaac			1768
caagtatctt tttttatgta attatttatt tgttcttaat tggaaaatag gatgttcaaa			1828
attaaagggtg tgtttttaaaa agaatttggc cccaagtcct actatcaaca gataagggtg			1888
tatcttgtat atcctgtata gaaataatca tgcataact cccaaggaga tattttatat			1948
gggttcattt catcaacagt attcctatca gcattcctta caatgcctat attgcatctc			2008
ctagtgtgaa caaacigtgt gtaacatagt cattccctcg ggggggattc aagtgcattc			2068
tctcagtgcc ctccacagtg ttcttaaatg atgtttaatg tcttgcttgg ctcatcata			2128
gtagicttcc aggggggtgct ttgaattctg acagccagat ggggtgtggct gccaccatac			2188
caaggcgcca ctctgtictt gtaatgccac ctggaaaaga atcctgtctc atttgcigtg			2248
ttaatttata catctgatat caagttgaat aaaatttatt ggtggaaagc tttcacaatt			2308

<210> 283

<211> 430

<212> PRT

<213> Mus musculus

<400> 283

```

Met Ala Leu Arg Val Thr Arg Asn Thr Lys Ile Asn Ala Glu Asn Lys
  1           5           10           15
Ala Lys Val Ser Met Ala Gly Ala Met Arg Val Pro Val Thr Val Thr
      20           25           30
Ala Ala Ser Lys Pro Gly Leu Arg Pro Arg Thr Ala Leu Gly Asp Ile
      35           40           45
Gly Asn Lys Val Ser Glu Glu Leu Gln Ala Arg Val Pro Leu Lys Arg
      50           55           60
Glu Ala Lys Thr Leu Gly Thr Gly Lys Gly Thr Val Lys Ala Leu Pro
      65           70           75           80
Lys Pro Val Glu Lys Val Pro Val Cys Glu Pro Glu Val Glu Leu Ala
      85           90           95
Glu Pro Glu Pro Glu Pro Glu Leu Glu His Val Arg Glu Glu Lys Leu
      100          105          110
Ser Pro Glu Pro Ile Leu Val Asp Asn Pro Ser Pro Ser Pro Met Glu
      115          120          125
Thr Ser Gly Cys Ala Pro Ala Glu Glu Tyr Leu Cys Gln Ala Phe Ser
      130          135          140
Asp Val Ile Leu Ala Val Ser Asp Val Asp Ala Asp Asp Gly Ala Asp
      145          150          155          160
Pro Asn Leu Cys Ser Glu Tyr Val Lys Asp Ile Tyr Ala Tyr Leu Arg
      165          170          175
Gln Leu Glu Glu Glu Gln Ser Val Arg Pro Lys Tyr Leu Gln Gly Arg
      180          185          190
Glu Val Thr Gly Asn Met Arg Ala Ile Leu Ile Asp Trp Leu Ile Gln
      195          200          205

```

Val Gln Met Lys Phe Arg Leu Leu Gln Glu Thr Met Tyr Met Thr Val
 210 215 220
 Ser Ile Ile Asp Arg Phe Met Gln Asn Ser Cys Val Pro Lys Lys Met
 225 230 235 240
 Leu Gln Leu Val Gly Val Thr Ala Met Phe Ile Ala Ser Lys Tyr Glu
 245 250 255
 Glu Met Tyr Pro Pro Glu Ile Gly Asp Phe Ala Phe Val Thr Asn Asn
 260 265 270
 Thr Tyr Thr Lys His Gln Ile Arg Gln Met Glu Met Lys Ile Leu Arg
 275 280 285
 Val Leu Asn Phe Ser Leu Gly Arg Pro Leu Pro Leu His Phe Leu Arg
 290 295 300
 Arg Ala Ser Lys Val Gly Glu Val Asp Val Glu Gln His Thr Leu Ala
 305 310 315 320
 Lys Tyr Leu Met Glu Leu Ser Met Leu Asp Cys Asp Met Val His Phe
 325 330 335
 Ala Pro Ser Gln Ile Ala Ala Gly Ala Phe Cys Leu Ala Leu Lys Ile
 340 345 350
 Leu Asp Asn Gly Glu Trp Thr Pro Thr Leu Gln His Tyr Leu Ser Tyr
 355 360 365
 Ser Glu Asp Ser Leu Leu Pro Val Met Gln His Leu Ala Lys Asn Val
 370 375 380
 Val Met Val Asn Cys Gly Leu Thr Lys His Met Thr Val Lys Asn Lys
 385 390 395 400
 Tyr Ala Ala Ser Lys His Ala Lys Ile Ser Thr Leu Ala Gln Leu Asn
 405 410 415
 Cys Thr Leu Val Gln Asn Leu Ser Lys Ala Val Thr Lys Ala
 420 425 430

<210> 284

<211> 355

<212> DNA

<213> *Mus musculus*

<400> 284

```
agaggggtcc cgagcgcgga tgcgggagga ttacgacagt gtggagcagg acggcgatga 60
acctggacca cagcgctctg ttgaagggtg gattctcttt gtcactggag tccacgaaga 120
agccactgaa gaagatatcc atgacaaatt cgctgaatat ggggaaataa aaaatatcca 180
ccttaatttg gacaggcgca cgggatactt gaaggggtat actctagttg aatatgaaac 240
atacaaagag gctcaggctg ccatggaagg actaaatggt caagatttga tggggcagcc 300
aatcagtgtg gactggigtg ttgttcgttg accaccaaag ggcaagagga gagga      355
```

<210> 285

<211> 268

<212> DNA

<213> *Mus musculus*

<400> 285

```
cactatcgaa gacaagctgg atacaaagca ctaccatac atctctaccc gctcgicccg 60
gtccttcagc accactgctg tgagtgcccg ctatggacat tggcacaaga ataaggcccc 120
cggggagtac cgcagcggtc cccgcctcat tattttcatt cttgggggtg tgagcctgaa 180
tgagatgcgc tgtgcttacg aagtgacca ggccaacgca aggtgggaag tgctgatatg 240
atccacgcac attctaccc cacagaaa      268
```

<210> 286

<211> 2453

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (188).. (1030)

<400> 286

```

aggtcgggct gtagctcgca gctgagccag tcactgctga tgcaatccgc agcggagcgc 60
gccagctct ccatttccg cgcttgccga ccgacctga gcgccacgtg tcactgcaca 120
gccgcctcct ccagaggaga ctacatttg caccaggag ccggagccac gacccaagcc 180
acgagaa atg aag gac tgc agt aat gga tgc tcc gcg ccg ttt gct gga 229
      Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Pro Phe Ala Gly
      1             5             10
gaa aga gga tca gaa gaa gtg gca gag act ttt agg gcc aaa gat ctc 277
Glu Arg Gly Ser Glu Glu Val Ala Glu Thr Phe Arg Ala Lys Asp Leu
      15             20             25             30
atc atc aca cca gcc act gtc tta aaa gag aag ccg gac ccg gat tcg 325
Ile Ile Thr Pro Ala Thr Val Leu Lys Glu Lys Pro Asp Pro Asp Ser
      35             40             45
ctg gtc ttt gga gct acg ttt act gac cac atg ctg acg gtg gag tgg 373
Leu Val Phe Gly Ala Thr Phe Thr Asp His Met Leu Thr Val Glu Trp
      50             55             60
tcc tct gcg tct gga tgg gag aaa cct cac att aag cct ttt gga aac 421
Ser Ser Ala Ser Gly Trp Glu Lys Pro His Ile Lys Pro Phe Gly Asn
      65             70             75
ttg ccc ata cat ccc gct gcc tct gtt ttg cac tac gct gtg gaa ctg 469
Leu Pro Ile His Pro Ala Ala Ser Val Leu His Tyr Ala Val Glu Leu
      80             85             90
ttt gaa ggc ttg aaa gcc ttt cgg gga gtt gat aac aag atc cga ttg 517
Phe Glu Gly Leu Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu

```

95	100	105	110	
ttc cgg ccg gac ctc aac atg gat aga atg tgc cga tct gct gtg agg	565			
Phe Arg Pro Asp Leu Asn Met Asp Arg Met Cys Arg Ser Ala Val Arg				
115	120	125		
acc acg ctg ccg atg ttt gac aag gag gag ctc cta aag tgt att ctt	613			
Thr Thr Leu Pro Met Phe Asp Lys Glu Glu Leu Leu Lys Cys Ile Leu				
130	135	140		
cag ctt cta cag atc gac caa gaa tgg gtt ccc tac tcc acc tct gcc	661			
Gln Leu Leu Gln Ile Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala				
145	150	155		
agc ctc tac atc cgc ccc aca ttt atc gga act gag cca tct ctt ggc	709			
Ser Leu Tyr Ile Arg Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu Gly				
160	165	170		
gtc aag aag cct tcc aaa gcc cta ctc ttt gtg atc ctg agc ccc gtg	757			
Val Lys Lys Pro Ser Lys Ala Leu Leu Phe Val Ile Leu Ser Pro Val				
175	180	185	190	
gga cct tat ttt tct agt gga tct ttt act ccg gtg tcc ctg tgg gcc	805			
Gly Pro Tyr Phe Ser Ser Gly Ser Phe Thr Pro Val Ser Leu Trp Ala				
195	200	205		
aat cca aag tac atc aga gcc tgg aaa ggt ggg act gga gac tgc aag	853			
Asn Pro Lys Tyr Ile Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys				
210	215	220		
atg ggc ggc aat tat gga gcc tcc ctt ctg gca cag tgc gag gcc gtg	901			
Met Gly Gly Asn Tyr Gly Ala Ser Leu Leu Ala Gln Cys Glu Ala Val				
225	230	235		
gag aat ggc tgt cag cag gtc ctg tgg ctg tac ggc aag gac aac cag	949			
Glu Asn Gly Cys Gln Gln Val Leu Trp Leu Tyr Gly Lys Asp Asn Gln				
240	245	250		
ata act gaa gta ggc aca atg aat ctt ttc ctc tac tgg ata aac gaa	997			

Ile Thr Glu Val Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu

255

260

265

270

gac gga gaa gag gag ctg caa cgc ccc cac tag atggcatcat tctcccgga 1050

Asp Gly Glu Glu Glu Leu Gln Arg Pro His

275

280

gtgaccaggc agagcatcct ggagctggca caacagtggg gtgaatttaa ggtatgtgag 1110

agacacctca ccatggatga cctggccacc gcccttgagg ggaacagagt gaaggagatg 1170

ttcggctcag ggacagcctg cgttgtctgc ccagttctcg atattctgta caagggccag 1230

atgctgcata tccaacgat ggagaatggc ccaagcttgc aagtcgaatc ctgggaaagc 1290

tgactgatat ccagtatgga agggctggaga gtgactggac aatcgagcta ccctgacggc 1350

aaagctcagg gtatcggatga cggctgccaca gaagagcgac tcctgcccctc gagctgggac 1410

cacctgtgac catctagtct tgcacattgt agtcgcgttc ctcatgtgtt accaaatgag 1470

gttttttccct tgagccacag aaagttgcc a gtgttcaatg ccacctatat acatggtagc 1530

aattgccttac tgtagtctcc ctaccctgt accagatcct tagtaggaga atgggttccc 1590

aaaccaataa gatgtctatg tgctggaagg gctactgagg aaatgtcaca ggcgccctcc 1650

ctgtgactca ggggcactct cagagcagga cactttgttt cttttgctgg tgaggttctt 1710

ttgttttttt tttttggttg gttttttttt tttgttttgt ttctaattgg ggcagatttg 1770

ggctccccat gcagccccgc tggcctggta ttccctaattg ttacccccgg ctggtctcag 1830

actcagagca gccttcccgt ctccctcagc cttctggatg ctggggtgat tgacagggtg 1890

cctaccatga tttgtttttg tttttaatc aaaagttcgg tcacctggat ttcttttctc 1950

cgttgggtccc tgagtccacg ctaaggtagc tgtcccttct tegtatcacg gtctgcacta 2010

atctcaccca aggtgtctga ggctggttgt ccgcactgcc ctttttacgt aactataact 2070

ggctgctcac tgcgctgcta tgagactagg ggtcctgtgc cttctagatc ttgcatcct 2130

caaagcccag cacatagtag gtattttcag tacatgttta ctctaagaat gaacatagaa 2190

gtgtactttc tgtctctcca tgctgaaacc ctttcggaag ccaggcctga tttgggcagc 2250

atgtagcagt atttacctca ggctgtcttt cctgtccatg gactcctcca gacagcacag 2310

tcagttggaa gaattgtctt atgttttaag attatcttgg aattgaagcg attgccctgg 2370

aaagatgaaa tactaaccac atggaagtga cagatactat acattatgtg ttaaattgcca 2430

aataaagggt caggttggga gat

2453

<210> 287

<211> 280

<212> PRT

<213> Mus musculus

<400> 287

Met Lys Asp Cys Ser Asn Gly Cys Ser Ala Pro Phe Ala Gly Glu Arg

1 5 10 15

Gly Ser Glu Glu Val Ala Glu Thr Phe Arg Ala Lys Asp Leu Ile Ile

20 25 30

Thr Pro Ala Thr Val Leu Lys Glu Lys Pro Asp Pro Asp Ser Leu Val

35 40 45

Phe Gly Ala Thr Phe Thr Asp His Met Leu Thr Val Glu Trp Ser Ser

50 55 60

Ala Ser Gly Trp Glu Lys Pro His Ile Lys Pro Phe Gly Asn Leu Pro

65 70 75 80

Ile His Pro Ala Ala Ser Val Leu His Tyr Ala Val Glu Leu Phe Glu

85 90 95

Gly Leu Lys Ala Phe Arg Gly Val Asp Asn Lys Ile Arg Leu Phe Arg

100 105 110

Pro Asp Leu Asn Met Asp Arg Met Cys Arg Ser Ala Val Arg Thr Thr

115 120 125

Leu Pro Met Phe Asp Lys Glu Glu Leu Leu Lys Cys Ile Leu Gln Leu

130 135 140

Leu Gln Ile Asp Gln Glu Trp Val Pro Tyr Ser Thr Ser Ala Ser Leu

145 150 155 160

Tyr Ile Arg Pro Thr Phe Ile Gly Thr Glu Pro Ser Leu Gly Val Lys

165 170 175

Lys Pro Ser Lys Ala Leu Leu Phe Val Ile Leu Ser Pro Val Gly Pro

180

185

190

Tyr Phe Ser Ser Gly Ser Phe Thr Pro Val Ser Leu Trp Ala Asn Pro

195

200

205

Lys Tyr Ile Arg Ala Trp Lys Gly Gly Thr Gly Asp Cys Lys Met Gly

210

215

220

Gly Asn Tyr Gly Ala Ser Leu Leu Ala Gln Cys Glu Ala Val Glu Asn

225

230

235

240

Gly Cys Gln Gln Val Leu Trp Leu Tyr Gly Lys Asp Asn Gln Ile Thr

245

250

255

Glu Val Gly Thr Met Asn Leu Phe Leu Tyr Trp Ile Asn Glu Asp Gly

260

265

270

Glu Glu Glu Leu Gln Arg Pro His

275

280

<210> 288

<211> 2188

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (57).. (2024)

<400> 288

tagggggaac gcgagaagga gacggacgtt gagagaacga ggaggaaggc gagaaa atg 59

Met

1

gcg tcc acg gat tac agt acc tat agt caa gct gca gcc cag cag ggc 107

Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Gly	
5 10 15	
tac agt gct tac acc gcc cag cca act caa gga tat gca cag acc acc	155
Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr Thr	
20 25 30	
cag gca tat ggg caa caa agc tat gga acc tat gga cag cct act gat	203
Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr Asp	
35 40 45	
gtc agc tat act cag gct cag acc act gcc acc tac ggg cag act gca	251
Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr Ala	
50 55 60 65	
tat gca act tct tac gga cag cct ccc act ggt tat agt act cca act	299
Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Ser Thr Pro Thr	
70 75 80	
gcc ccc cag gcg tac agc cag cct gtg cag gga tat ggc act ggg gct	347
Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly Ala	
85 90 95	
tat gac agc acc act gct aca gtc acc aca acg cag gcc tct tac gca	395
Tyr Asp Ser Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr Ala	
100 105 110	
gct cag tca gca tat ggc acc cag cct gcc tac ccc acc tat ggc cag	443
Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Thr Tyr Gly Gln	
115 120 125	
cag cca aca gcc acc gca cct acc aga cca cag gat ggt aac aag cct	491
Gln Pro Thr Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys Pro	
130 135 140 145	
gct gag act agc caa cct caa tct agc aca ggg ggt tat aac caa ccc	539
Ala Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln Pro	
150 155 160	

agc cta gga tat gga cag agt aac tac agc tat ccc cag gta cct ggg 587
 Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro Gly
 165 170 175
 agc tac cca atg cag cca gtc acc gca cct cca tct tat cct cct acc 635
 Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro Thr
 180 185 190
 agc tac tcc tct tca cag ccg act agt tac gat cag agc agt tac tct 683
 Ser Tyr Ser Ser Ser Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr Ser
 195 200 205
 cag cag aac acc tat ggg cag ccg agc agc tat gga caa cag agt agc 731
 Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser Ser
 210 215 220 225
 tat ggt caa caa agc agc tat ggg cag cag cct cct act agt tac ccg 779
 Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr Pro
 230 235 240
 cct cag act gga tcc tac agc cag gct cca agt caa tat agc caa cag 827
 Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln Gln
 245 250 255
 agc agc agc tac ggg cag cag agt tca ttc cga cag gac cac ccc agt 875
 Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro Ser
 260 265 270
 agc atg ggt gtt tat ggg cag gag tct gga gga ttt tcc gga cca gga 923
 Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro Gly
 275 280 285
 gag aac cgg agc ttg agt ggc cct gat aac cgg ggc agg gga aga ggg 971
 Glu Asn Arg Ser Leu Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg Gly
 290 295 300 305
 gga ttt gat cgt gga ggc atg agc aga ggt ggg cgg gga gga gga cgc 1019
 Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly Arg

310	315	320	
ggt gga ctg ggc gct gga gag cga ggt ggc ttc aat aag cct ggt gga	1067		
Gly Gly Leu Gly Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly Gly			
325	330	335	
ccc atg gat gaa gga cca gat ctt gat cta ggc ctt cct ata gat ccc	1115		
Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Leu Pro Ile Asp Pro			
340	345	350	
gat gaa gac tct gac aac agt gca att tat gtg caa gga tta aat gac	1163		
Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn Asp			
355	360	365	
aat gtg act ctg gat gat ctg gca gac ttc ttt aag cag tgt ggg gtt	1211		
Asn Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly Val			
370	375	380	385
gtc aag atg aac aag aga act gga caa ccc atg atc cat atc tac ctg	1259		
Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr Leu			
390	395	400	
gat aag gag aca gga aag cct aaa ggg gac gcc aca gtg tcc tat gaa	1307		
Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr Glu			
405	410	415	
gat cca cca act gca aag gct gcc gtg gaa tgg ttt gat ggg aaa gat	1355		
Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys Asp			
420	425	430	
ttt caa gga agc aaa ctt aaa gtg tct ctt gcc cga aag aag cct cca	1403		
Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro Pro			
435	440	445	
atg aac agc atg cgg gga ggc atg cca cct cgt gag ggc agg ggt atg	1451		
Met Asn Ser Met Arg Gly Gly Met Pro Pro Arg Glu Gly Arg Gly Met			
450	455	460	465
cca cca cca ctt cgt gga ggt cct ggt ggc cca gga ggc cct gga gga	1499		

Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly Gly
 470 475 480
 ccc atg ggt cgc atg gga ggc cgt gga gga gac aga ggg ggc ttc cct 1547
 Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe Pro
 485 490 495
 cca aga ggg ccc cga ggc tcc aga gga aac ccc tct gga gga gga aat 1595
 Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly Asn
 500 505 510
 gtc cag cac cga gct gga gac tgg cag tgt ccc aat ccg ggc tgt gga 1643
 Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys Gly
 515 520 525
 aac cag aac ttc gct tgg aga aca gaa tgc aac cag tgt aag gcc cct 1691
 Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala Pro
 530 535 540 545
 aag ccc gag ggc ttc ctc ccg cca ccc ttt cca cct ccg ggt ggt gat 1739
 Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly Asp
 550 555 560
 cgt gga cga ggt ggc cct ggt ggc atg cga gga gga aga gga gga ctc 1787
 Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly Gly Leu
 565 570 575
 atg gac cgt ggt ggt cct gga gga atg ttc aga ggt ggc aga ggt gga 1835
 Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly
 580 585 590
 gac aga gga ggc ttc cga ggt ggc cgt gga atg gac cga ggt ggc ttt 1883
 Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe
 595 600 605
 ggt gga gga aga cga ggt ggt cct ggg ggg cct cct gga cct tta atg 1931
 Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro Leu Met
 610 615 620 625

gaa cag atg gga gga aga aga ggc gga cgt gga gga cct ggg aaa atg 1979
 Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly Lys Met

630

635

640

gat aaa ggc gag cac cgt cag gaa cgc aga gac cgg ccc tac tag 2024
 Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr

645

650

655

agacctgcag agctgcattg agtaccagat ttatattttta aaccaggaaa tgttttaaatt 2084
 ttataattcc atatttataa tgttggcgac aacattatga ttattccttg tctgtacttt 2144
 agtatttttc accatttgtg gagaaacatt aaaacaagtt aaat 2188

<210> 289

<211> 655

<212> PRT

<213> Mus musculus

<400> 289

Met Ala Ser Thr Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln

1

5

10

15

Gly Tyr Ser Ala Tyr Thr Ala Gln Pro Thr Gln Gly Tyr Ala Gln Thr

20

25

30

Thr Gln Ala Tyr Gly Gln Gln Ser Tyr Gly Thr Tyr Gly Gln Pro Thr

35

40

45

Asp Val Ser Tyr Thr Gln Ala Gln Thr Thr Ala Thr Tyr Gly Gln Thr

50

55

60

Ala Tyr Ala Thr Ser Tyr Gly Gln Pro Pro Thr Gly Tyr Ser Thr Pro

65

70

75

80

Thr Ala Pro Gln Ala Tyr Ser Gln Pro Val Gln Gly Tyr Gly Thr Gly

85

90

95

Ala Tyr Asp Ser Thr Thr Ala Thr Val Thr Thr Thr Gln Ala Ser Tyr

100	105	110
Ala Ala Gln Ser Ala Tyr Gly Thr Gln Pro Ala Tyr Pro Thr Tyr Gly		
115	120	125
Gln Gln Pro Thr Ala Thr Ala Pro Thr Arg Pro Gln Asp Gly Asn Lys		
130	135	140
Pro Ala Glu Thr Ser Gln Pro Gln Ser Ser Thr Gly Gly Tyr Asn Gln		
145	150	155
Pro Ser Leu Gly Tyr Gly Gln Ser Asn Tyr Ser Tyr Pro Gln Val Pro		
165	170	175
Gly Ser Tyr Pro Met Gln Pro Val Thr Ala Pro Pro Ser Tyr Pro Pro		
180	185	190
Thr Ser Tyr Ser Ser Ser Gln Pro Thr Ser Tyr Asp Gln Ser Ser Tyr		
195	200	205
Ser Gln Gln Asn Thr Tyr Gly Gln Pro Ser Ser Tyr Gly Gln Gln Ser		
210	215	220
Ser Tyr Gly Gln Gln Ser Ser Tyr Gly Gln Gln Pro Pro Thr Ser Tyr		
225	230	235
Pro Pro Gln Thr Gly Ser Tyr Ser Gln Ala Pro Ser Gln Tyr Ser Gln		
245	250	255
Gln Ser Ser Ser Tyr Gly Gln Gln Ser Ser Phe Arg Gln Asp His Pro		
260	265	270
Ser Ser Met Gly Val Tyr Gly Gln Glu Ser Gly Gly Phe Ser Gly Pro		
275	280	285
Gly Glu Asn Arg Ser Leu Ser Gly Pro Asp Asn Arg Gly Arg Gly Arg		
290	295	300
Gly Gly Phe Asp Arg Gly Gly Met Ser Arg Gly Gly Arg Gly Gly Gly		
305	310	315
Arg Gly Gly Leu Gly Ala Gly Glu Arg Gly Gly Phe Asn Lys Pro Gly		
325	330	335

Gly Pro Met Asp Glu Gly Pro Asp Leu Asp Leu Gly Leu Pro Ile Asp
 340 345 350
 Pro Asp Glu Asp Ser Asp Asn Ser Ala Ile Tyr Val Gln Gly Leu Asn
 355 360 365
 Asp Asn Val Thr Leu Asp Asp Leu Ala Asp Phe Phe Lys Gln Cys Gly
 370 375 380
 Val Val Lys Met Asn Lys Arg Thr Gly Gln Pro Met Ile His Ile Tyr
 385 390 395 400
 Leu Asp Lys Glu Thr Gly Lys Pro Lys Gly Asp Ala Thr Val Ser Tyr
 405 410 415
 Glu Asp Pro Pro Thr Ala Lys Ala Ala Val Glu Trp Phe Asp Gly Lys
 420 425 430
 Asp Phe Gln Gly Ser Lys Leu Lys Val Ser Leu Ala Arg Lys Lys Pro
 435 440 445
 Pro Met Asn Ser Met Arg Gly Gly Met Pro Pro Arg Glu Gly Arg Gly
 450 455 460
 Met Pro Pro Pro Leu Arg Gly Gly Pro Gly Gly Pro Gly Gly Pro Gly
 465 470 475 480
 Gly Pro Met Gly Arg Met Gly Gly Arg Gly Gly Asp Arg Gly Gly Phe
 485 490 495
 Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly Gly
 500 505 510
 Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Gly Cys
 515 520 525
 Gly Asn Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Lys Ala
 530 535 540
 Pro Lys Pro Glu Gly Phe Leu Pro Pro Pro Phe Pro Pro Pro Gly Gly
 545 550 555 560
 Asp Arg Gly Arg Gly Gly Pro Gly Gly Met Arg Gly Gly Arg Gly Gly

	565	570	575
Leu Met Asp Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly			
	580	585	590
Gly Asp Arg Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly			
	595	600	605
Phe Gly Gly Gly Arg Arg Gly Gly Pro Gly Gly Pro Pro Gly Pro Leu			
	610	615	620
Met Glu Gln Met Gly Gly Arg Arg Gly Gly Arg Gly Gly Pro Gly Lys			
625	630	635	640
Met Asp Lys Gly Glu His Arg Gln Glu Arg Arg Asp Arg Pro Tyr			
	645	650	655

<210> 290

<211> 3295

<212> DNA

<213> Mus musculus

<400> 290

atccactcag gttcaggtgg tgtgggcaa gcggccattt ccattgccct cagtctgggc 60
tgccgcgtct tcaccactgt gggctctgca gagaagcgag catacctcca ggccaggttc 120
cctcagcttg atgacaccag ctttgccaac tcgagggaca catcatttga gcagcacgtg 180
ttactgcaca caggtggcaa aggggtcgac ctggctccta actcactggc agaagagaag 240
ctgcaggcca gtgtgcggtg ctggctcag catggctcgt tcttagagat tggcaaattt 300
gatctttcta acaaccaccc tctgggcatg gctatcttct tgaagaacgt cactttccat 360
gggatcctgc tggacgccct ttttgaggag gccaatgaca gctggcgsga ggtggcggca 420
ctcctgaagg ctggcattcg tgatggagtc gtgaagcccc tcaagtgcac agtgtttccc 480
aaggcccagg tggaagatgc ctccgctac atggctcagg ggaaacactt ggcaaagtcc 540
ttgtccaggt acgggaggag gagcctaggc tgtgctgcca ggggctcagc caccctgatt 600
tctgccatct ccaagacctt ctgccagcc cataagagtt acatcatcac tgggtggccta 660

ggiggcittg gcctggagct ggcccgggtg ctcgtgcttc gcggagccca gaggcttgtg 720
ctgacttccc gatctggaat cgcaccggc taccaagcca agcacaticg ggagtggaga 780
cgccagggca tccaagtgtc cgtgtcaaca agcaacgtga gctcacatga gggggcccg 840
gctctcatcg ccgaagccac aaagctgggg cccgttgggg gtgtcttcaa cctggggccat 900
ggtttgaggg atgcatgtc ggagaaccag accccagagc tcttccagga tgtcaacaag 960
cccaaataca atggcaacct gaaccttgac agggcaacce gggaagcctg ccttgagctg 1020
gactactttg tggccttctc ctcgtgaagc tgcgggcgtg gtaatgttg ccaaactaac 1080
tattgcttcg ccaactctac catggagcgt atatgtgaac agcgcaggca cgatgtcctc 1140
ccaggccttg ccgtgcagtg gggtgccatt ggtgacgttg gcatgtcct ggaagcgatg 1200
ggcaccaatg acacagtcac cggaggtacg ctgcctcagc gcatctcctc ctgcatggag 1260
giactggacc tcttctgaa tcagccccac gcagtcctga gcagctttgt gctggcagag 1320
aagaaagctg tggcccatgg ggacggggac aaccagaggg atctggtgaa agctgtagca 1380
cacatcctag gcatccgaga cctcgcaggt attaacctgg acagcacgtt ggcagacctc 1440
ggcctggact cgctcatggg tgtggaagtt cgtcagatcc tggaacgaga acacgatctg 1500
gtgctgccc a tgcgtgaggt gcgaaggctc acgtgcgga aacttcagga aatgtcctcc 1560
aagactgact cggctactga cagcacagcc cccaagtcca ggagtgcac gtctctgaag 1620
cagaaccaac tgaacctgag cacactgtct gtgaacctg agggctcctac cctaaccag 1680
ctcaactcgg tgcagagctc tgagcggcct ctgttccctg tgcaccccat tgagggttcc 1740
accacgtgt tccacagtct ggctgccaag ctcagtgtgc ccacctacgg cctgcagtgc 1800
acccaagctg ccccccctga tagcatlccg aacctggctg cctactacat agattgcac 1860
aagcaagtgc agcctgaggg accccaccgc atagctgggt actcatttgg agcctgtgta 1920
gccttcgaga tgtgctccca gctgcaggcc cagcagggcc cagccccgac ccacaacaac 1980
ctcttctgt tlgacggctc acacacctac gtgttggcct acaccagag ctaccgggca 2040
aagatgacce caggctgtga agccgaggcc gaggctgagg ccttatgtct cttcataaag 2100
cagtttcttg atgtggaaca cagcaaggtg ctggaggccc tgcctgacct gaagagcctg 2160
gaagatcggg tggctgcctc cgtggacctt atcactaaga gtcaccacag cctggaccgc 2220
cgagagctga gctttgtgc cgtgtcctc taccacaagc tccgggcagc tgatcagtat 2280
aagcccaagg ccaagtacca tggcaacgtg acactgtctg gtgccaagac aggcggcacc 2340
tatggcgagg acttgggtgc tgactacaac ctctcccagg tgtgtgacgg gaagggtgt 2400

gtgcacatca ttgaggggtga ccaccgcaca ctgctggagg gcagtggcct ggaatccatc 2460
 atcaacatca tccatagctc cctggctgag ccacgagtga gtgtacggga gggctagacc 2520
 tccacatga agccacgctc cacacctgcc accagagatg ctccgatccc caccacaccc 2580
 tgagtgcagg aactggggag ggtcctgctg gtgggacccc tccccccagt ggcccagcac 2640
 caccgctcc cctgggtggct gctacaaaca gaccatcacg cgtgtgttcc cagccgcgta 2700
 gtggggttcc cagagccact gacttggaga caccctggtc tgtgaagagt cagtggaggc 2760
 aggagccaaa ctgagccitt tctaccgtgt ggcatitgcc acgttggtcg tttctccatt 2820
 aaattctcat atttattgca ttgctgggaa agacccccag ggttgactca ttccagaacc 2880
 ccctaaaatg ggagaagcca tgtggggaag atttctggga aagtttctag actcaataca 2940
 caggctgctg gctggagccc ctttttgtct tgcctgttcc ctgctcactg cagggcagga 3000
 tatggagagg gctggttccc aggaacaag gaccccagca gacactgtag cccgtggccc 3060
 ttgggtccca gcatccccgg ctgccccatg atgcagggcc atcctgactc tgcggaccgc 3120
 accgggcact gactgtctgt ttccaagac gaaaatgatg cttgggtttt gacttttctg 3180
 cagctgtcag tgtgaagaag tgtctggact gtgtcatttt tacaccaacc tggtaaaaat 3240
 gctgctcttg atgtcttctt gatcccacaa ttaaactgca cgtgagcgaa aaaaa 3295

<210> 291

<211> 1127

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (50).. (1033)

<400> 291

gagtcgggga cgccgcagg tgcctgaatc gcgcgaccag aacgcagta atg aag cca 58

Met Lys Pro

1

ggt ttc cgc ccc cgt ggg ggt ggc ttt ggt ggc aga ggc ggc ttt ggt 106
 Gly Phe Arg Pro Arg Gly Gly Gly Phe Gly Gly Arg Gly Gly Phe Gly
 5 10 15
 gac aga ggc ggt aga gga ggt gga aga gga ggc cga gga ggc ttt ggc 154
 Asp Arg Gly Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly Gly Phe Gly
 20 25 30 35
 ggt gga cga gga ggc ttt ggc ggt gga ggt cga ggt cga ggc gga ggg 202
 Gly Gly Arg Gly Gly Phe Gly Gly Gly Gly Arg Gly Arg Gly Gly Gly
 40 45 50
 ggt ggt ggc ttc agg gga cga gga ggt ggc ggt gtc cga ggt ggg ggc 250
 Gly Gly Gly Phe Arg Gly Arg Gly Gly Gly Gly Val Arg Gly Gly Gly
 55 60 65
 ttc cag tct ggg ggc aac cgg ggt cga ggt ggt ggc cgg gga ggc aag 298
 Phe Gln Ser Gly Gly Asn Arg Gly Arg Gly Gly Gly Arg Gly Gly Lys
 70 75 80
 aga gga aac cag tca ggg aag aat gtg atg gtg gag ccg cat cgt cat 346
 Arg Gly Asn Gln Ser Gly Lys Asn Val Met Val Glu Pro His Arg His
 85 90 95
 gaa ggt gtc ttt atc tgt cgc gga aag gag gat gcc ctt ttc aca aag 394
 Glu Gly Val Phe Ile Cys Arg Gly Lys Glu Asp Ala Leu Phe Thr Lys
 100 105 110 115
 aat ctg gtc cct gga gag tct gtg tat gga gag aag aga gtc tct att 442
 Asn Leu Val Pro Gly Glu Ser Val Tyr Gly Glu Lys Arg Val Ser Ile
 120 125 130
 tca gaa gga gat gac aca att gag tac aga gcc tgg aac ccc ttc cgc 490
 Ser Glu Gly Asp Asp Thr Ile Glu Tyr Arg Ala Trp Asn Pro Phe Arg
 135 140 145
 tcc aag ctg gca gca gct atc ctg ggc ggc gta gac cag atc cac atc 538
 Ser Lys Leu Ala Ala Ala Ile Leu Gly Gly Val Asp Gln Ile His Ile

150	155	160	
aag cca gga gcc aag gtg ctc tac ctt ggg gca gcc tca ggc acc acc			586
Lys Pro Gly Ala Lys Val Leu Tyr Leu Gly Ala Ala Ser Gly Thr Thr			
165	170	175	
gtc tcc cac gtc tct gat att gtc ggc ccg gat ggt ctg gtc tac gca			634
Val Ser His Val Ser Asp Ile Val Gly Pro Asp Gly Leu Val Tyr Ala			
180	185	190	195
gtt gag ttc tcc cac cgc tct ggc cgt gac ctc atc aac ttg gcc aag			682
Val Glu Phe Ser His Arg Ser Gly Arg Asp Leu Ile Asn Leu Ala Lys			
200	205	210	
aag agg act aac att att cct gta att gaa gat gct cga cac cca cac			730
Lys Arg Thr Asn Ile Ile Pro Val Ile Glu Asp Ala Arg His Pro His			
215	220	225	
aaa tac cgc atg ctt atc gca atg gtg gat gtc atc ttt gcc gat gtg			778
Lys Tyr Arg Met Leu Ile Ala Met Val Asp Val Ile Phe Ala Asp Val			
230	235	240	
gcc cag cca gac caa acc cga att gtg gcc ctg aac gcc cac acc ttc			826
Ala Gln Pro Asp Gln Thr Arg Ile Val Ala Leu Asn Ala His Thr Phe			
245	250	255	
ctg cgg aat gga gga cac ttt gtg att tcc att aag gcc aac tgc att			874
Leu Arg Asn Gly Gly His Phe Val Ile Ser Ile Lys Ala Asn Cys Ile			
260	265	270	275
gac tcc act gcg tca gca gag gct gtg ttt gca tct gaa gtg aag aag			922
Asp Ser Thr Ala Ser Ala Glu Ala Val Phe Ala Ser Glu Val Lys Lys			
280	285	290	
atg cag cag gag aac atg aag ccg cag gag cag ctg acg cta gag cct			970
Met Gln Gln Glu Asn Met Lys Pro Gln Glu Gln Leu Thr Leu Glu Pro			
295	300	305	
tat gag cga gac cac gcc gtg gtt gtc ggt gtg tac agg cca cct ccc			1018

Tyr Glu Arg Asp His Ala Val Val Val Gly Val Tyr Arg Pro Pro Pro

310

315

320

aag gtg aag aac tga aactcagagc tgtctggatt gaagagatgt gtgttggttac 1073

Lys Val Lys Asn

325

tgttgcacgt gttgcttgtg attttttggg ggcgggggag ttgttttgtt tttc 1127

<210> 292

<211> 327

<212> PRT

<213> Mus musculus

<400> 292

Met Lys Pro Gly Phe Arg Pro Arg Gly Gly Gly Phe Gly Gly Arg Gly

1

5

10

15

Gly Phe Gly Asp Arg Gly Gly Arg Gly Gly Gly Arg Gly Gly Arg Gly

20

25

30

Gly Phe Gly Gly Gly Arg Gly Gly Phe Gly Gly Gly Gly Arg Gly Arg

35

40

45

Gly Gly Gly Gly Gly Gly Phe Arg Gly Arg Gly Gly Gly Gly Val Arg

50

55

60

Gly Gly Gly Phe Gln Ser Gly Gly Asn Arg Gly Arg Gly Gly Gly Arg

65

70

75

80

Gly Gly Lys Arg Gly Asn Gln Ser Gly Lys Asn Val Met Val Glu Pro

85

90

95

His Arg His Glu Gly Val Phe Ile Cys Arg Gly Lys Glu Asp Ala Leu

100

105

110

Phe Thr Lys Asn Leu Val Pro Gly Glu Ser Val Tyr Gly Glu Lys Arg

115

120

125

Val Ser Ile Ser Glu Gly Asp Asp Thr Ile Glu Tyr Arg Ala Trp Asn
 130 135 140
 Pro Phe Arg Ser Lys Leu Ala Ala Ala Ile Leu Gly Gly Val Asp Gln
 145 150 155 160
 Ile His Ile Lys Pro Gly Ala Lys Val Leu Tyr Leu Gly Ala Ala Ser
 165 170 175
 Gly Thr Thr Val Ser His Val Ser Asp Ile Val Gly Pro Asp Gly Leu
 180 185 190
 Val Tyr Ala Val Glu Phe Ser His Arg Ser Gly Arg Asp Leu Ile Asn
 195 200 205
 Leu Ala Lys Lys Arg Thr Asn Ile Ile Pro Val Ile Glu Asp Ala Arg
 210 215 220
 His Pro His Lys Tyr Arg Met Leu Ile Ala Met Val Asp Val Ile Phe
 225 230 235 240
 Ala Asp Val Ala Gln Pro Asp Gln Thr Arg Ile Val Ala Leu Asn Ala
 245 250 255
 His Thr Phe Leu Arg Asn Gly Gly His Phe Val Ile Ser Ile Lys Ala
 260 265 270
 Asn Cys Ile Asp Ser Thr Ala Ser Ala Glu Ala Val Phe Ala Ser Glu
 275 280 285
 Val Lys Lys Met Gln Gln Glu Asn Met Lys Pro Gln Glu Gln Leu Thr
 290 295 300
 Leu Glu Pro Tyr Glu Arg Asp His Ala Val Val Val Gly Val Tyr Arg
 305 310 315 320
 Pro Pro Pro Lys Val Lys Asn
 325

<210> 293

<211> 2060

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (14).. (1633)

<400> 293

```

ggcaccgagcc aac atg gcg gag ctg acg gtg gag gtt cgc ggc tcc aac      49
      Met Ala Glu Leu Thr Val Glu Val Arg Gly Ser Asn
              1              5              10
ggg gct ttc tac aag gga ttt atc aaa gat gtc cac gaa gac tcc ctc      97
Gly Ala Phe Tyr Lys Gly Phe Ile Lys Asp Val His Glu Asp Ser Leu
      15              20              25
aca gtt gtt ttt gaa aat aat tgg caa cca gaa cgc cag gtt ccg ttt      145
Thr Val Val Phe Glu Asn Asn Trp Gln Pro Glu Arg Gln Val Pro Phe
      30              35              40
aat gaa gtg cga tta cca cca cca cct gat ata aaa aaa gaa att agt      193
Asn Glu Val Arg Leu Pro Pro Pro Pro Asp Ile Lys Lys Glu Ile Ser
      45              50              55              60
gaa gga gat gaa gta gag gta tat tca aga gca aat gac caa gag cca      241
Glu Gly Asp Glu Val Glu Val Tyr Ser Arg Ala Asn Asp Gln Glu Pro
      65              70              75
tgt gga tgg tgg ctg gct aaa gtt cgg atg atg aaa ggc gag ttt tat      289
Cys Gly Trp Trp Leu Ala Lys Val Arg Met Met Lys Gly Glu Phe Tyr
      80              85              90
gtc att gaa tat gct gct tgt gat gcc act tac aat gaa ata gtc aca      337
Val Ile Glu Tyr Ala Ala Cys Asp Ala Thr Tyr Asn Glu Ile Val Thr
      95              100              105

```

```

    ttt gaa cga ctt cgg cct gtc aat caa aat aaa act gtc aaa aaa aat 385
Phe Glu Arg Leu Arg Pro Val Asn Gln Asn Lys Thr Val Lys Lys Asn
      110              115              120
    acc ttc ttt aag tgc aca gtg gat gtt cct gag gac ctg aga gaa gcg 433
Thr Phe Phe Lys Cys Thr Val Asp Val Pro Glu Asp Leu Arg Glu Ala
    125              130              135              140
    tgt gct aat gaa aat gcc cat aaa gat ttt aag aaa gca gta gga gca 481
Cys Ala Asn Glu Asn Ala His Lys Asp Phe Lys Lys Ala Val Gly Ala
      145              150              155
    tgc aga atc ttt tat cat cct gaa act acc cag cta atg ata ctg tcg 529
Cys Arg Ile Phe Tyr His Pro Glu Thr Thr Gln Leu Met Ile Leu Ser
      160              165              170
    gcc agt gaa gca act gtg aag aga gta aat atc tta agt gat atg cat 577
Ala Ser Glu Ala Thr Val Lys Arg Val Asn Ile Leu Ser Asp Met His
      175              180              185
    ttg aga agt att cgg acg aag ttg atg ctt atg tcc aga aat gaa gag 625
Leu Arg Ser Ile Arg Thr Lys Leu Met Leu Met Ser Arg Asn Glu Glu
      190              195              200
    gcc act aag cat tta gaa tgc aca aaa caa ctt gca gca gct ttt cat 673
Ala Thr Lys His Leu Glu Cys Thr Lys Gln Leu Ala Ala Ala Phe His
    205              210              215              220
    gaa gaa ttt gtt gtg aga gaa gat tta atg ggc ctg gcg ata gga acg 721
Glu Glu Phe Val Val Arg Glu Asp Leu Met Gly Leu Ala Ile Gly Thr
      225              230              235
    cat ggc agt aac ata cag caa gct agg aag gtt cct gga gtt act gcc 769
His Gly Ser Asn Ile Gln Gln Ala Arg Lys Val Pro Gly Val Thr Ala
      240              245              250
    att gag tta gat gaa gac acc gga acg ttt aga atc tat gga gag agt 817
Ile Glu Leu Asp Glu Asp Thr Gly Thr Phe Arg Ile Tyr Gly Glu Ser

```


255	260	265	
gct gag gct gta aaa aaa gct aga ggt ttc ttg gaa ttt gtg gaa gat	865		
Ala Glu Ala Val Lys Lys Ala Arg Gly Phe Leu Glu Phe Val Glu Asp			
270	275	280	
ttt att caa gtt ccc agg aat ctt gtt gga aaa gta att gga aaa aat	913		
Phe Ile Gln Val Pro Arg Asn Leu Val Gly Lys Val Ile Gly Lys Asn			
285	290	295	300
ggc aaa gtt att caa gaa ata gtg gat aaa tct ggt gtg gtt cga gta	961		
Gly Lys Val Ile Gln Glu Ile Val Asp Lys Ser Gly Val Val Arg Val			
305	310	315	
aga att gaa gga gac aat gaa aat aaa cta cct aga gaa gac gga atg	1009		
Arg Ile Glu Gly Asp Asn Glu Asn Lys Leu Pro Arg Glu Asp Gly Met			
320	325	330	
gtt cca ttt gta ttt gtt ggc act aaa gaa agc att ggg aat gtg caa	1057		
Val Pro Phe Val Phe Val Gly Thr Lys Glu Ser Ile Gly Asn Val Gln			
335	340	345	
gtt ctt cta gag tat cac atc gct tac tta aag gaa gtg gaa caa cta	1105		
Val Leu Leu Glu Tyr His Ile Ala Tyr Leu Lys Glu Val Glu Gln Leu			
350	355	360	
aga atg gaa cgt ctg cag att gat gag cag ctg cga cag att ggt tct	1153		
Arg Met Glu Arg Leu Gln Ile Asp Glu Gln Leu Arg Gln Ile Gly Ser			
365	370	375	380
agg tct tat agt gga aga ggc aga ggt cgt cgg ggc cct aat tac acc	1201		
Arg Ser Tyr Ser Gly Arg Gly Arg Gly Arg Arg Gly Pro Asn Tyr Thr			
385	390	395	
tcc ggt tat ggt aca aat tct gag ctg tct aac ccc tcc gaa aca gaa	1249		
Ser Gly Tyr Gly Thr Asn Ser Glu Leu Ser Asn Pro Ser Glu Thr Glu			
400	405	410	
tct gag cgt aaa gat gag ctg agt gat tgg tca ttg gca gga gaa gat	1297		

Ser Glu Arg Lys Asp Glu Leu Ser Asp Trp Ser Leu Ala Gly Glu Asp
 415 420 425
 gat cga gag act cga cat cag cga gac agc agg aga cgc cca gga gga 1345
 Asp Arg Glu Thr Arg His Gln Arg Asp Ser Arg Arg Arg Pro Gly Gly
 430 435 440
 aga ggc aga agt gtt tct ggg gga cga ggt cgt ggt gga cca cgt ggt 1393
 Arg Gly Arg Ser Val Ser Gly Gly Arg Gly Arg Gly Gly Pro Arg Gly
 445 450 455 460
 ggc aaa tcc tcc atc agt tct gtg ctc aaa gat cca gac agc aat cca 1441
 Gly Lys Ser Ser Ile Ser Ser Val Leu Lys Asp Pro Asp Ser Asn Pro
 465 470 475
 tac agc tta ctt gat aat aca gaa tcc gat cag act gca gac act gac 1489
 Tyr Ser Leu Leu Asp Asn Thr Glu Ser Asp Gln Thr Ala Asp Thr Asp
 480 485 490
 gcc agc gaa tct cac cac agt act aac cgt cgt agg cgg tct cgt aga 1537
 Ala Ser Glu Ser His His Ser Thr Asn Arg Arg Arg Arg Ser Arg Arg
 495 500 505
 cgg agg act gat gaa gat gct gtt ctg atg gat gga ctg act gaa tct 1585
 Arg Arg Thr Asp Glu Asp Ala Val Leu Met Asp Gly Leu Thr Glu Ser
 510 515 520
 gat aca gcc tca gtt aat gag aat ggg cta ggc aaa aga tgt gat tga 1633
 Asp Thr Ala Ser Val Asn Glu Asn Gly Leu Gly Lys Arg Cys Asp
 525 530 535 540
 agagcatggt ccttcagaaa aggcaataaa tggccaact agcgcttctg gcgatgaaat 1693
 tcctaagcta ccgcgtactc tgggagaaga aaagactaag accttaaaag aagacagcac 1753
 tcaagaagca gcagtcctga atggigtgttc ataactgaag gaagttccta gtttacagtt 1813
 cttttacatt acagttacaa tagtgcttgt acaagcttgc caaagataga atacggatcg 1873
 ccagtcttac atcgcacttt cagttcctcc atttgggaatt cagaaagggg agggatcctg 1933
 aagaaatcat atgttaaaca tactttgaca cctacttgtt taaaaatata tcatcagatg 1993

tgcccttgaga atagtataatg taacattaaa aaaagttgct ggctaaaaaa aaaaaaaaaa 2053
 aaaaaaa 2060

<210> 294

<211> 539

<212> PRT

<213> Mus musculus

<400> 294

Met Ala Glu Leu Thr Val Glu Val Arg Gly Ser Asn Gly Ala Phe Tyr
 1 5 10 15
 Lys Gly Phe Ile Lys Asp Val His Glu Asp Ser Leu Thr Val Val Phe
 20 25 30
 Glu Asn Asn Trp Gln Pro Glu Arg Gln Val Pro Phe Asn Glu Val Arg
 35 40 45
 Leu Pro Pro Pro Pro Asp Ile Lys Lys Glu Ile Ser Glu Gly Asp Glu
 50 55 60
 Val Glu Val Tyr Ser Arg Ala Asn Asp Gln Glu Pro Cys Gly Trp Trp
 65 70 75 80
 Leu Ala Lys Val Arg Met Met Lys Gly Glu Phe Tyr Val Ile Glu Tyr
 85 90 95
 Ala Ala Cys Asp Ala Thr Tyr Asn Glu Ile Val Thr Phe Glu Arg Leu
 100 105 110
 Arg Pro Val Asn Gln Asn Lys Thr Val Lys Lys Asn Thr Phe Phe Lys
 115 120 125
 Cys Thr Val Asp Val Pro Glu Asp Leu Arg Glu Ala Cys Ala Asn Glu
 130 135 140
 Asn Ala His Lys Asp Phe Lys Lys Ala Val Gly Ala Cys Arg Ile Phe
 145 150 155 160

Tyr His Pro Glu Thr Thr Gln Leu Met Ile Leu Ser Ala Ser Glu Ala
 165 170 175
 Thr Val Lys Arg Val Asn Ile Leu Ser Asp Met His Leu Arg Ser Ile
 180 185 190
 Arg Thr Lys Leu Met Leu Met Ser Arg Asn Glu Glu Ala Thr Lys His
 195 200 205
 Leu Glu Cys Thr Lys Gln Leu Ala Ala Ala Phe His Glu Glu Phe Val
 210 215 220
 Val Arg Glu Asp Leu Met Gly Leu Ala Ile Gly Thr His Gly Ser Asn
 225 230 235 240
 Ile Gln Gln Ala Arg Lys Val Pro Gly Val Thr Ala Ile Glu Leu Asp
 245 250 255
 Glu Asp Thr Gly Thr Phe Arg Ile Tyr Gly Glu Ser Ala Glu Ala Val
 260 265 270
 Lys Lys Ala Arg Gly Phe Leu Glu Phe Val Glu Asp Phe Ile Gln Val
 275 280 285
 Pro Arg Asn Leu Val Gly Lys Val Ile Gly Lys Asn Gly Lys Val Ile
 290 295 300
 Gln Glu Ile Val Asp Lys Ser Gly Val Val Arg Val Arg Ile Glu Gly
 305 310 315 320
 Asp Asn Glu Asn Lys Leu Pro Arg Glu Asp Gly Met Val Pro Phe Val
 325 330 335
 Phe Val Gly Thr Lys Glu Ser Ile Gly Asn Val Gln Val Leu Leu Glu
 340 345 350
 Tyr His Ile Ala Tyr Leu Lys Glu Val Glu Gln Leu Arg Met Glu Arg
 355 360 365
 Leu Gln Ile Asp Glu Gln Leu Arg Gln Ile Gly Ser Arg Ser Tyr Ser
 370 375 380
 Gly Arg Gly Arg Gly Arg Arg Gly Pro Asn Tyr Thr Ser Gly Tyr Gly

385 390 395 400
 Thr Asn Ser Glu Leu Ser Asn Pro Ser Glu Thr Glu Ser Glu Arg Lys
 405 410 415
 Asp Glu Leu Ser Asp Trp Ser Leu Ala Gly Glu Asp Asp Arg Glu Thr
 420 425 430
 Arg His Gln Arg Asp Ser Arg Arg Arg Pro Gly Gly Arg Gly Arg Ser
 435 440 445
 Val Ser Gly Gly Arg Gly Arg Gly Gly Pro Arg Gly Gly Lys Ser Ser
 450 455 460
 Ile Ser Ser Val Leu Lys Asp Pro Asp Ser Asn Pro Tyr Ser Leu Leu
 465 470 475 480
 Asp Asn Thr Glu Ser Asp Gln Thr Ala Asp Thr Asp Ala Ser Glu Ser
 485 490 495
 His His Ser Thr Asn Arg Arg Arg Arg Ser Arg Arg Arg Arg Thr Asp
 500 505 510
 Glu Asp Ala Val Leu Met Asp Gly Leu Thr Glu Ser Asp Thr Ala Ser
 515 520 525
 Val Asn Glu Asn Gly Leu Gly Lys Arg Cys Asp
 530 535

<210> 295

<211> 3069

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (113)...(1555)

<400> 295

gtcgaccgcg gaggccggtg gcgtcgacgt ctagtgtctc agtgtgctcc cgctctgtggc 60
 taactaagca gccagcagca ggcagctcgc gactgcggcc aggcagccaa cc atg ctc 118

Met Leu

1

aac ttc ggg gcg ctt ctc tcc agc aag ctt cgg agg gga aaa ttg gaa 166
 Asn Phe Gly Ala Leu Leu Ser Ser Lys Leu Arg Arg Gly Lys Leu Glu

5

10

15

cta att tct gaa aag ccc aga gag ggg atg cat ccc tgg gac aaa gct 214
 Leu Ile Ser Glu Lys Pro Arg Glu Gly Met His Pro Trp Asp Lys Ala

20

25

30

gag cag agt gac ttt gaa gcg gtg gaa gcg ctc atg tcc atg agc tgc 262
 Glu Gln Ser Asp Phe Glu Ala Val Glu Ala Leu Met Ser Met Ser Cys

35

40

45

50

gac tgg aag tct cat ttc aag aaa tac ctt gaa aac agg cct gtc aca 310
 Asp Trp Lys Ser His Phe Lys Lys Tyr Leu Glu Asn Arg Pro Val Thr

55

60

65

cca gtg tct gat acc tcc gag gat gac agc ttg ctt cca ggg acg cct 358
 Pro Val Ser Asp Thr Ser Glu Asp Asp Ser Leu Leu Pro Gly Thr Pro

70

75

80

gac ctt cag aca gtc cca gca ttt tgt tta acg cca cct tac agc ccc 406
 Asp Leu Gln Thr Val Pro Ala Phe Cys Leu Thr Pro Pro Tyr Ser Pro

85

90

95

tct gac ttc gaa ccc tcc caa ggg tca aat ctg act gca tca gcg cca 454
 Ser Asp Phe Glu Pro Ser Gln Gly Ser Asn Leu Thr Ala Ser Ala Pro

100

105

110

tct act ggc cac ttc aaa tct ttc tcc gat tct gcc aag cct cca ggc 502
 Ser Thr Gly His Phe Lys Ser Phe Ser Asp Ser Ala Lys Pro Pro Gly

115

120

125

130

```

gcc act cct ttc aaa gag gag gaa aag aat cct tta gct gcc cct cct 550
Ala Thr Pro Phe Lys Glu Glu Glu Lys Asn Pro Leu Ala Ala Pro Pro
          135                140                145
ctt cct aag gct caa gcc acc agt gtc atc cgt cac aca gct gat gcc 598
Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His Thr Ala Asp Ala
          150                155                160
caa ctg tgc aac cac cag tcc tgc ccc gtg aaa gca gct agc atc ctc 646
Gln Leu Cys Asn His Gln Ser Cys Pro Val Lys Ala Ala Ser Ile Leu
          165                170                175
aac tat cag gac aat tct ttc cgg aga aga acc cac gga aat gtt gag 694
Asn Tyr Gln Asp Asn Ser Phe Arg Arg Arg Thr His Gly Asn Val Glu
          180                185                190
gct act cga aag aac ata ccc tgt gct gca gtg tca cca aac aga tcc 742
Ala Thr Arg Lys Asn Ile Pro Cys Ala Ala Val Ser Pro Asn Arg Ser
          195                200                205                210
aag cct gag ccc agc aca gtg tcc gat ggt gat gag aag gcg ggc gct 790
Lys Pro Glu Pro Ser Thr Val Ser Asp Gly Asp Glu Lys Ala Gly Ala
          215                220                225
gca cta tat gac ttt gct gtg cct tcc tca gag aca gta att tgt agg 838
Ala Leu Tyr Asp Phe Ala Val Pro Ser Ser Glu Thr Val Ile Cys Arg
          230                235                240
tct cag cca gct tcc ttt cgt ccc cag tgc aga agt cag tac tgg tgt 886
Ser Gln Pro Ala Ser Phe Arg Pro Gln Cys Arg Ser Gln Tyr Trp Cys
          245                250                255
ctt cac cta cag tat cca ctg ggg gag tgc cac ccc tgc ctg tca tct 934
Leu His Leu Gln Tyr Pro Leu Gly Glu Cys His Pro Cys Leu Ser Ser
          260                265                270
gcc aga tgg ttc ccc ttc ctg cca aca act ctc ttg tta gca caa gtt 982
Ala Arg Trp Phe Pro Phe Leu Pro Thr Thr Leu Leu Leu Ala Gln Val

```

275	280	285	290	
gtc ccc agc act cct cct agc cag cca cca gct gtc tgc tca cct gtg	1030			
Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys Ser Pro Val				
295	300	305		
ttg ttc atg gca ctc atg cct gag ggc acc gta cgt gtt tgt ggt acc	1078			
Leu Phe Met Ala Leu Met Pro Glu Gly Thr Val Arg Val Cys Gly Thr				
310	315	320		
cca gcc cgt tgt gca gag cca agg cct cca gtg gtg agc ccc agt ggc	1126			
Pro Ala Arg Cys Ala Glu Pro Arg Pro Pro Val Val Ser Pro Ser Gly				
325	330	335		
acc aga ctg tct ccc att gcc cct gct cct gga ttc tct cct tca gca	1174			
Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro Ser Ala				
340	345	350		
gca agg gtc act cct cag att gac tcg tcc aga gta aga agt cac atc	1222			
Ala Arg Val Thr Pro Gln Ile Asp Ser Ser Arg Val Arg Ser His Ile				
355	360	365	370	
tgt agc cac cca ggg gtt ggc aag act tac ttt aaa agt tcc cat ctg	1270			
Cys Ser His Pro Gly Val Gly Lys Thr Tyr Phe Lys Ser Ser His Leu				
375	380	385		
aag gcc cac gtg agg aca cac aca ggg gaa aaa cct ttc agc tgc agc	1318			
Lys Ala His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser Cys Ser				
390	395	400		
tgg aaa ggc tgt gaa agg agg ttt gct cgc tcc gat gaa ctg tcc aga	1366			
Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu Ser Arg				
405	410	415		
cac cgg cgg aca cac aca ggt gag aag aag ttt gcc tgt ccc atg tgt	1414			
His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro Met Cys				
420	425	430		
gac cgt cgg ttt atg agg agc gac cat tta acc aag cat gcc cga cgc	1462			

Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala Arg Arg
 435 440 445 450
 cac cta tca gcc aag aag ctg cca aac tgg caa atg gaa gtt agc aag 1510
 His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val Ser Lys
 455 460 465
 tta aat gac att gct ctg cct ccg acc cct gct tcc gca cag tga 1555
 Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Ser Ala Gln
 470 475 480
 cggccagaag atggagacgc agaataaact ttggtcagag tcaggagcca gtgatggtgt 1615
 caagtgttc tgcaaggctg tggcctccaa agctaaagta gaagccctgg cctggggagg 1675
 cccgtggtg aaatgacaga gtgctcagca caggcaggtc acagaggaca gggctcagtt 1735
 cttaccacag agagagagga gaacctttt attcctccct tatttttagtc tggaaagttt 1795
 cggctgaggt gagcgacga caggttttga atcacataca cattggggac ttgtttttg 1855
 ccatttatac ttgagaccag ctttgcagtg tgattctttc aaaggattgg ttccaagaat 1915
 atagaggctg gaaattacgg tacagaaatg gagctagaaa atgagtttgt gttacacaga 1975
 gatgtcatct tctcctagag ttatcttgtt tcttattcct agtctttcca gtcaaatccg 2035
 tggatgtagc taagtatatc taaaactcat ttttccacta ttgttggtat ttgaagtga 2095
 acacagctgt acattgctgt gggggagcca aaggattgga accctcatta atttaattgc 2155
 ttggaaatgc agctaaaatt cttctttggc attttgtttt gaaagtttag gcattttact 2215
 ctactttaga ttttagtttg cttgcagttt ttgtgtaga ttgaaaatt gtataccaat 2275
 gtgttttctg taggcttaaa atacactgca cttgttttag aaaaaaatct ggagatgaaa 2335
 atatgtattt taaagaagag atgtcaagaa ttgagataa ctccctgaga aagttggcaa 2395
 gtttgagata actccttgag aagttggctt tatgctacag caaggcctaa cgtcaagcta 2455
 acactgtggt ttttttgttt ttttgtttt ttttttcaa ttagaaagt aattgaccgt 2515
 tacagatgga cagtgtcttt ttatttatag gagtttttca ggaatgcaga gtagataggt 2575
 aggaaaattg ttattagaac attcgcttct accttgaaaa ggatgttaat gtggctatgt 2635
 tcttagcacc acagtgtctg ggcatctggg aaactccgag acttttttaa agtgtcatag 2695
 atgtgatcac acacctgcag ttggggcat cgaatccagg gccttgcatg tcttcigtta 2755
 gagctctcat cgctgacctg tatccccgca agagcaatga cttttgctaa cagtatttct 2815

tttctgttgt aaagtggaca gatgatacac ttggtacgca aaggtaaact atcaaaatcc 2875
 acagtgtaaa cctcaccaca ctttccatt taaactatit ccataatcica gaggtttctg 2935
 acatgcaaac ttgaaccctt gaaagaagag ttttcttaaa aattataaaa aatcacgagt 2995
 tacaatttgc acaatatitit ttgttgaact ttataccttg ttacaataa agactititct 3055
 ttggtataaa aaaa 3069

<210> 296

<211> 480

<212> PRT

<213> Mus musculus

<400> 296

Met Leu Asn Phe Gly Ala Leu Leu Ser Ser Lys Leu Arg Arg Gly Lys

1 5 10 15

Leu Glu Leu Ile Ser Glu Lys Pro Arg Glu Gly Met His Pro Trp Asp

20 25 30

Lys Ala Glu Gln Ser Asp Phe Glu Ala Val Glu Ala Leu Met Ser Met

35 40 45

Ser Cys Asp Trp Lys Ser His Phe Lys Lys Tyr Leu Glu Asn Arg Pro

50 55 60

Val Thr Pro Val Ser Asp Thr Ser Glu Asp Asp Ser Leu Leu Pro Gly

65 70 75 80

Thr Pro Asp Leu Gln Thr Val Pro Ala Phe Cys Leu Thr Pro Pro Tyr

85 90 95

Ser Pro Ser Asp Phe Glu Pro Ser Gln Gly Ser Asn Leu Thr Ala Ser

100 105 110

Ala Pro Ser Thr Gly His Phe Lys Ser Phe Ser Asp Ser Ala Lys Pro

115 120 125

Pro Gly Ala Thr Pro Phe Lys Glu Glu Glu Lys Asn Pro Leu Ala Ala

130	135	140	
Pro Pro Leu Pro Lys Ala Gln Ala Thr Ser Val Ile Arg His Thr Ala			
145	150	155	160
Asp Ala Gln Leu Cys Asn His Gln Ser Cys Pro Val Lys Ala Ala Ser			
	165	170	175
Ile Leu Asn Tyr Gln Asp Asn Ser Phe Arg Arg Arg Thr His Gly Asn			
	180	185	190
Val Glu Ala Thr Arg Lys Asn Ile Pro Cys Ala Ala Val Ser Pro Asn			
	195	200	205
Arg Ser Lys Pro Glu Pro Ser Thr Val Ser Asp Gly Asp Glu Lys Ala			
	210	215	220
Gly Ala Ala Leu Tyr Asp Phe Ala Val Pro Ser Ser Glu Thr Val Ile			
225	230	235	240
Cys Arg Ser Gln Pro Ala Ser Phe Arg Pro Gln Cys Arg Ser Gln Tyr			
	245	250	255
Trp Cys Leu His Leu Gln Tyr Pro Leu Gly Glu Cys His Pro Cys Leu			
	260	265	270
Ser Ser Ala Arg Trp Phe Pro Phe Leu Pro Thr Thr Leu Leu Leu Ala			
	275	280	285
Gln Val Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys Ser			
	290	295	300
Pro Val Leu Phe Met Ala Leu Met Pro Glu Gly Thr Val Arg Val Cys			
305	310	315	320
Gly Thr Pro Ala Arg Cys Ala Glu Pro Arg Pro Pro Val Val Ser Pro			
	325	330	335
Ser Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro			
	340	345	350
Ser Ala Ala Arg Val Thr Pro Gln Ile Asp Ser Ser Arg Val Arg Ser			
	355	360	365

His Ile Cys Ser His Pro Gly Val Gly Lys Thr Tyr Phe Lys Ser Ser

370

375

380

His Leu Lys Ala His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser

385

390

395

400

Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu

405

410

415

Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro

420

425

430

Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala

435

440

445

Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val

450

455

460

Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Thr Pro Ala Ser Ala Gln

465

470

475

480

<210> 297

<211> 3227

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (241).. (2142)

<400> 297

gaattcggca cgaggagcgc gcaggcaacg cggcggggcg ggaggactgg cggctgcaga 60
gagcctcggg aggctgatgc aactttccct ttaagaaagc cacctgggcg caccgcgtgc 120
ggaccagca cgcctgggcc ggggcagcag tatctcttga ggctgttgt ctgaaaggca 180
ctgaacgcaa gactctgcaa gtgtgggtcca gatctccaga tcccccaacc cactgccacc 240

atg gta gga aaa ggt gcc aaa ggg atg ttg aat ggt gct gtg ccc agc	288
Met Val Gly Lys Gly Ala Lys Gly Met Leu Asn Gly Ala Val Pro Ser	
1 5 10 15	
gag gcc acc aag aag gac cag aac ctc aca cgg ggc aac tgg ggc aac	336
Glu Ala Thr Lys Lys Asp Gln Asn Leu Thr Arg Gly Asn Trp Gly Asn	
20 25 30	
cag atc gag ttt gta ctg acg agc gtg ggc tat gcc gtg ggc ctg ggc	384
Gln Ile Glu Phe Val Leu Thr Ser Val Gly Tyr Ala Val Gly Leu Gly	
35 40 45	
aat gtc tgg cgt ttc cca tac ctc tgc tat cgc aac ggg gga gga gcc	432
Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Arg Asn Gly Gly Gly Ala	
50 55 60	
ttc atg ttc ccc tac ttc atc atg ctg atc ttc tgc ggg att cct ctc	480
Phe Met Phe Pro Tyr Phe Ile Met Leu Ile Phe Cys Gly Ile Pro Leu	
65 70 75 80	
ttc ttc atg gag ctt tcc ttc ggc cag ttt gca agc cag ggc tgc ctg	528
Phe Phe Met Glu Leu Ser Phe Gly Gln Phe Ala Ser Gln Gly Cys Leu	
85 90 95	
ggg gtc tgg cgg atc agc ccc atg ttc aaa ggc gtg ggc tat ggt atg	576
Gly Val Trp Arg Ile Ser Pro Met Phe Lys Gly Val Gly Tyr Gly Met	
100 105 110	
atg gtg gtg tcc aca tac att ggc atc tac tac aac gtg gtc atc tgc	624
Met Val Val Ser Thr Tyr Ile Gly Ile Tyr Tyr Asn Val Val Ile Cys	
115 120 125	
atc gcc ttc tac tac ttc ttc tcg tcc atg acg cac gtg ctg ccc tgg	672
Ile Ala Phe Tyr Tyr Phe Phe Ser Ser Met Thr His Val Leu Pro Trp	
130 135 140	
gcg tac tgc aac aac ccc tgg aac aca cct gac tgt gcc ggt gtg ctg	720
Ala Tyr Cys Asn Asn Pro Trp Asn Thr Pro Asp Cys Ala Gly Val Leu	

145	150	155	160	
gac gct tcc aac ctc acc aat ggc tcc cgg ccc gct gcc ctg tct ggc				768
Asp Ala Ser Asn Leu Thr Asn Gly Ser Arg Pro Ala Ala Leu Ser Gly				
	165	170	175	
aac ctg tct cac ctg ttc aac tac acc ttg caa agg acc agc ccc agc				816
Asn Leu Ser His Leu Phe Asn Tyr Thr Leu Gln Arg Thr Ser Pro Ser				
	180	185	190	
gag gag tac tgg agg ctg tat gtg ctg aag ctg tca gac gac att gga				864
Glu Glu Tyr Trp Arg Leu Tyr Val Leu Lys Leu Ser Asp Asp Ile Gly				
	195	200	205	
aac ttt ggg gaa gtg cgg ctt ccc ctc cta ggc tgc ctc ggc gtc tcc				912
Asn Phe Gly Glu Val Arg Leu Pro Leu Leu Gly Cys Leu Gly Val Ser				
	210	215	220	
tgg gtg gtt gtc ttc ctc tgt ctc atc cga gga gtc aag tct tca ggg				960
Trp Val Val Val Phe Leu Cys Leu Ile Arg Gly Val Lys Ser Ser Gly				
	225	230	235	240
aaa gtg gtg tac ttc acg gcc aca ttc ccc tat gtg gtg ctg acc att				1008
Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Tyr Val Val Leu Thr Ile				
	245	250	255	
ctg ttt gtt cgt gga gtg acc ctg gaa gga gcc ttc acg ggt atc atg				1056
Leu Phe Val Arg Gly Val Thr Leu Glu Gly Ala Phe Thr Gly Ile Met				
	260	265	270	
tac tac ctg acc cca caa tgg gac aag tac ctg gag gcc aag gtc tgg				1104
Tyr Tyr Leu Thr Pro Gln Trp Asp Lys Tyr Leu Glu Ala Lys Val Trp				
	275	280	285	
ggg gat gca gcc tct cag atc ttc tat tcc ctg ggc tgt gca tgg ggt				1152
Gly Asp Ala Ala Ser Gln Ile Phe Tyr Ser Leu Gly Cys Ala Trp Gly				
	290	295	300	
ggc ctc atc acc atg gcg tcc tac aac aaa ttt cac aac aac tgc tac				1200

Gly	Leu	Ile	Thr	Met	Ala	Ser	Tyr	Asn	Lys	Phe	His	Asn	Asn	Cys	Tyr		
305					310					315					320		
cgg	gac	agc	gtc	att	atc	agt	atc	acc	aac	tgt	gct	acc	agg	ctc	tac	1248	
Arg	Asp	Ser	Val	Ile	Ile	Ser	Ile	Thr	Asn	Cys	Ala	Thr	Arg	Leu	Tyr		
				325						330					335		
gcc	ggc	ttc	gtc	atc	ttc	tcc	atc	ctg	ggc	ttc	atg	gcc	aat	cac	ctg	1296	
Ala	Gly	Phe	Val	Ile	Phe	Ser	Ile	Leu	Gly	Phe	Met	Ala	Asn	His	Leu		
				340						345					350		
ggt	gtg	gat	gtg	tct	cgg	gtg	gca	gac	cat	ggg	cct	ggg	cta	gct	ttt	1344	
Gly	Val	Asp	Val	Ser	Arg	Val	Ala	Asp	His	Gly	Pro	Gly	Leu	Ala	Phe		
				355						360					365		
gtc	gct	tac	cct	gag	gct	ctc	acg	ctg	ctt	ccc	atc	tct	cca	ctc	tgg	1392	
Val	Ala	Tyr	Pro	Glu	Ala	Leu	Thr	Leu	Leu	Pro	Ile	Ser	Pro	Leu	Trp		
				370						375					380		
tcc	tta	ttg	ttt	ttc	ttc	atg	ctc	atc	ttg	ctg	ggg	ctg	ggt	act	cag	1440	
Ser	Leu	Leu	Phe	Phe	Phe	Met	Leu	Ile	Leu	Leu	Gly	Leu	Gly	Thr	Gln		
385						390					395				400		
ttc	tgc	ctc	cta	gag	acc	ctg	gtc	act	gcc	att	gtg	gat	gag	gia	ggg	1488	
Phe	Cys	Leu	Leu	Glu	Thr	Leu	Val	Thr	Ala	Ile	Val	Asp	Glu	Val	Gly		
						405					410				415		
aat	gag	tgg	att	ctg	cag	aag	aag	acc	tac	gtg	acc	ttg	ggc	gtc	gct	1536	
Asn	Glu	Trp	Ile	Leu	Gln	Lys	Lys	Thr	Tyr	Val	Thr	Leu	Gly	Val	Ala		
				420							425				430		
gtg	gct	ggc	ttc	ttg	ctg	ggc	atc	ccc	ctt	acc	agc	cag	gca	ggc	atc	1584	
Val	Ala	Gly	Phe	Leu	Leu	Gly	Ile	Pro	Leu	Thr	Ser	Gln	Ala	Gly	Ile		
				435							440				445		
tac	tgg	ctg	ctg	ctg	atg	gac	aac	tat	gca	gcc	agc	ttc	tcc	ttg	gtt	1632	
Tyr	Trp	Leu	Leu	Leu	Met	Asp	Asn	Tyr	Ala	Ala	Ser	Phe	Ser	Leu	Val		
				450							455				460		

```

gtc atc tcc tgt atc atg tgt gta tcc atc atg tac atc tat ggg cac 1680
Val Ile Ser Cys Ile Met Cys Val Ser Ile Met Tyr Ile Tyr Gly His
465          470          475          480
cgt aac tac ttc cag gac atc cag atg atg cta gga ttt ccc ccg cct 1728
Arg Asn Tyr Phe Gln Asp Ile Gln Met Met Leu Gly Phe Pro Pro Pro
          485          490          495
ctc ttc ttc cag atc tgt tgg cgc ttt gtt tct ccg gct atc atc ttt 1776
Leu Phe Phe Gln Ile Cys Trp Arg Phe Val Ser Pro Ala Ile Ile Phe
          500          505          510
ttc att ctc atc ttc acg gtg atc cag tac cgg cca atc acc tac aac 1824
Phe Ile Leu Ile Phe Thr Val Ile Gln Tyr Arg Pro Ile Thr Tyr Asn
          515          520          525
cac tac cag tac cca ggc tgg gct gtg cgc atc ggc ttc ctc atg gct 1872
His Tyr Gln Tyr Pro Gly Trp Ala Val Arg Ile Gly Phe Leu Met Ala
          530          535          540
ttg tgc tct gtc atc tgc atc cca ctg tac gcg ctg ttc cag ctc tgc 1920
Leu Ser Ser Val Ile Cys Ile Pro Leu Tyr Ala Leu Phe Gln Leu Cys
545          550          555          560
cgc aca gat ggg gac aca ctt ctt cag cgt ttg aaa aat gcc aca aag 1968
Arg Thr Asp Gly Asp Thr Leu Leu Gln Arg Leu Lys Asn Ala Thr Lys
          565          570          575
cca agc aga gac tgg ggc ccc gct ctc ctg gag cac cgg act ggg cgc 2016
Pro Ser Arg Asp Trp Gly Pro Ala Leu Leu Glu His Arg Thr Gly Arg
          580          585          590
tac gct ccc act aca acc ccc tct ccc gaa gac ggg ttt gag gtc cag 2064
Tyr Ala Pro Thr Thr Thr Pro Ser Pro Glu Asp Gly Phe Glu Val Gln
          595          600          605
cca ctg cac ccg gac aag gcc cag att ccc atc gtg ggc agt aac ggc 2112
Pro Leu His Pro Asp Lys Ala Gln Ile Pro Ile Val Gly Ser Asn Gly

```


610	615	620	
tcc agc cgc ttc cag gac tcc cgg ata tga gcgcaattgt tgcaagggga			2162
Ser Ser Arg Phe Gln Asp Ser Arg Ile			
625	630		
gaaacccac ccaacccttg ctcccaccac ggagactggg aggcggacag gtggaggcct			2222
gccccatcac accctgtctg ggatggctgc tgtcaccttg accaccactg ctcattgtccc			2282
cagtgtttac acatcctttg gatgccaaaga cagcagctgg gggtagggaaa gcgatggggg			2342
aattgggggg agcgggcatg gggaagcagt gtccaaagca ctttgaggga ggccctgccag			2402
gcttcctatg gcctctgata cctcattgct ctgccctgag ctgtttcact atgggataag			2462
aggttctgtg tccacatccc accggttccc ctccagcctcg tgaccagtgt tcctgacccc			2522
agaacagacc ctaccctctg cccaggaaaa tctgtatctt cctcctccag acaaggtag			2582
ggccccgggg ctgtacagtg ttacttgttg gactgcacca ctccagcctg tttatttgtg			2642
taattatitt ttttttaaat tgtattacct gtggttgcca tcccctgccc cagccttggg			2702
tccagtgtgt ctccaggcc tgcctgcacc tcacttggct gctccagggt ctctatcctt			2762
tgttccaacc ctggttgta gggccagcca gcaaaggccc acgaccagc agcctgcca			2822
aagcattgt ttatggaggg aaagaagggg acttctctgt aggaagcttg agcccagagc			2882
cctggggaag gggaccctgt tccacattcc ctggcccacc ctccaccagg tcggaggccc			2942
agtcttccca gacgtgctaa cccattcaa tgtgccaaat ggcttcagtc catgtgccc			3002
tccccctct gcagttcctg caccctctcc caagaccgc agtccgtttg tccgtcctct			3062
gtgccctctg cagtacagc cctggccaag ccacttctaa tctctgttag caataacggt			3122
gtgccgccc cgcctgcca gtgtgtgcag aactagggtt ttaaagtcg taggttttaa			3182
tgaaatttct attcctgtct ctgaaaaaaaa aaaaaaaaaa aaaaa			3227

<210> 298

<211> 633

<212> PRT

<213> Mus musculus

<400> 298

Met Val Gly Lys Gly Ala Lys Gly Met Leu Asn Gly Ala Val Pro Ser
 1 5 10 15
 Glu Ala Thr Lys Lys Asp Gln Asn Leu Thr Arg Gly Asn Trp Gly Asn
 20 25 30
 Gln Ile Glu Phe Val Leu Thr Ser Val Gly Tyr Ala Val Gly Leu Gly
 35 40 45
 Asn Val Trp Arg Phe Pro Tyr Leu Cys Tyr Arg Asn Gly Gly Gly Ala
 50 55 60
 Phe Met Phe Pro Tyr Phe Ile Met Leu Ile Phe Cys Gly Ile Pro Leu
 65 70 75 80
 Phe Phe Met Glu Leu Ser Phe Gly Gln Phe Ala Ser Gln Gly Cys Leu
 85 90 95
 Gly Val Trp Arg Ile Ser Pro Met Phe Lys Gly Val Gly Tyr Gly Met
 100 105 110
 Met Val Val Ser Thr Tyr Ile Gly Ile Tyr Tyr Asn Val Val Ile Cys
 115 120 125
 Ile Ala Phe Tyr Tyr Phe Phe Ser Ser Met Thr His Val Leu Pro Trp
 130 135 140
 Ala Tyr Cys Asn Asn Pro Trp Asn Thr Pro Asp Cys Ala Gly Val Leu
 145 150 155 160
 Asp Ala Ser Asn Leu Thr Asn Gly Ser Arg Pro Ala Ala Leu Ser Gly
 165 170 175
 Asn Leu Ser His Leu Phe Asn Tyr Thr Leu Gln Arg Thr Ser Pro Ser
 180 185 190
 Glu Glu Tyr Trp Arg Leu Tyr Val Leu Lys Leu Ser Asp Asp Ile Gly
 195 200 205
 Asn Phe Gly Glu Val Arg Leu Pro Leu Leu Gly Cys Leu Gly Val Ser
 210 215 220
 Trp Val Val Val Phe Leu Cys Leu Ile Arg Gly Val Lys Ser Ser Gly

225	230	235	240
Lys Val Val Tyr Phe Thr Ala Thr Phe Pro Tyr Val Val Leu Thr Ile			
	245	250	255
Leu Phe Val Arg Gly Val Thr Leu Glu Gly Ala Phe Thr Gly Ile Met			
	260	265	270
Tyr Tyr Leu Thr Pro Gln Trp Asp Lys Tyr Leu Glu Ala Lys Val Trp			
	275	280	285
Gly Asp Ala Ala Ser Gln Ile Phe Tyr Ser Leu Gly Cys Ala Trp Gly			
	290	295	300
Gly Leu Ile Thr Met Ala Ser Tyr Asn Lys Phe His Asn Asn Cys Tyr			
305	310	315	320
Arg Asp Ser Val Ile Ile Ser Ile Thr Asn Cys Ala Thr Arg Leu Tyr			
	325	330	335
Ala Gly Phe Val Ile Phe Ser Ile Leu Gly Phe Met Ala Asn His Leu			
	340	345	350
Gly Val Asp Val Ser Arg Val Ala Asp His Gly Pro Gly Leu Ala Phe			
	355	360	365
Val Ala Tyr Pro Glu Ala Leu Thr Leu Leu Pro Ile Ser Pro Leu Trp			
	370	375	380
Ser Leu Leu Phe Phe Phe Met Leu Ile Leu Leu Gly Leu Gly Thr Gln			
385	390	395	400
Phe Cys Leu Leu Glu Thr Leu Val Thr Ala Ile Val Asp Glu Val Gly			
	405	410	415
Asn Glu Trp Ile Leu Gln Lys Lys Thr Tyr Val Thr Leu Gly Val Ala			
	420	425	430
Val Ala Gly Phe Leu Leu Gly Ile Pro Leu Thr Ser Gln Ala Gly Ile			
	435	440	445
Tyr Trp Leu Leu Leu Met Asp Asn Tyr Ala Ala Ser Phe Ser Leu Val			
	450	455	460

Val Ile Ser Cys Ile Met Cys Val Ser Ile Met Tyr Ile Tyr Gly His
 465 470 475 480
 Arg Asn Tyr Phe Gln Asp Ile Gln Met Met Leu Gly Phe Pro Pro Pro
 485 490 495
 Leu Phe Phe Gln Ile Cys Trp Arg Phe Val Ser Pro Ala Ile Ile Phe
 500 505 510
 Phe Ile Leu Ile Phe Thr Val Ile Gln Tyr Arg Pro Ile Thr Tyr Asn
 515 520 525
 His Tyr Gln Tyr Pro Gly Trp Ala Val Arg Ile Gly Phe Leu Met Ala
 530 535 540
 Leu Ser Ser Val Ile Cys Ile Pro Leu Tyr Ala Leu Phe Gln Leu Cys
 545 550 555 560
 Arg Thr Asp Gly Asp Thr Leu Leu Gln Arg Leu Lys Asn Ala Thr Lys
 565 570 575
 Pro Ser Arg Asp Trp Gly Pro Ala Leu Leu Glu His Arg Thr Gly Arg
 580 585 590
 Tyr Ala Pro Thr Thr Thr Pro Ser Pro Glu Asp Gly Phe Glu Val Gln
 595 600 605
 Pro Leu His Pro Asp Lys Ala Gln Ile Pro Ile Val Gly Ser Asn Gly
 610 615 620
 Ser Ser Arg Phe Gln Asp Ser Arg Ile
 625 630

<210> 299

<211> 1619

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (74).. (484)

<400> 299

```

gaattccgitt cgagcgccttc cagctcgcct cggctctcagc aagggcccca gactcggcctt 60
tgggtgaaaa aaa atg gcc cga acc aag cag acc gct agg aag tcc acc 109
      Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr
            1             5             10
ggt ggg aaa gcc ccc cgc aaa cag ctg gcc acc aag gcg gct cgg aaa 157
Gly Gly Lys Ala Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys
      15             20             25
agc gcg ccc tct acc ggc ggg gtg aag aag cct cac cgc tac agg cca 205
Ser Ala Pro Ser Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro
      30             35             40
ggg acc gtg gct ctg aga gag atc cgt cgt tac cag aaa tcg act gag 253
Gly Thr Val Ala Leu Arg Glu Ile Arg Arg Tyr Gln Lys Ser Thr Glu
      45             50             55             60
ctg ctc atc cgg aag ctg cca ttc cag aga ttg gtg agg gag atc gcc 301
Leu Leu Ile Arg Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala
            65             70             75
cag gat ttc aaa acc gac ttg agg ttt caa agt gca gcc atc ggt gcc 349
Gln Asp Phe Lys Thr Asp Leu Arg Phe Gln Ser Ala Ala Ile Gly Ala
            80             85             90
ctt cag gag gct agc gaa gca tac ctg gtg ggg ttg ttt gaa gat acc 397
Leu Gln Glu Ala Ser Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr
            95             100             105
aat ctg tgt gcc atc cac gcc aag aga gtc acc atc atg ccc aaa gac 445
Asn Leu Cys Ala Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp
            110             115             120

```

atc cag ttg gct cgc cgg ata cgg ggg gag aga gct taa gttgaagcgg 494
 Ile Gln Leu Ala Arg Arg Ile Arg Gly Glu Arg Ala
 125 130 135
 tttttatggc atttttagt aaattctgta aaatactttg gtttaatttg tgactttttt 554
 tgtaagaaat tgtttataat atgttgcatt tgtacttaag tcatccatc tttcactcag 614
 gatgaatggg aagagtgact gactgttcac agacctcagt gatgtgagca ctgtggctca 674
 ggagtgacaa gttgctaata cgcagaaggg atgggtgata ctcttgctt ttcattgatgc 734
 atgtttctgt atgttaatga ctgttgggt agctattaag gtactagaat tgataaatgt 794
 gtacagggtc cttttgcaat aaaactgggt atgacttgat ccaagtgttt aaccatacat 854
 cactgtgata gaatgtgggc tttttcaaag gttgaagata caagttttag ccacagtgt 914
 acagtttctt ttaaaaaaaaa aaagtaaacc tggcagctat agaatacact atgtgcattt 974
 ataatagcta ttttatatat tgtagtgttc aacattttta aattaaatgt tttacattca 1034
 caagtggigg ggagtcctgt cattaagggt tgtgtaatit agtccagtig gtatttctg 1094
 actagactgc atttgttttt aacagtagaa aaatgctaig cgtattaaac ctigcataag 1154
 tcttcattct accacatgtt cactaacccc tgacctctg gctggtaaca caacactaac 1214
 ggggatttta tttataaggg ctctagagta aaataacaag ctattcacac cagcatcatc 1274
 tattactaat ctagttagt cagcttttca ttgtgtttgg tcttaggcct agattgagtt 1334
 cggtttctgt tctttttaat ctttaagggg gaaaactgta caaggtttgt ttttcttgt 1394
 agagtttata aacatgggag taagaacaca gcttcaactt ctiggacctc tgccaatgaa 1454
 gatgggttag gttacacctg gttactatac tggcaaaatc ctttttatag agatggcctt 1514
 caagtggitt ttaaaagtat cctattgaag tttttaggtc aattatgtat gttgactaaa 1574
 tttacaaata aacttgttta ttcaaaaaaaaa aaaaaaggga attcc 1619

<210> 300

<211> 136

<212> PRT

<213> Mus musculus

<400> 300

Met Ala Arg Thr Lys Gln Thr Ala Arg Lys Ser Thr Gly Gly Lys Ala

1

5

10

15

Pro Arg Lys Gln Leu Ala Thr Lys Ala Ala Arg Lys Ser Ala Pro Ser

20

25

30

Thr Gly Gly Val Lys Lys Pro His Arg Tyr Arg Pro Gly Thr Val Ala

35

40

45

Leu Arg Glu Ile Arg Arg Tyr Gln Lys Ser Thr Glu Leu Leu Ile Arg

50

55

60

Lys Leu Pro Phe Gln Arg Leu Val Arg Glu Ile Ala Gln Asp Phe Lys

65

70

75

80

Thr Asp Leu Arg Phe Gln Ser Ala Ala Ile Gly Ala Leu Gln Glu Ala

85

90

95

Ser Glu Ala Tyr Leu Val Gly Leu Phe Glu Asp Thr Asn Leu Cys Ala

100

105

110

Ile His Ala Lys Arg Val Thr Ile Met Pro Lys Asp Ile Gln Leu Ala

115

120

125

Arg Arg Ile Arg Gly Glu Arg Ala

130

135

<210> 301

<211> 548

<212> DNA

<213> Mus musculus

<400> 301

cgcitttgta aaggccaatt tcatgaattt caagagagta ccattggggc tgcctttcta 60

acccaaactg tgtgtcttga tgacacaaca gtaaaatttg aaataatggga tacagctggt 120

caagaacggt atcatagctt agcaccaatg tactaccgag gagcacaagc agccatagtt 180

gtgtatgata tcacaaatga ggaatccttt gcgagagcaa aaaactgggt taaagaactt 240

caaaggcaag caagtcctaa tattgtgata gctttgtcag gaaacaaagc tgacttagca 300
 aataaaagag ctgttgactt ccaggaagca cagtcctatg cagatgacaa cagcttatta 360
 tttatggaga catcagctaa gacatcaatg aatgtaaatg aaatatttat ggcaatagct 420
 aaaaagctgc caaagaatga accacagaat cctgggtgcaa ctgagccaga ggacgaggag 480
 tagaccttac tgagcgtgca cagccagcca gaagccagtt gtggtggtaa ctgagctcca 540
 gtgtgaac 548

<210> 302

<211> 8601

<212> DNA

<213> Mus musculus

<400> 302

ctgcctggtg ggtatgtgca gggagagcgt tctgtgagca ggcgccacag cgctctgact 60
 ttcttcagta cgcgtgtcct cccggaggcc cgcccgaaac aagcctttcc ttccgctggc 120
 ggggccggtg gccgggtggg ggactcgagt ggggcaggcc ggccggcaaa caagccccgg 180
 gagacaggct ggccggcagc agagctctgg gccggtgtc tccaacgcgc actatcacag 240
 gcgcttagta gatgtcgtg ttgtccgtgc ttgcggcca gccggccggg ctggggaaca 300
 ctgacctgca aggaggctgc ggctcaaggc catttcaaata ctcatgtgtt ggttgtcatg 360
 tggcggcaga ggcatccaca attaccccg gaaatgtttc ctagegatgt cctttcccaa 420
 cagctctcct gctgctaata cttttttagt agattccttg atcagtgcc tgcaggagtga 480
 cagtttttat tcgagcagcg ccagcatgta catgccacca cctagcgcag acatggggac 540
 ctatggaatg caaacctgtg gactgtctcc gtccttggcc aaaagagaag tgaaccacca 600
 aaataiggggt atgaatgtac atccttata accitcaagta gacagttgga cagacccgaa 660
 cagatcttgt cgaatagagc aacctgttac acagcaagtc cccacttgct cattcaccgc 720
 caacattaaa gaagaatcca attgtgtcat gtattctgat aagcgcaaca aactcatttc 780
 tgccgaggtc ccttcgtacc agaggctggg ccccgagtct tgtcctgttg agaaccgccg 840
 ggttcctgtc cctggatatt ttagactgag tcagacctac gccaccggga aaaccgaaga 900
 gtacaataac agccccgaag gcagctccac tgtcatgtc cagctcaacc ctgctgcggc 960

ggccaagccc gagctctcgg ctgcccagct gcagatggaa aagaagatga acgaaagcgc 1020
gagcgcccag gagcccacta aagtctccca agtggagagc cccgaggcca aaggcggcct 1080
tccagaagac aggagctgcc tggctgaggt ttccgtgtcc agtcccgaag tgcaggagaa 1140
ggaaagcaaa ggtcggtaig aacagagtig ccaccccagc gcgtgcagtc cggtaaaacc 1200
tcgaaaaggg agcgctcggg tgcccagagc agagcccggg cagcggacgc cccagagccc 1260
atactccgca gtgctgtctc acccggtttt tagaaggat atccctgcct tgaaagggtc 1320
ggggcttctc tcccgtgct ccgccagcct ggcccgaagc tgtggcgctt gggcagagga 1380
caggcttgcc gggtttatca gtcttgagcc agatccgaaa tacaacaaaa gagctaaaag 1440
gagaccagcc gtttgtaaac agggctccag tgcccgtttt tctttggctc agatttgagc 1500
ccctagtitt tgccctgaac ccagggatca ttttaaggta gcctaagaca ccgtgtttgt 1560
gttcaagggt ttgcaccccg catcctgcga tctaagaggg aaaggaaatg gtttggcctg 1620
ttgggtgttg ggtggggaag cagaggtaac ctgggtttg tctggcgaaa gtgcgcaggc 1680
tttgcaatct tctacaaagg gggcaaaggc ggaggagggg gagaacagat ctgcattgcc 1740
cacctagggc tggggtaatg caaagaacca gggatatggg tttctaagaa ggaatcttga 1800
gccccacgc ccatttctgc agtctgtccc tcaactgtct cccgggtgagc cacagagtta 1860
catttctgga ggaaggcttt tgtgtgagag caaagaaaaa ttgaggaaat tctgggggga 1920
aggggggaac tgtaagaatg cccagtcagg gtggacaagg gatcctgctt cctcattatc 1980
tcttgaaaca gccctgatcc ctataaacct ggttgtggat ctcttgtct gcctaggagg 2040
ggtgggtaag aagcggccga ctggggccc tggagcagta gtgagatact ggtagatgaa 2100
gcaagctatg gttctttctg gtggcctgac ggcttagaat gtttttgggg ggacggagga 2160
atcctgtaaa gtttgctatt atagtcacat tttgtgcaag ccagaaaagt tgtgtaggag 2220
agagagagag agagagagag agagaatatg aggaggcagc ctcccagaa tctcctttca 2280
ttcatcgtgt taagtattta gttctaactt ggtaccaatt tacaatcccc ttcatgccac 2340
cttcgtaagt gatgtttaat accagcattg tccaaagcag cccatctggc agcagggtca 2400
tggccaaggg atatttgaat ggactgagag aaaaaaaaaa tcttgatttt tttttcttct 2460
ccctttaatt ttgttaggaa atcaagtctg atactccaac cagcaattgg ctactgcaa 2520
agagtggcag agagaagagg tgcccttaca ccaagcacca aacgctggaa ttggaaaaag 2580
agticttgtt caatatgtac ctaccccgcg agcgccgctt agagatcagt aagagcgtta 2640
acctcaccga caggcaggtc aagatttggg ttcaaaaccg ccgaatgaaa ctcaagaaga 2700

tgagccgaga gaatcgaatc cgagaactga ccgccaacct caccitttct taggtctgag 2760
gcccgatgtg aggccaggat ccgagagggg gcaccgagtg ttccaggcct gaggctgga 2820
ggactggcaa ggcggaaaca aacccttcat tgctcttttg tttttttgtt ttgttttgtt 2880
ctgttctgtt ctgttttcc tctagaatgt gactttgggg tcatctgtt cgtgctgcaa 2940
gtgatctgta atccctatga gtatacatat atatatatat taaaaaaact tagcacgtgt 3000
aatttatitt ttttcatcgt aatgcagggt aactattact gcgcatttca ttggggctta 3060
acttatggga actgtagaac atccatctaa acgtatccat cgcateccac ccatctatcc 3120
cgccagcaat gtgacttttc catgtttttc ctaacataaa agttctctgt gtgtgggttag 3180
cccatgaact catggcattt tgaaaacatc cagtatttaa aaaaacaaac aacctatata 3240
tatatatatt tcaaaagatt aagaaaaccc acaagctttg gggggagggg gactttaaaa 3300
agcacattac aatgtatctt ttacaaaatg aacttagcaa ttgtccttgg tgaaatggaa 3360
tattgatgac ttatgccttg tagcctttcc ttgtggtgca tctgtggttt ggtagaagta 3420
caagcgcaac ctgtgctttt ctgtgcatgt tctggctgca tgtgtaatgc aataaactct 3480
ggaaatgggt ttgtttcttc tgctttcctg aaatggaaat ccaaataaac cttttgggtg 3540
gaggaaagcc ttgggggagg gtttcttctg accaaactgc tcttcgaggg ggcagtgga 3600
taggggactg ggaggggcag gagaaaggag atgggaggag aaaaactgga gaagacctag 3660
gctgttagaa tatgcaatga tgggtttgag aagggttctg gattcagcct gagagctcag 3720
tcttcataac tgggaagacc gtctcgcct cteccccccc ctaatcttat taatataatt 3780
gtattctcaa tgggatgagc ttccctctac ccttgagcct ggtaagtaag aaccactgc 3840
aggcttttgc tccagtcctc catttgttg ttttcttctc ttgggttttg gttatgttat 3900
ttttaatgct ttcagtgagc tcttggtgac ttctggcttg ggaagcatct tcaggggcta 3960
ggttgaaact agtaatgccc acctggaacc tggctggcct ccttagcagg aacaagcaac 4020
agcttagcag ggcactggat ccaattgtgc ccccccaagt ccttttctct tcccaccg 4080
ccccaagctc aagacaacca gaccagtgga agccaagggt gggtgagttt tctcatttta 4140
ttctaccttg gtccctttct gaaaaggatt aatatctgc cattgccttt gaggggcca 4200
cagtaactat tttaaaggaa aaaaatgaaa ctattccccc agtcaaatct ctcactattt 4260
aattacaaaa ttttcatttg cagccactgt gctgagctg tcaggtgact gaaagcagtt 4320
gcaagtgacc atgactgctc aacaagtctg tccaatgggc cttttacata catgggttgg 4380
aaaattcaaa ccaacgtctg tagaatccct gtcattgagc ccacattcat cttgtgctac 4440

caggaaaaag ggaagaggig actgaactcg ttgccccaaag tctggcctcg tggtttttaa 4500
cccatcttca aagaatttca caaaacagga tccccccccc cccaacacag gcccttttcc 4560
tcccaaagaa cgggtgcattc agcgtctctg agctgcctcg ccccatccag acagtccttg 4620
ggaigctcgg tactgatitit ttaaaacctc ctctcccaga ccccaaattc tctcaaattc 4680
caagacagat cccctttaggg acgtattttt ctgaggctag cagagagaga gagagagaga 4740
gagagagaga gagagagaga gaagtgtctg attccattct agcttgagag gactggaata 4800
aatttgcccc tgacttacct tggatgggca aaagaagtag agtgatttta acctctgcgt 4860
ttctcccagc gatgtgggga gcgccattag ttgctgatgg ggggaaacct gtgctacagg 4920
aaagggcagg ccccttgaaa caaaatcaga aagccattcg ccaaggcaat caatcaggtc 4980
ctaagtagcc atttaccccc ttcttggcg gggctagagg tgggttggga gccctccaag 5040
ggtgctctgg gcaacttgta gagcgaggaa tatgtcctct cagccgcccgc tggcgtcgg 5100
ctttgtctc ggctcccagg caggctttgt accatggatt tgggagtac aatgggcatt 5160
tctctcagat tcaaggctgc ccggccctac ctctcaaggg gaaaactgga aaggggggtg 5220
atcaaggacc tgttctttcg tctggatttt gaagacatct tcagaatccg ttgacaggca 5280
cgtgtgaaag gcacgcagcg aacctaccct cggagatgag gtctctgcag gcctctctga 5340
ggctgggcta attccggcta gtgagaaccg gtctcactgg cctttaggtt tccccctctg 5400
tggcatgttt tcttgaggcg ccattccaga aggttgggga aagatgaggc accatggcca 5460
tactgtcgg ctccctggga ctccagtgt caccacccat gcgagggcag agagacagcc 5520
cttgagggcc gcccttgga agccatgctg agctggacca ggcccgagag tccagttagc 5580
ccagctcacc ccctgggcct cggggcggtg gcctagcttt ttgtcgaggg ttacatgtg 5640
gtgccccgg gagtgtgagc gcggtagagg gaggggcact ccgagctgct ccatccgtcc 5700
gttttattag ggacacatta atctataatc aaatacacct cataaaattt ttattgaaag 5760
gcataatata attacagagg tcttccacct gttttaaaca acagccaag ctgtgtgtgt 5820
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtaggg atgggtttag 5880
gtaagaaaag aggcgagggg agaacgactc cctttgggcg acaggggtcc gcccttaaag 5940
gccagcctgc ctggggcagc ccgggccccca ggagccacca actgtctcgg ggctttggat 6000
aatgccttag gtgtgactta gaagcccggc ccaggggctc agagcccagg agtcggagag 6060
ccagagtcgg ggtggagatc gcaggaccca gagaggcaag aagagatgaa caaatagtc 6120
ccagcgccctc ctgcggccgc agttaggcct gtggccgccc ccgccaccag ggcgggctga 6180

gccgggccag gccgggctgg tgcgtggacc tgggcccggc agctctaatt gcaacgctcc 6240
tgttgatgat gatTTTTTT tttttaaatc acagcagccc ccagtttagc ggactgattt 6300
actccgggta ttggtaaata tgatcacgtg ggccgcgcga ccaatgggtg tgcgcagcc 6360
tgcgaactag tcggcggctc gggcccggcg aggagcctcg gcggtgggca gtggaacctt 6420
gggtgggagc gagcggcgcc tcaccatgtc gtccagtggc accctcagca actactacgt 6480
ggactcgctc ataggccatg agggcgacga ggtgttcgcc gcgcgctttg ggccaccggg 6540
gccggggaca cagggccggc ccgcagggtg ggccgatggc ccagccgcg ccaccgccga 6600
gttcgcctcg ttagtTTTg cccccaaatc gtccgtgttc tccgcctcgt ggtccgcggt 6660
ggccgcccag ccccgggcg cggcgacgat gagcggcctg taccaccgt acgtgtcccc 6720
gccgcccctg gctgcgcgcg agccgggacg ctacgtacgc tcctggaagg agccgtgcc 6780
cggttcccc ggcggcgcag gcggtggcgg tggcagtgtt ggcgggcggt gcggagggcc 6840
gggtcccggt cccagccccg gtggcccagc caacgggcgc cactacggga ttaagcctga 6900
aaccggagcg gccccggccc ccgctgcagc ctccacctc tcctctcct ccacctctc 6960
gtctctctc tccaaaagga ctgagtgtc cgcgccccgc gattcccagg ggagcggcg 7020
cccagaattc ccgtgcaact cgttcttgcg ggacaaggca gcggcggcga cagggaacgg 7080
gcccggggtg ggaatcgga cccggccagg ggcggtaggc tcgtccgagc cctcagctt 7140
cagcgatcac ccagccccg gctgtctcgt gaaggaggag gagaagcagc cgccgcagcc 7200
gccgcagcag caacttgacc caagtaagt caaaagaaat tgccccctga ttatttgtg 7260
aaacctgtaa ggctcgaatg tgcaaaactg atagttttac taacctataa aaacgtctag 7320
acgcctaccc aagcctaggc agcaacacgt atccataaaa agcttcccat aaccacctac 7380
cttgggcggc gcggtttgta cggtaaacag agcgcgggca ttaaggcttt ttatgataat 7440
tcccccaagt tgtgaaaagc gtccatcctt ggtgaaattt atttaacgac ctctcttccc 7500
caccctgtcg tctctccctg cctccctcc gccctcgtt ccttgtctg caaaccccc 7560
tcttcttaga caaccctgca gcgaactgga tccacgctcg ctccaccgg aaaaagcgct 7620
gtccctacac caaataaccag acgctagagc tggagaagga attcctctc aacatgtacc 7680
tcaccggga ccggcgctac gaggtggcta ggattctgaa ccttacagag agacaagtca 7740
aaatctggtt ccagaaccgt aggatgaaaa tgaaaaagat gagcaaggag aagtgccta 7800
aaggagactg acccagtgcg ggtcttgcc tgcagcactc aaaaggcagc cgggtttttt 7860
ggttggttgg ttggttgggt tggTTTTTg ttttggtg tgggtggtt cctttgtggg 7920

tgccttgattc agaaactctg agcgactcgg acttcttctt tttttaggta gaagtgactg 7980
 tgtggttggt ctctctgagt tatctggggg acactgtatt tcctcgcata tgtattggag 8040
 aaaccagtgg ctttggagtc ttgtccctgc ccactccctc ccttccctgct cccctgattc 8100
 cttaggaaat gctatatatt gtgagtgac gcaggcttga tggagcccta ttctatgtaa 8160
 atgtccctca tgtttctgaa aagtgcctga gtttagtctc accctatcca gcctcccaaa 8220
 cagggccaac gatctaattc cgagaatctg aaggaagaca gagtgtggac acccccaccc 8280
 tgctctccca actaaaatcc aactcagctg ctcaaggcag gaaaacccct ttccctcggg 8340
 agccggcgga ctgacttcca cagaggcccta ccgagaaacc ttgggcccctg gggcgcgaga 8400
 ttgggggtgg ggtggggata ggcttagtcc tcagagcacc ggggaagcta ctttctcccc 8460
 gggagggctg agctcccatt gggcgggcctc gggaggttgc cttccatatt cctgcctgag 8520
 gaccagtgt aaatgttacc gcttccaaca aataaatgct gatctgaaca aaaaaaaccc 8580
 ttgaccgtaa gacatgaatt c 8601

<210> 303

<211> 505

<212> DNA

<213> Mus musculus

<400> 303

ggctgtttgt tccttgagaa tcagaccacc agaaatctgg acacctgtgc cttcagacct 60
 gacctgtggg aatggggcga tcggcacatc cctcagacac cgggagcagc tgagagagaa 120
 ggcttcagag aaagggaccc acggagaccg ttggccacgc ctgaattggg cagaccaacc 180
 tggatcttgc ctttctggag aatgcagctt caaggacctg tctttgtagg tgtgcccctg 240
 ctgggccatc ctgatttgta tgcctattca tcagccatcc agtcggtgtg aggatgagag 300
 aaagttaccc tgggtcccaac ctcaaaaggt catattgctt gtgtgggtga ccatctactc 360
 tgicattggc tatgtcctta cctggatatg aaggaactcg gagggggcct ccggtggccc 420
 ctgacactgc ccttgggtct ctactcttc cagctggccc tcagctggac tttcttgggtg 480
 ctcttccctg cagccgacag ccctg 505

<210> 304

<211> 484

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (46).. (321)

<400> 304

acacattgaa ttccctgctct ccaatcatct aggtgactcg cagcc atg aag aaa ctt 57

Met Lys Lys Leu

1

gtc ctc ctc ttt gcc ctt gtc ctg ctt gca ttc cag gtc cag gct gat 105

Val Leu Leu Phe Ala Leu Val Leu Leu Ala Phe Gln Val Gln Ala Asp

5

10

15

20

tct atc caa aac aca gat gaa gag act aaa act gag gag cag cca ggg 153

Ser Ile Gln Asn Thr Asp Glu Glu Thr Lys Thr Glu Glu Gln Pro Gly

25

30

35

gaa aag gac cag gct gtg tct gtc tct ttt gga gac cca caa ggc tct 201

Glu Lys Asp Gln Ala Val Ser Val Ser Phe Gly Asp Pro Gln Gly Ser

40

45

50

gct ctt caa gat gca gcc cta gga tgg ggt cgg cgg tgc cca caa tgc 249

Ala Leu Gln Asp Ala Ala Leu Gly Trp Gly Arg Arg Cys Pro Gln Cys

55

60

65

cct aga tgc cgg tca tgc cca tct tgc ccg aga tgc ccg agg tgc ccg 297

Pro Arg Cys Pro Ser Cys Pro Ser Cys Pro Arg Cys Pro Arg Cys Pro

70

75

80

agg tgc aaa tgc aat cca aaa taa gccatgcaatt ggcaccaaag atccaaataa 351

Arg Cys Lys Cys Asn Pro Lys

85

90

acagcataaa ttctgctgca gctgagcatg gaatctgggt caagataacc atgttctttg 411

gaacctcact atctgtcaag acccttggtc ttagccttga ttgctcttgc ttctccaata 471

aactccttgc aga

484

<210> 305

<211> 91

<212> PRT

<213> Mus musculus

<400> 305

Met Lys Lys Leu Val Leu Leu Phe Ala Leu Val Leu Leu Ala Phe Gln

1

5

10

15

Val Gln Ala Asp Ser Ile Gln Asn Thr Asp Glu Glu Thr Lys Thr Glu

20

25

30

Glu Gln Pro Gly Glu Lys Asp Gln Ala Val Ser Val Ser Phe Gly Asp

35

40

45

Pro Gln Gly Ser Ala Leu Gln Asp Ala Ala Leu Gly Trp Gly Arg Arg

50

55

60

Cys Pro Gln Cys Pro Arg Cys Pro Ser Cys Pro Ser Cys Pro Arg Cys

65

70

75

80

Pro Arg Cys Pro Arg Cys Lys Cys Asn Pro Lys

85

90

<210> 306

<211> 658

<212> DNA

<213> Mus musculus

<400> 306

gccgggccgg agctggcggg cgcgcgggccc gggagctgga ccacaagccc ctggggcagg 60
 agcgccccgcc cgcctacaac ctggaggccg gccaggggcga ctacgcgtgc ggccccgcacg 120
 gctacgggggc catccccacc gcgccccccgc cgccgccccta cccctacctc gtcacaggga 180
 tccccaccag ccacccccgg gtctataaca tccacagtcg aacggtcacc cggtatcctg 240
 ccaactccat cgtcgtggtc ggaggctgcc cggctctgcag ggttggtgtc ctggagtact 300
 gcttcacctg cctgggcata ttcctggcca tcgtcctgtt cccctttggg ttcctctgct 360
 gctttgcact gaggaagcga agatgcccc aactgtggagc ggtctttact tagagggaac 420
 agcacacca gttttcctac attcagctat gttttctaata gtaaagtgtg tgtacaatag 480
 ttttatttga ttaagcttct ggactgtttt gtaaagtgtg gcgggctaga ctggcatagg 540
 ggtgacgcaa aggtggaaag cagcgacttg cccccaaggg taagggtaac gtgcigcttc 600
 cattttggca gcctcacttt gagaatgggt ggaatactgt tgtaaaaaat gggatcat 658

<210> 307

<211> 2775

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (5).. (2665)

<400> 307

ggct atg tgg tgg ccc tgc ctt gtc ttg gct ctg ctc tct ggc ttg gag 49
 Met Trp Trp Pro Cys Leu Val Leu Ala Leu Leu Ser Gly Leu Glu
 1 5 10 15
 acc tct ggc ttt ccg aga agt ccc ctc cgg ctg ctt ggg aaa cgg agc 97
 Thr Ser Gly Phe Pro Arg Ser Pro Leu Arg Leu Leu Gly Lys Arg Ser

20	25	30	
cic cca gag ggg gtg gtg gat ggc att gag gtt tac agc acc aag atc			145
Leu Pro Glu Gly Val Val Asp Gly Ile Glu Val Tyr Ser Thr Lys Ile			
35	40	45	
agc tgc aag gig acc tcc cgc ttt gct cac aat gtt gtc acc aca agg			193
Ser Cys Lys Val Thr Ser Arg Phe Ala His Asn Val Val Thr Thr Arg			
50	55	60	
gct gtc aac cgt gca gac aca gcc aag gag gtg tcc ttt gat gtg gaa			241
Ala Val Asn Arg Ala Asp Thr Ala Lys Glu Val Ser Phe Asp Val Glu			
65	70	75	
ctg ccc aag aca gcc ttc atc acc aac ttc acc ttg acc att gat ggt			289
Leu Pro Lys Thr Ala Phe Ile Thr Asn Phe Thr Leu Thr Ile Asp Gly			
80	85	90	95
gtc acc tac ccc ggg aac gtc aag gag aag gaa gtt gcc cag aaa caa			337
Val Thr Tyr Pro Gly Asn Val Lys Glu Lys Glu Val Ala Gln Lys Gln			
100	105	110	
tat gaa aag gct gtg tcc cag ggc aag aca gcc ggt ttg gtc aag gcc			385
Tyr Glu Lys Ala Val Ser Gln Gly Lys Thr Ala Gly Leu Val Lys Ala			
115	120	125	
tct ggg agg aaa ctg gag aaa ttc aca gtg tct gtc aac gtg gct gca			433
Ser Gly Arg Lys Leu Glu Lys Phe Thr Val Ser Val Asn Val Ala Ala			
130	135	140	
ggc agc aaa gtc acc ttt gag cta acc tat gaa gaa ctg ctc aag aga			481
Gly Ser Lys Val Thr Phe Glu Leu Thr Tyr Glu Glu Leu Leu Lys Arg			
145	150	155	
aac aag ggc aag tac gag atg tac ctt aag gtc cag ccc aaa caa ctg			529
Asn Lys Gly Lys Tyr Glu Met Tyr Leu Lys Val Gln Pro Lys Gln Leu			
160	165	170	175
gtc aga cac ttt gag att gat gca cac atc ttc gag cca cag ggc att			577

Val Arg His Phe Glu Ile Asp Ala His Ile Phe Glu Pro Gln Gly Ile	
180	185
190	
agc atg cta gat gct gaa gcc tca ttc atc act aat gac ctc ctg gga	625
Ser Met Leu Asp Ala Glu Ala Ser Phe Ile Thr Asn Asp Leu Leu Gly	
195	200
205	
agc gcc ctc acc aag tcc ttc tca ggc aag aag ggg cac gtg tct ttc	673
Ser Ala Leu Thr Lys Ser Phe Ser Gly Lys Lys Gly His Val Ser Phe	
210	215
220	
aag ccc agc tta gac cag cag cgt tca tgc ccg acc tgt aca gac tcc	721
Lys Pro Ser Leu Asp Gln Gln Arg Ser Cys Pro Thr Cys Thr Asp Ser	
225	230
235	
ctc ctc aac ggg gac ttc acc att gtc tac gat gtg aac aga gag tct	769
Leu Leu Asn Gly Asp Phe Thr Ile Val Tyr Asp Val Asn Arg Glu Ser	
240	245
250	255
cca ggg aat gtg cag ata gtc aat ggc tac ttt gtg cac ttc ttt gca	817
Pro Gly Asn Val Gln Ile Val Asn Gly Tyr Phe Val His Phe Phe Ala	
260	265
270	
ccc caa ggc ctt cca gtg gtc cct aag aac ata gtc ttt gtg att gat	865
Pro Gln Gly Leu Pro Val Val Pro Lys Asn Ile Val Phe Val Ile Asp	
275	280
285	
gtc agc ggc tcc atg tct ggt cgg aaa atc cag cag acc agg gaa gcc	913
Val Ser Gly Ser Met Ser Gly Arg Lys Ile Gln Gln Thr Arg Glu Ala	
290	295
300	
ctt ctt aaa atc ctg gat gac gtg aaa gaa gat gac tac ctg aat ttc	961
Leu Leu Lys Ile Leu Asp Asp Val Lys Glu Asp Asp Tyr Leu Asn Phe	
305	310
315	
att ctc ttc agc acc gat gtg acc acc tgg aaa gat cac cta gtt caa	1009
Ile Leu Phe Ser Thr Asp Val Thr Thr Trp Lys Asp His Leu Val Gln	
320	325
330	335

```

gcc acc cct gca aac ctc aag gag gcc aag aca ttt gtg aag aac atc 1057
Ala Thr Pro Ala Asn Leu Lys Glu Ala Lys Thr Phe Val Lys Asn Ile
          340          345          350
cat gat caa agc atg acc aac atc aat gat ggg ctg ctg aag ggt att 1105
His Asp Gln Ser Met Thr Asn Ile Asn Asp Gly Leu Leu Lys Gly Ile
          355          360          365
gaa atg ctg aac aag gcc cga gag gac cac act gtc cca gag agg agc 1153
Glu Met Leu Asn Lys Ala Arg Glu Asp His Thr Val Pro Glu Arg Ser
          370          375          380
acc tcc atc atc atc atg ttg aca gac ggg gat gcc aat act ggc gag 1201
Thr Ser Ile Ile Ile Met Leu Thr Asp Gly Asp Ala Asn Thr Gly Glu
          385          390          395
agc aga cca gaa aag atc cag gaa aac gtc cgg aat gcc atc ggg ggc 1249
Ser Arg Pro Glu Lys Ile Gln Glu Asn Val Arg Asn Ala Ile Gly Gly
400          405          410          415
aag ttc cct ttg tat aac ctg ggt ttt ggc aac aat ctg aat tat aat 1297
Lys Phe Pro Leu Tyr Asn Leu Gly Phe Gly Asn Asn Leu Asn Tyr Asn
          420          425          430
ttc ctg gag act ctg gcc ctg gag aac cat ggg ctt gcc cgg cgc att 1345
Phe Leu Glu Thr Leu Ala Leu Glu Asn His Gly Leu Ala Arg Arg Ile
          435          440          445
tat gaa gat tct gat gcc aac ttg cag ctg cag ggc ttc tat gaa gag 1393
Tyr Glu Asp Ser Asp Ala Asn Leu Gln Leu Gln Gly Phe Tyr Glu Glu
          450          455          460
gta gct aat cca ctg ctg act aat gtg gag gtg gaa tac ccc gag aac 1441
Val Ala Asn Pro Leu Leu Thr Asn Val Glu Val Glu Tyr Pro Glu Asn
          465          470          475
gcc atc cta gac ctc acc agg aac agt tac ccc cac ttc tac gat ggc 1489
Ala Ile Leu Asp Leu Thr Arg Asn Ser Tyr Pro His Phe Tyr Asp Gly

```

480	485	490	495	
tct gag att gtt gta gca ggg cgc ctg gtg gac agg aac atg gac aac	1537			
Ser Glu Ile Val Val Ala Gly Arg Leu Val Asp Arg Asn Met Asp Asn				
500	505	510		
ttc aaa gca gat gtg aag ggc cat ggg gcc ttg aat gac ctg acc ttc	1585			
Phe Lys Ala Asp Val Lys Gly His Gly Ala Leu Asn Asp Leu Thr Phe				
515	520	525		
aca gag gag gta gac atg gag gaa atg gat gca gcc ctg aag gag caa	1633			
Thr Glu Glu Val Asp Met Glu Glu Met Asp Ala Ala Leu Lys Glu Gln				
530	535	540		
ggc tac att ttt ggg gac tac att gag cga ctc tgg gcc tac ctc act	1681			
Gly Tyr Ile Phe Gly Asp Tyr Ile Glu Arg Leu Trp Ala Tyr Leu Thr				
545	550	555		
att gag cag cta ctg gag aaa cgc aag aat gcc aaa ggg gat gag aag	1729			
Ile Glu Gln Leu Leu Glu Lys Arg Lys Asn Ala Lys Gly Asp Glu Lys				
560	565	570	575	
gag aac atc aca gcg gag gcc ctg gat ctg tcc ctc aag tac cac ttt	1777			
Glu Asn Ile Thr Ala Glu Ala Leu Asp Leu Ser Leu Lys Tyr His Phe				
580	585	590		
gta acc cca ctg acc tcc atg gtg gtg acc aag cct gag gac aat gaa	1825			
Val Thr Pro Leu Thr Ser Met Val Val Thr Lys Pro Glu Asp Asn Glu				
595	600	605		
gac cag aca tcc att gct gac aac gct ggg gaa gaa gcc ttc gct gag	1873			
Asp Gln Thr Ser Ile Ala Asp Asn Ala Gly Glu Glu Ala Phe Ala Glu				
610	615	620		
acc acg acc atg tcc ttc ttg acc act cag cag tcc agt cag agc ccc	1921			
Thr Thr Thr Met Ser Phe Leu Thr Thr Gln Gln Ser Ser Gln Ser Pro				
625	630	635		
tac tat tat gtg gat ggg gac ccc cac ttt atc atc caa atc ccg gga	1969			

gca cag aca cat ggg ctg ctg ggc cag ttc ttc caa ccc ttt gac ttt 2449
 Ala Gln Thr His Gly Leu Leu Gly Gln Phe Phe Gln Pro Phe Asp Phe
 800 805 810 815
 aaa gtg ttt ggc atc cgc cca ggc tct gac cct aca aag cca gat gcc 2497
 Lys Val Phe Gly Ile Arg Pro Gly Ser Asp Pro Thr Lys Pro Asp Ala
 820 825 830
 aca atg gtg gtg aag aat cat cgg ttg act gtc aca agg ggc tcc cag 2545
 Thr Met Val Val Lys Asn His Arg Leu Thr Val Thr Arg Gly Ser Gln
 835 840 845
 aaa gat tac agg aag gat gcc agt gtt ggc acc aag gtc atc tgc tgg 2593
 Lys Asp Tyr Arg Lys Asp Ala Ser Val Gly Thr Lys Val Ile Cys Trp
 850 855 860
 ttt gtc cat aac aat gga gaa gga cta att gat ggt gtc cat acc gac 2641
 Phe Val His Asn Asn Gly Glu Gly Leu Ile Asp Gly Val His Thr Asp
 865 870 875
 tat att gtc ccc agc ttg ttc tga gtagcatgtc agctgctgat gaagtagaag 2695
 Tyr Ile Val Pro Ser Leu Phe
 880 885
 gcctgggtgg cctggaaaaa ggacacagaa tggggcttgt gggaaagacc gggacagtaa 2755
 agcccaccat gtaaaccaaa 2775

<210> 308

<211> 886

<212> PRT

<213> Mus musculus

<400> 308

Met Trp Trp Pro Cys Leu Val Leu Ala Leu Leu Ser Gly Leu Glu Thr

1

5

10

15

Ser Gly Phe Pro Arg Ser Pro Leu Arg Leu Leu Gly Lys Arg Ser Leu
 20 25 30
 Pro Glu Gly Val Val Asp Gly Ile Glu Val Tyr Ser Thr Lys Ile Ser
 35 40 45
 Cys Lys Val Thr Ser Arg Phe Ala His Asn Val Val Thr Thr Arg Ala
 50 55 60
 Val Asn Arg Ala Asp Thr Ala Lys Glu Val Ser Phe Asp Val Glu Leu
 65 70 75 80
 Pro Lys Thr Ala Phe Ile Thr Asn Phe Thr Leu Thr Ile Asp Gly Val
 85 90 95
 Thr Tyr Pro Gly Asn Val Lys Glu Lys Glu Val Ala Gln Lys Gln Tyr
 100 105 110
 Glu Lys Ala Val Ser Gln Gly Lys Thr Ala Gly Leu Val Lys Ala Ser
 115 120 125
 Gly Arg Lys Leu Glu Lys Phe Thr Val Ser Val Asn Val Ala Ala Gly
 130 135 140
 Ser Lys Val Thr Phe Glu Leu Thr Tyr Glu Glu Leu Leu Lys Arg Asn
 145 150 155 160
 Lys Gly Lys Tyr Glu Met Tyr Leu Lys Val Gln Pro Lys Gln Leu Val
 165 170 175
 Arg His Phe Glu Ile Asp Ala His Ile Phe Glu Pro Gln Gly Ile Ser
 180 185 190
 Met Leu Asp Ala Glu Ala Ser Phe Ile Thr Asn Asp Leu Leu Gly Ser
 195 200 205
 Ala Leu Thr Lys Ser Phe Ser Gly Lys Lys Gly His Val Ser Phe Lys
 210 215 220
 Pro Ser Leu Asp Gln Gln Arg Ser Cys Pro Thr Cys Thr Asp Ser Leu
 225 230 235 240
 Leu Asn Gly Asp Phe Thr Ile Val Tyr Asp Val Asn Arg Glu Ser Pro

	245		250		255
Gly Asn Val Gln Ile Val Asn Gly Tyr Phe Val His Phe Phe Ala Pro					
	260		265		270
Gln Gly Leu Pro Val Val Pro Lys Asn Ile Val Phe Val Ile Asp Val					
	275		280		285
Ser Gly Ser Met Ser Gly Arg Lys Ile Gln Gln Thr Arg Glu Ala Leu					
	290		295		300
Leu Lys Ile Leu Asp Asp Val Lys Glu Asp Asp Tyr Leu Asn Phe Ile					
305		310		315	320
Leu Phe Ser Thr Asp Val Thr Thr Trp Lys Asp His Leu Val Gln Ala					
	325		330		335
Thr Pro Ala Asn Leu Lys Glu Ala Lys Thr Phe Val Lys Asn Ile His					
	340		345		350
Asp Gln Ser Met Thr Asn Ile Asn Asp Gly Leu Leu Lys Gly Ile Glu					
	355		360		365
Met Leu Asn Lys Ala Arg Glu Asp His Thr Val Pro Glu Arg Ser Thr					
	370		375		380
Ser Ile Ile Ile Met Leu Thr Asp Gly Asp Ala Asn Thr Gly Glu Ser					
385		390		395	400
Arg Pro Glu Lys Ile Gln Glu Asn Val Arg Asn Ala Ile Gly Gly Lys					
	405		410		415
Phe Pro Leu Tyr Asn Leu Gly Phe Gly Asn Asn Leu Asn Tyr Asn Phe					
	420		425		430
Leu Glu Thr Leu Ala Leu Glu Asn His Gly Leu Ala Arg Arg Ile Tyr					
	435		440		445
Glu Asp Ser Asp Ala Asn Leu Gln Leu Gln Gly Phe Tyr Glu Glu Val					
	450		455		460
Ala Asn Pro Leu Leu Thr Asn Val Glu Val Glu Tyr Pro Glu Asn Ala					
465		470		475	480

Ile	Leu	Asp	Leu	Thr	Arg	Asn	Ser	Tyr	Pro	His	Phe	Tyr	Asp	Gly	Ser
				485					490					495	
Glu	Ile	Val	Val	Ala	Gly	Arg	Leu	Val	Asp	Arg	Asn	Met	Asp	Asn	Phe
				500					505					510	
Lys	Ala	Asp	Val	Lys	Gly	His	Gly	Ala	Leu	Asn	Asp	Leu	Thr	Phe	Thr
				515					520					525	
Glu	Glu	Val	Asp	Met	Glu	Glu	Met	Asp	Ala	Ala	Leu	Lys	Glu	Gln	Gly
				530					535					540	
Tyr	Ile	Phe	Gly	Asp	Tyr	Ile	Glu	Arg	Leu	Trp	Ala	Tyr	Leu	Thr	Ile
545									550					555	560
Glu	Gln	Leu	Leu	Glu	Lys	Arg	Lys	Asn	Ala	Lys	Gly	Asp	Glu	Lys	Glu
									565					570	575
Asn	Ile	Thr	Ala	Glu	Ala	Leu	Asp	Leu	Ser	Leu	Lys	Tyr	His	Phe	Val
									580					585	590
Thr	Pro	Leu	Thr	Ser	Met	Val	Val	Thr	Lys	Pro	Glu	Asp	Asn	Glu	Asp
									595					600	605
Gln	Thr	Ser	Ile	Ala	Asp	Asn	Ala	Gly	Glu	Glu	Ala	Phe	Ala	Glu	Thr
									610					615	620
Thr	Thr	Met	Ser	Phe	Leu	Thr	Thr	Gln	Gln	Ser	Ser	Gln	Ser	Pro	Tyr
625														630	635
Tyr	Tyr	Val	Asp	Gly	Asp	Pro	His	Phe	Ile	Ile	Gln	Ile	Pro	Gly	Lys
									645					650	655
Asn	Asp	Ser	Ile	Cys	Phe	Asn	Ile	Asp	Glu	Lys	Pro	Gly	Thr	Val	Leu
									660					665	670
Arg	Leu	Ile	Gln	Asp	Pro	Val	Thr	Gly	Ile	Thr	Val	Thr	Gly	Gln	Ile
									675					680	685
Ile	Gly	Asp	Lys	Arg	Ser	Asn	Ala	Ser	Ser	Arg	Thr	Gly	Lys	Thr	Tyr
									690					695	700
Phe	Gly	Lys	Leu	Gly	Ile	Thr	Asn	Ala	Trp	Met	Asp	Phe	Arg	Val	Glu

705 710 715 720
 Val Thr Thr Glu Lys Ile Ile Leu Gly Thr Gly Ala Glu Leu Ser Thr
 725 730 735
 Phe Ser Trp Leu Asp Thr Val Thr Val Thr Gln Thr Gly Leu Ser Val
 740 745 750
 Thr Ile Asn Arg Lys Lys Asn Met Val Val Ser Phe Gly Asp Gly Ile
 755 760 765
 Ser Phe Val Ile Ile Leu His Gln Val Trp Lys Lys His Pro Val His
 770 775 780
 Gln Asp Phe Leu Gly Phe Tyr Val Val Asp Ser His Arg Met Ser Ala
 785 790 795 800
 Gln Thr His Gly Leu Leu Gly Gln Phe Phe Gln Pro Phe Asp Phe Lys
 805 810 815
 Val Phe Gly Ile Arg Pro Gly Ser Asp Pro Thr Lys Pro Asp Ala Thr
 820 825 830
 Met Val Val Lys Asn His Arg Leu Thr Val Thr Arg Gly Ser Gln Lys
 835 840 845
 Asp Tyr Arg Lys Asp Ala Ser Val Gly Thr Lys Val Ile Cys Trp Phe
 850 855 860
 Val His Asn Asn Gly Glu Gly Leu Ile Asp Gly Val His Thr Asp Tyr
 865 870 875 880
 Ile Val Pro Ser Leu Phe
 885

<210> 309

<211> 460

<212> DNA

<213> Mus musculus

<400> 309

ggctgaggct ccggggaaga tcccaccgcg gaaacgggta caagagtgcg tcctttcctg 60
tccttgtcag ccccttggcc ttiggattgg cgtcaaagat cagttgctct ttaaataatt 120
aagccgcgat atgggccttg tggacagact ttcaggtttg ctiggcctga agaagaagga 180
ggttcatggt ctgtgccttg ggctggataa cagtgggaaa accacaatca ttaacaagct 240
gaagccttcc aacgctcaat ctcaagatat agttccaacc ataggattta gcatagagaa 300
attcaagtcc tccagtttgt cttttacagt gtttgacatg tcaggtaag gaaggtacag 360
gaatctctgg gaacactatt ataaagatgg acaagccatt atttttgtca ttgatagtag 420
tgataagtta agaatgggtg tggcaaagaa gagcttgata 460

<210> 310

<211> 70

<212> DNA

<213> Mus musculus

<400> 310

gtctgtcaac gtcaaccgca gcgtgtcaga ccagttctat cgctacaaga tgccccgttt 60
gattctaaag 70

<210> 311

<211> 3424

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (75).. (2744)

<400> 311

attaacttcc tcgcctgtgt gctccgggaa ctgcactgtg agcgtttttc agagacacgt 60
 gaccatcaat aagc atg aag aac cca ttt gca cac ctt gct gag ccc ttg 110
 Met Lys Asn Pro Phe Ala His Leu Ala Glu Pro Leu
 1 5 10
 gac gct gcc caa cca gga aag agg ttc ttc aac ttg aat aaa ttg gag 158
 Asp Ala Ala Gln Pro Gly Lys Arg Phe Phe Asn Leu Asn Lys Leu Glu
 15 20 25
 gac tca aga tac gga cgc tta cca ttt tct atc aga gtt ctc ctg gag 206
 Asp Ser Arg Tyr Gly Arg Leu Pro Phe Ser Ile Arg Val Leu Leu Glu
 30 35 40
 gca gcc gtt cgg aac tgt gat gag ttt ctg gtg aag aaa aat gac atc 254
 Ala Ala Val Arg Asn Cys Asp Glu Phe Leu Val Lys Lys Asn Asp Ile
 45 50 55 60
 gag aat atc ctg aat tgg aat gtc atg caa cat aag aac ata gaa gtg 302
 Glu Asn Ile Leu Asn Trp Asn Val Met Gln His Lys Asn Ile Glu Val
 65 70 75
 ccg ttt aag cca gcc cga gtc ata ctg caa gac ttt acg ggt gtg cct 350
 Pro Phe Lys Pro Ala Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro
 80 85 90
 gct gtg gtg gat ttt gca gca atg cgc gat gct gtg aag aag ttg gga 398
 Ala Val Val Asp Phe Ala Ala Met Arg Asp Ala Val Lys Lys Leu Gly
 95 100 105
 ggg aat ccg gag aaa att aac cct gtc tgc ccc gct gac ctt gta att 446
 Gly Asn Pro Glu Lys Ile Asn Pro Val Cys Pro Ala Asp Leu Val Ile
 110 115 120
 gat cat tcc atc cag gtt gat ttc aac aga agg gca gac agt tta cag 494
 Asp His Ser Ile Gln Val Asp Phe Asn Arg Arg Ala Asp Ser Leu Gln
 125 130 135 140
 aag aat caa gac ctg gag ttt gaa aga aat aaa gaa cga ttt gaa ttt 542

Lys Asn Gln Asp Leu Glu Phe Glu Arg Asn Lys Glu Arg Phe Glu Phe
 145 150 155
 cta aag tgg ggt tcc cag gcc ttt tgc aac atg cgg ata atc cct cct 590
 Leu Lys Trp Gly Ser Gln Ala Phe Cys Asn Met Arg Ile Ile Pro Pro
 160 165 170
 ggc tcg gga atc att cac caa gtg aac ctg gag tat ttg gca aga gta 638
 Gly Ser Gly Ile Ile His Gln Val Asn Leu Glu Tyr Leu Ala Arg Val
 175 180 185
 gtg ttt gat cag gat gga tgc tac tac cca gac agc ctc gtg ggc aca 686
 Val Phe Asp Gln Asp Gly Cys Tyr Tyr Pro Asp Ser Leu Val Gly Thr
 190 195 200
 gat tca cac acg acc atg att gac ggc ctg gga gtt ctt ggt tgg ggt 734
 Asp Ser His Thr Thr Met Ile Asp Gly Leu Gly Val Leu Gly Trp Gly
 205 210 215 220
 gtg ggt ggt att gaa gca gaa gct gtc atg ctg ggt cag ccc atc agc 782
 Val Gly Gly Ile Glu Ala Glu Ala Val Met Leu Gly Gln Pro Ile Ser
 225 230 235
 atg gtg ctt ccc cag gtg att ggc tac aag ctg atg ggg aag cct cac 830
 Met Val Leu Pro Gln Val Ile Gly Tyr Lys Leu Met Gly Lys Pro His
 240 245 250
 cct ctg gtg aca tcc acg gac atc gtg ctc acc att acc aag cac ctc 878
 Pro Leu Val Thr Ser Thr Asp Ile Val Leu Thr Ile Thr Lys His Leu
 255 260 265
 cga caa gtg gga gtt gtg ggc aaa ttt gtg gag ttt ttc ggg cca gga 926
 Arg Gln Val Gly Val Val Gly Lys Phe Val Glu Phe Phe Gly Pro Gly
 270 275 280
 gtg gct cag ctg tcc att gct gac cga gct acg att gcc aat atg tgc 974
 Val Ala Gln Leu Ser Ile Ala Asp Arg Ala Thr Ile Ala Asn Met Cys
 285 290 295 300

cca gag tat ggt gcg aca gca gcc ttc ttc ccg gtt gat gaa gtt agc 1022
 Pro Glu Tyr Gly Ala Thr Ala Ala Phe Phe Pro Val Asp Glu Val Ser
 305 310 315
 atc gcg tac ctg ctg cag aca ggc cgc gag gaa gac aaa gtc aag cac 1070
 Ile Ala Tyr Leu Leu Gln Thr Gly Arg Glu Glu Asp Lys Val Lys His
 320 325 330
 att cag aag tat ctt cag gct gta ggc atg ttt cga gat ttc aac gac 1118
 Ile Gln Lys Tyr Leu Gln Ala Val Gly Met Phe Arg Asp Phe Asn Asp
 335 340 345
 acc tct caa gac cca gac ttc act cag gtt gtg gag tta gat ctg aaa 1166
 Thr Ser Gln Asp Pro Asp Phe Thr Gln Val Val Glu Leu Asp Leu Lys
 350 355 360
 aca gtt gtg cct tgc tgc agt gga ccc aaa aga cct cag gac aaa gtc 1214
 Thr Val Val Pro Cys Cys Ser Gly Pro Lys Arg Pro Gln Asp Lys Val
 365 370 375 380
 gcg gtg tct gag atg aaa aag gac ttt gaa agc tgc ctt gga gcc aag 1262
 Ala Val Ser Glu Met Lys Lys Asp Phe Glu Ser Cys Leu Gly Ala Lys
 385 390 395
 caa gga ttt aaa ggt ttc caa gtt gct cca gac cgt cac aat gac cgc 1310
 Gln Gly Phe Lys Gly Phe Gln Val Ala Pro Asp Arg His Asn Asp Arg
 400 405 410
 aag acg ttc ctc tat agt aac agt gaa ttc act ctc gct cat ggc tct 1358
 Lys Thr Phe Leu Tyr Ser Asn Ser Glu Phe Thr Leu Ala His Gly Ser
 415 420 425
 gtg gta atc gct gcc atc act acg tgc aca aac acc agc aat cca tcc 1406
 Val Val Ile Ala Ala Ile Thr Thr Cys Thr Asn Thr Ser Asn Pro Ser
 430 435 440
 gtg atg tta gga gca gga ttg tta gca aag aaa gct gtg gag gcg ggg 1454
 Val Met Leu Gly Ala Gly Leu Leu Ala Lys Lys Ala Val Glu Ala Gly

445	450	455	460	
ctg agt gtg aag cct tac atc aaa acc agc ctg tct cct gga agt gga	1502			
Leu Ser Val Lys Pro Tyr Ile Lys Thr Ser Leu Ser Pro Gly Ser Gly				
	465	470	475	
gtg gtc acc tac tac ctt cga gag agt gga gtc atg cct tac ctg tcc	1550			
Val Val Thr Tyr Tyr Leu Arg Glu Ser Gly Val Met Pro Tyr Leu Ser				
	480	485	490	
cag tta ggg ttt gat gtg gtg ggc tac ggc tgc atg acc tgc atc ggc	1598			
Gln Leu Gly Phe Asp Val Val Gly Tyr Gly Cys Met Thr Cys Ile Gly				
	495	500	505	
aac agt gga ccc ctt cct gaa cct gtg gtc gag gca atc acc cag gga	1646			
Asn Ser Gly Pro Leu Pro Glu Pro Val Val Glu Ala Ile Thr Gln Gly				
	510	515	520	
gac ctc gta gct gtt ggc gtt ctg tct ggg aat agg aat ttt gaa ggc	1694			
Asp Leu Val Ala Val Gly Val Leu Ser Gly Asn Arg Asn Phe Glu Gly				
	525	530	535	540
cga gtc cat cct aac aca cga gcc aac tac tta gca tcc ccc cct ctg	1742			
Arg Val His Pro Asn Thr Arg Ala Asn Tyr Leu Ala Ser Pro Pro Leu				
	545	550	555	
gta ata gca tat gcg att gca ggc acc gtc agg att gac ttc gag aaa	1790			
Val Ile Ala Tyr Ala Ile Ala Gly Thr Val Arg Ile Asp Phe Glu Lys				
	560	565	570	
gag cct ttg gga gtg aac gca cag ggc cgg caa gtg ttt ctg aag gac	1838			
Glu Pro Leu Gly Val Asn Ala Gln Gly Arg Gln Val Phe Leu Lys Asp				
	575	580	585	
atc tgg ccc acg cga gat gag atc cag gcg gtg gaa agg cag cat gtc	1886			
Ile Trp Pro Thr Arg Asp Glu Ile Gln Ala Val Glu Arg Gln His Val				
	590	595	600	
atc ccc ggg atg ttt aag gag gtc tat cag aaa ata gag act gta aac	1934			

Ile Pro Gly Met Phe Lys Glu Val Tyr Gln Lys Ile Glu Thr Val Asn
 605 610 615 620
 aaa agc tgg aat gcc tta gca gcc ccg tca gag aag ctg tat gcg tgg 1982
 Lys Ser Trp Asn Ala Leu Ala Ala Pro Ser Glu Lys Leu Tyr Ala Trp
 625 630 635
 aat ccc aaa tct act tac att aag tgc cca cca ttc ttt gaa agc ttg 2030
 Asn Pro Lys Ser Thr Tyr Ile Lys Ser Pro Pro Phe Phe Glu Ser Leu
 640 645 650
 act tta gat ctc cag cca ccc aag tcc ata gtg gat gcc tat gtg cta 2078
 Thr Leu Asp Leu Gln Pro Pro Lys Ser Ile Val Asp Ala Tyr Val Leu
 655 660 665
 ctg aat tta gga gat tca gta aca acg gac cat atc tct ccc gcc ggc 2126
 Leu Asn Leu Gly Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Gly
 670 675 680
 aat att gca aga aac agc cct gcg gct cgc tac ttg acg aac aga ggc 2174
 Asn Ile Ala Arg Asn Ser Pro Ala Ala Arg Tyr Leu Thr Asn Arg Gly
 685 690 695 700
 cta aca cca cga gag ttc aac tcc tat ggc tcc cgc cgg ggt aac gac 2222
 Leu Thr Pro Arg Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly Asn Asp
 705 710 715
 gcc atc atg gcc cgg ggg aca ttt gcc aac att cgc ttg ctg aac aag 2270
 Ala Ile Met Ala Arg Gly Thr Phe Ala Asn Ile Arg Leu Leu Asn Lys
 720 725 730
 ttt ctg aac aag cag gca cct cag act gtc cat ctc ccc tca gga gaa 2318
 Phe Leu Asn Lys Gln Ala Pro Gln Thr Val His Leu Pro Ser Gly Glu
 735 740 745
 acc ctt gat gta ttc gac gct gct gag cgg tac cag cag gct gga ctt 2366
 Thr Leu Asp Val Phe Asp Ala Ala Glu Arg Tyr Gln Gln Ala Gly Leu
 750 755 760


```

ccc ctg att gtt ctg gct ggg aaa gaa tac ggt tca ggc agc tcc cga 2414
Pro Leu Ile Val Leu Ala Gly Lys Glu Tyr Gly Ser Gly Ser Ser Arg
765          770          775          780
gac tgg gca gcc aaa ggc cct ttc ctg ctg gga atc aaa gct gtc ctg 2462
Asp Trp Ala Ala Lys Gly Pro Phe Leu Leu Gly Ile Lys Ala Val Leu
          785          790          795
gca gag agc tat gag cgc att cac cgc agc aac ttg gtt ggc atg ggg 2510
Ala Glu Ser Tyr Glu Arg Ile His Arg Ser Asn Leu Val Gly Met Gly
          800          805          810
gig atc ccc ctt gag tat ctc cct ggt gaa act gca gac tct ctg gga 2558
Val Ile Pro Leu Glu Tyr Leu Pro Gly Glu Thr Ala Asp Ser Leu Gly
          815          820          825
ctc aca ggt cgg gaa aga tac act atc aac atc cct gaa gac ctc aag 2606
Leu Thr Gly Arg Glu Arg Tyr Thr Ile Asn Ile Pro Glu Asp Leu Lys
          830          835          840
cct cgc atg acg gtg cag atc aag ctg gac act ggg aag acc ttc cag 2654
Pro Arg Met Thr Val Gln Ile Lys Leu Asp Thr Gly Lys Thr Phe Gln
          845          850          855          860
gcc gtg atg agg ttc gac act gat gtg gag ctc acg tac ttc cac aat 2702
Ala Val Met Arg Phe Asp Thr Asp Val Glu Leu Thr Tyr Phe His Asn
          865          870          875
gga ggc atc ctg aac tac atg atc cga aag atg gcc cag tag 2744
Gly Gly Ile Leu Asn Tyr Met Ile Arg Lys Met Ala Gln
          880          885          890
gtgctgacct ctgaggagac ccgcacttgg tgctagaccc aatgaggaac aggccccac 2804
tggtggaggc ctggcagagc agccacatct acttctgatg agggtgctgg caggatgagc 2864
aagtgggcac tgccattcct ggaggcacag agccaggagt ctctagtitt gtgatttgtt 2924
catcttttta tccctttctg taatctggat tctagaatca cgggaaggtc ctagtacca 2984
aagagaactc gcttctcttt aaagtcacgg acattgattt tttccctct gactaatctt 3044

```

gagctcagca ctagccagta ttctcagaag tggctcctac cctttctgtt gttctgtgtt 3104
 tgctctgtct cggtagacacc cttccctgga gagcccagtc ctccgtgtat tacaccagtg 3164
 ttaactgaca tagcatagac cttcttcaca cttcagattc atagcagcga tgggatccct 3224
 tcctttgaag tgaacaagtc cttgtagata ggtcacccgt caaaagtgtt tgattatcta 3284
 cctttcaatc aacatgagat tgcctcttac cattttcaac gattgttgac aggggtcctt 3344
 tgtttgaaaa taactgggga gagatacggg atttctaatt tgaataagat taaatatatt 3404
 ttcatgaaaa aaaaaaaaaa 3424

<210> 312

<211> 889

<212> PRT

<213> Mus musculus

<400> 312

Met Lys Asn Pro Phe Ala His Leu Ala Glu Pro Leu Asp Ala Ala Gln
 1 5 10 15
 Pro Gly Lys Arg Phe Phe Asn Leu Asn Lys Leu Glu Asp Ser Arg Tyr
 20 25 30
 Gly Arg Leu Pro Phe Ser Ile Arg Val Leu Leu Glu Ala Ala Val Arg
 35 40 45
 Asn Cys Asp Glu Phe Leu Val Lys Lys Asn Asp Ile Glu Asn Ile Leu
 50 55 60
 Asn Trp Asn Val Met Gln His Lys Asn Ile Glu Val Pro Phe Lys Pro
 65 70 75 80
 Ala Arg Val Ile Leu Gln Asp Phe Thr Gly Val Pro Ala Val Val Asp
 85 90 95
 Phe Ala Ala Met Arg Asp Ala Val Lys Lys Leu Gly Gly Asn Pro Glu
 100 105 110
 Lys Ile Asn Pro Val Cys Pro Ala Asp Leu Val Ile Asp His Ser Ile

115	120	125
Gln Val Asp Phe Asn Arg Arg Ala Asp Ser Leu Gln Lys Asn Gln Asp		
130	135	140
Leu Glu Phe Glu Arg Asn Lys Glu Arg Phe Glu Phe Leu Lys Trp Gly		
145	150	155
Ser Gln Ala Phe Cys Asn Met Arg Ile Ile Pro Pro Gly Ser Gly Ile		
165	170	175
Ile His Gln Val Asn Leu Glu Tyr Leu Ala Arg Val Val Phe Asp Gln		
180	185	190
Asp Gly Cys Tyr Tyr Pro Asp Ser Leu Val Gly Thr Asp Ser His Thr		
195	200	205
Thr Met Ile Asp Gly Leu Gly Val Leu Gly Trp Gly Val Gly Gly Ile		
210	215	220
Glu Ala Glu Ala Val Met Leu Gly Gln Pro Ile Ser Met Val Leu Pro		
225	230	235
Gln Val Ile Gly Tyr Lys Leu Met Gly Lys Pro His Pro Leu Val Thr		
245	250	255
Ser Thr Asp Ile Val Leu Thr Ile Thr Lys His Leu Arg Gln Val Gly		
260	265	270
Val Val Gly Lys Phe Val Glu Phe Phe Gly Pro Gly Val Ala Gln Leu		
275	280	285
Ser Ile Ala Asp Arg Ala Thr Ile Ala Asn Met Cys Pro Glu Tyr Gly		
290	295	300
Ala Thr Ala Ala Phe Phe Pro Val Asp Glu Val Ser Ile Ala Tyr Leu		
305	310	315
Leu Gln Thr Gly Arg Glu Glu Asp Lys Val Lys His Ile Gln Lys Tyr		
325	330	335
Leu Gln Ala Val Gly Met Phe Arg Asp Phe Asn Asp Thr Ser Gln Asp		
340	345	350

Pro Asp Phe Thr Gln Val Val Glu Leu Asp Leu Lys Thr Val Val Pro
 355 360 365
 Cys Cys Ser Gly Pro Lys Arg Pro Gln Asp Lys Val Ala Val Ser Glu
 370 375 380
 Met Lys Lys Asp Phe Glu Ser Cys Leu Gly Ala Lys Gln Gly Phe Lys
 385 390 395 400
 Gly Phe Gln Val Ala Pro Asp Arg His Asn Asp Arg Lys Thr Phe Leu
 405 410 415
 Tyr Ser Asn Ser Glu Phe Thr Leu Ala His Gly Ser Val Val Ile Ala
 420 425 430
 Ala Ile Thr Thr Cys Thr Asn Thr Ser Asn Pro Ser Val Met Leu Gly
 435 440 445
 Ala Gly Leu Leu Ala Lys Lys Ala Val Glu Ala Gly Leu Ser Val Lys
 450 455 460
 Pro Tyr Ile Lys Thr Ser Leu Ser Pro Gly Ser Gly Val Val Thr Tyr
 465 470 475 480
 Tyr Leu Arg Glu Ser Gly Val Met Pro Tyr Leu Ser Gln Leu Gly Phe
 485 490 495
 Asp Val Val Gly Tyr Gly Cys Met Thr Cys Ile Gly Asn Ser Gly Pro
 500 505 510
 Leu Pro Glu Pro Val Val Glu Ala Ile Thr Gln Gly Asp Leu Val Ala
 515 520 525
 Val Gly Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Val His Pro
 530 535 540
 Asn Thr Arg Ala Asn Tyr Leu Ala Ser Pro Pro Leu Val Ile Ala Tyr
 545 550 555 560
 Ala Ile Ala Gly Thr Val Arg Ile Asp Phe Glu Lys Glu Pro Leu Gly
 565 570 575
 Val Asn Ala Gln Gly Arg Gln Val Phe Leu Lys Asp Ile Trp Pro Thr

580	585	590
Arg Asp Glu Ile Gln Ala Val Glu Arg Gln His Val Ile Pro Gly Met		
595	600	605
Phe Lys Glu Val Tyr Gln Lys Ile Glu Thr Val Asn Lys Ser Trp Asn		
610	615	620
Ala Leu Ala Ala Pro Ser Glu Lys Leu Tyr Ala Trp Asn Pro Lys Ser		
625	630	635
Thr Tyr Ile Lys Ser Pro Pro Phe Phe Glu Ser Leu Thr Leu Asp Leu		
645	650	655
Gln Pro Pro Lys Ser Ile Val Asp Ala Tyr Val Leu Leu Asn Leu Gly		
660	665	670
Asp Ser Val Thr Thr Asp His Ile Ser Pro Ala Gly Asn Ile Ala Arg		
675	680	685
Asn Ser Pro Ala Ala Arg Tyr Leu Thr Asn Arg Gly Leu Thr Pro Arg		
690	695	700
Glu Phe Asn Ser Tyr Gly Ser Arg Arg Gly Asn Asp Ala Ile Met Ala		
705	710	715
Arg Gly Thr Phe Ala Asn Ile Arg Leu Leu Asn Lys Phe Leu Asn Lys		
725	730	735
Gln Ala Pro Gln Thr Val His Leu Pro Ser Gly Glu Thr Leu Asp Val		
740	745	750
Phe Asp Ala Ala Glu Arg Tyr Gln Gln Ala Gly Leu Pro Leu Ile Val		
755	760	765
Leu Ala Gly Lys Glu Tyr Gly Ser Gly Ser Ser Arg Asp Trp Ala Ala		
770	775	780
Lys Gly Pro Phe Leu Leu Gly Ile Lys Ala Val Leu Ala Glu Ser Tyr		
785	790	795
Glu Arg Ile His Arg Ser Asn Leu Val Gly Met Gly Val Ile Pro Leu		
805	810	815

Glu Tyr Leu Pro Gly Glu Thr Ala Asp Ser Leu Gly Leu Thr Gly Arg
 820 825 830
 Glu Arg Tyr Thr Ile Asn Ile Pro Glu Asp Leu Lys Pro Arg Met Thr
 835 840 845
 Val Gln Ile Lys Leu Asp Thr Gly Lys Thr Phe Gln Ala Val Met Arg
 850 855 860
 Phe Asp Thr Asp Val Glu Leu Thr Tyr Phe His Asn Gly Gly Ile Leu
 865 870 875 880
 Asn Tyr Met Ile Arg Lys Met Ala Gln
 885

<210> 313

<211> 416

<212> DNA

<213> Mus musculus

<400> 313

aattcgggac gagggcgcgg tgccgttctt cctgtcccgg ccgccatcgg agagcatcag 60
 ccatggctct gcgctacccc atggccgtgg gctcaacaag ggccacaagg tgacgaaaaa 120
 cgtcagtaag ccgagacaca gccggcgacg cgggcgcctc accaaacaca ccaagttcgt 180
 gcgggacatg atccgggagg tgtgcggtt cgcaccctac gagcggcgag ccatggagtt 240
 gctcaaagtg tccaaggaca agcgcgcact caagttcatc aagaagaggg tgggcacgca 300
 catccgcgcc aagagaaagc gggaggagct gagcaacgtg ctggcagcca tgaggaaggc 360
 ggcggaaga aggattgatg aaccctcccc caataaaaga tggttcctac aaaaaa 416

<210> 314

<211> 252

<212> DNA

<213> Mus musculus

<400> 314

ccactcatac ccagctcttt ctgctgatca gaagacggag ttgtcggata ttgctctacg 60
 gatcgtgact cccggcaagg ccattctggc tgcagatgag tccgtaggca gcatggccag 120
 aaggctgagc caaattgcgg ggggagaaca ctgaggagaa tcgccggctg gtaccgcagt 180
 ccgtattcag tgctgatgac cgtgtgaaaa agtgcattgg gtgggtcatt ttcttccatg 240
 agagactcta cc 252

<210> 315

<211> 423

<212> DNA

<213> Mus musculus

<400> 315

ttcccgaagc gcctgagaga ctgatgacag acaccattaa tgaaccaatc ctgctgtgtc 60
 gctttctgtt ggagatcaag tctttctata tgcagcgttg tcctgaggat cctcgactta 120
 ctgaatctgt ggacgtgttg atgcccacag ttggtgagat tglaggtggc tcgatgcgct 180
 cctgggacag tgaggagatt ctccaaggct ataagaggga agggattgac cccgctcctt 240
 actactggta tacagatcag agaaaataat gcaccctcat ggagggtact ggcttgggct 300
 tggaacgatt tcttagcttg attctgaaca ggtatcacat ccgagatgtg tgcctgtacc 360
 ctcgatttct ccagcgtgc aggcataac catggggccc tcaagcacga aggaaatgaa 420
 aag 423

<210> 316

<211> 261

<212> DNA

<213> Mus musculus

<400> 316

cctacagacg ctgcgaccgc aatggcagct gggaggtggt tccagggcac aaccggacgt 60
 gggccaacta cagcgagtgc ctcaagtctt accccgagtc taaagagaac aaggatgtgc 120
 ccaccggcag caggcgccga ggggcicctt gtcigccaga gtggaacaac atcgtttgct 180
 ggcaattggg ggaacgagtt aaagtgttgg cataacctgt ccccgatacc attaagtact 240
 ccaaccacaa ggccattgcc t 261

<210> 317

<211> 414

<212> DNA

<213> Mus musculus

<400> 317

ctgccncggc aggctcgccc atggcgtaac gtggccgaca cgaagctgta cgacatcctg 60
 ggcgtccctc ccggcgctac gcagaacgag ctgaagaagg cataccgaaa gttagccaaa 120
 gaataccacc ctgataagaa tccaaatgct ggagacaaat ttaaagaaat aagttttgca 180
 tatgaagtat tgtcaaatcc agagaagcga gactgtatga cagatatgga gaacaaggcc 240
 tacgggaagg cagcggcgga ggcggtggca tggatgatat cttctcacat atttttgggtg 300
 gaggattgtt tggctttatg ggcaatcaga gtagaagtcg aaatggcaga agaagaggcg 360
 aggacatgat gcattcacta aaagtatctt tagaagacct gtacaatggc aaga 414

<210> 318

<211> 414

<212> DNA

<213> Mus musculus

<400> 318

cacacaaggg gccttggcat gtcagccttt aagtaacggt tctcaaaacc tagaagtcac 60
 ggcatgggtg cttcgagagc tgggtacccc agccctaagg atgtctcaga ggcacaatga 120
 ggtggataat gaggtgggca tticagagggg cttctgcaaa cctagagtcc aggaggcaat 180

gggtgcagca gtgaggtagc tatgccacac agagaccata gtcactgtc attttcaagc 240
 ctcctatttc ccagctccat ggtgaggaca ccagctttcc caccaccga gtgtcccaga 300
 aaatgaaatt ggaaggaata agatgcatcg tggctgtgga ttgattcttg ggaccaaaaa 360
 gagactaggg agagaaagca cattagcagg tcaaccagga ctcatacctt ccag 414

<210> 319

<211> 3031

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (51).. (2348)

<400> 319

gggtgaggtg gcittgacct cgggtggccc ggccagcgcg accgaggaga atg aac 56
 Met Asn
 1
 gga gaa gcg gac tgt ccc aca gac ctg gaa atg gcc gcc ccc aaa ggc 104
 Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro Lys Gly
 5 10 15
 caa gac cgc tgg tcc cag gaa gat atg ctg act ctg ctg gaa tgc atg 152
 Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu Cys Met
 20 25 30
 aag aac aac ctc cca tcc aac gac agc tcc aag ttc aaa acc aca gag 200
 Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr Thr Glu
 35 40 45 50
 tcg cac atg gat tgg gaa aaa gtt gcg ttt aag gat ttt tca gga gat 248
 Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser Gly Asp

55	60	65	
atg tgc aag ctc aaa tgg gtg gag att tct aac gag gta agg aag ttc			296
Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg Lys Phe			
70	75	80	
cgt aca ttg aca gaa ttg atc ctc gat gct cag gaa cat gtt aaa aac			344
Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val Lys Asn			
85	90	95	
cct tac aaa ggc aaa aag ctc aag aaa cac ccg gat ttt cca aag aaa			392
Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro Lys Lys			
100	105	110	
cct ctc acc cct tac ttc cgc ttc ttc atg gag aag cgg gcc aag tac			440
Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala Lys Tyr			
115	120	125	130
gcg aag ctc cac ccg gag atg agc aac ctg gac ctg act aag atc ctg			488
Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys Ile Leu			
135	140	145	
tct aag aaa tac aag gaa ctt cca gag aag aag aag atg aaa tat att			536
Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys Tyr Ile			
150	155	160	
cag gac ttc cag agg gag aaa cag gag ttc gag cga aac ctg gcc cga			584
Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu Ala Arg			
165	170	175	
ttc agg gag gat cac cct gac ctt atc cag aat gcc aag aag tcg gac			632
Phe Arg Glu Asp His Pro Asp Leu Ile Gln Asn Ala Lys Lys Ser Asp			
180	185	190	
atc ccc gag aaa ccc aaa act ccc cag caa ctg tgg tac acc cac gag			680
Ile Pro Glu Lys Pro Lys Thr Pro Gln Gln Leu Trp Tyr Thr His Glu			
195	200	205	210
aag aag gtg tat ctc aaa gtg cgg ccg gat gcc act acg aag gag gtg			728

Lys Lys Val Tyr Leu Lys Val Arg Pro Asp Ala Thr Thr Lys Glu Val
 215 220 225
 aag gac tcc ctg ggg aag cag tgg tct cag ctc tcg gac aaa aag acg 776
 Lys Asp Ser Leu Gly Lys Gln Trp Ser Gln Leu Ser Asp Lys Lys Thr
 230 235 240
 ctg aaa tgg att cat aag gcc ctg gag cag cgg aag gag tac gag gag 824
 Leu Lys Trp Ile His Lys Ala Leu Glu Gln Arg Lys Glu Tyr Glu Glu
 245 250 255
 att atg cgg gac tat atc cag aag cac cct gag ctg aac atc agt gag 872
 Ile Met Arg Asp Tyr Ile Gln Lys His Pro Glu Leu Asn Ile Ser Glu
 260 265 270
 gaa ggc atc acc aag tcc acc ctc acc aag gcc gag cgc cag ctc aag 920
 Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys Ala Glu Arg Gln Leu Lys
 275 280 285 290
 gac aag ttc gat ggg cga cct acc aag ccg cct ccg aac agc tac tcc 968
 Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro Pro Pro Asn Ser Tyr Ser
 295 300 305
 ctg tac tgt gcg gag ctc atg gcc aac atg aag gat gtg ccc agc aca 1016
 Leu Tyr Cys Ala Glu Leu Met Ala Asn Met Lys Asp Val Pro Ser Thr
 310 315 320
 gag cgc atg gtg cta tgc agc cag caa tgg aag ctg ctc tct cag aag 1064
 Glu Arg Met Val Leu Cys Ser Gln Gln Trp Lys Leu Leu Ser Gln Lys
 325 330 335
 gag aag gat gcc tat cac aag aaa tgt gac cag aaa aag aaa gat tat 1112
 Glu Lys Asp Ala Tyr His Lys Lys Cys Asp Gln Lys Lys Lys Asp Tyr
 340 345 350
 gag gta gag ctg ctg cgg ttc ctt gag agc ttg ccg gag gaa gag cag 1160
 Glu Val Glu Leu Leu Arg Phe Leu Glu Ser Leu Pro Glu Glu Glu Gln
 355 360 365 370

cag cgg gtt ctg ggg gag gag aag atg ctg aac atc aat aag aag caa	1208
Gln Arg Val Leu Gly Glu Glu Lys Met Leu Asn Ile Asn Lys Lys Gln	
375 380 385	
acc acc agt ccg gcc tcc aag aag cct tca cag gaa ggt ggc aag ggt	1256
Thr Thr Ser Pro Ala Ser Lys Lys Pro Ser Gln Glu Gly Gly Lys Gly	
390 395 400	
ggc tcc gag aag ccc aag cgg cct gtg tct gct atg ttc atc ttc tct	1304
Gly Ser Glu Lys Pro Lys Arg Pro Val Ser Ala Met Phe Ile Phe Ser	
405 410 415	
gag gag aag cga agg cag cta cag gag gaa cga cct gag ctc tcc gaa	1352
Glu Glu Lys Arg Arg Gln Leu Gln Glu Glu Arg Pro Glu Leu Ser Glu	
420 425 430	
agc gaa ctg acc cgc ctt ctg gcc cgc atg tgg aac gac ttg acc gag	1400
Ser Glu Leu Thr Arg Leu Leu Ala Arg Met Trp Asn Asp Leu Thr Glu	
435 440 445 450	
aag aag aag gct aaa tac aag gcc cgg gag gct gca ctg aag gcg cag	1448
Lys Lys Lys Ala Lys Tyr Lys Ala Arg Glu Ala Ala Leu Lys Ala Gln	
455 460 465	
tct gag agg aag ccg ggc ggg gag cgt gaa gat agg ggc aag ctg ccg	1496
Ser Glu Arg Lys Pro Gly Gly Glu Arg Glu Asp Arg Gly Lys Leu Pro	
470 475 480	
gag tcg ccc aag agg gct gag gag atc tgg cag cag agt gtc atc gga	1544
Glu Ser Pro Lys Arg Ala Glu Glu Ile Trp Gln Gln Ser Val Ile Gly	
485 490 495	
gac tat ctg gcc cgc ttc aag aat gac cgg gtg aaa gcc ttg aaa gcc	1592
Asp Tyr Leu Ala Arg Phe Lys Asn Asp Arg Val Lys Ala Leu Lys Ala	
500 505 510	
atg gag atg act tgg aac aac atg gag aag aag gag aag ctg atg tgg	1640
Met Glu Met Thr Trp Asn Asn Met Glu Lys Lys Glu Lys Leu Met Trp	

515	520	525	530	
att aag aag gca gca gaa gac caa aaa cga tat gag aga gag tta agt				1688
Ile Lys Lys Ala Ala Glu Asp Gln-Lys Arg Tyr Glu Arg Glu Leu Ser				
	535	540	545	
	gag atg cgg gcc cct cca gct gct aca aac tct tcc aag aag atg aag			1736
	Glu Met Arg Ala Pro Pro Ala Ala Thr Asn Ser Ser Lys Lys Met Lys			
	550	555	560	
	ttc cag gga gaa ccc aag aaa cct cct atg aac ggt tac cag aag ttc			1784
	Phe Gln Gly Glu Pro Lys Lys Pro Pro Met Asn Gly Tyr Gln Lys Phe			
	565	570	575	
	tcc cag gag ctg ctg tcc aat ggg gag cta aat cac ctg ccg ctg aag			1832
	Ser Gln Glu Leu Leu Ser Asn Gly Glu Leu Asn His Leu Pro Leu Lys			
	580	585	590	
	gag cgc atg gtg gag att ggc agc cgc tgg cag cgc atc tcc cag agc			1880
	Glu Arg Met Val Glu Ile Gly Ser Arg Trp Gln Arg Ile Ser Gln Ser			
595	600	605	610	
cag aag gag cac tat aag aag ctg gcg gag gag caa cag agg cag tac				1928
Gln Lys Glu His Tyr Lys Lys Leu Ala Glu Glu Gln Gln Arg Gln Tyr				
	615	620	625	
	aag gtg cac ttg gac ctc tgg gtc aag agc ctg tct ccc cag gac cgc			1976
	Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln Asp Arg			
	630	635	640	
	gca gca tac aaa gaa tac atc tcc aat aaa cgt aag aac atg acc aag			2024
	Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Asn Met Thr Lys			
	645	650	655	
	ctc cga ggc cca aac ccc aag tct agc cgg acc acc ctg cag tcc aag			2072
	Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln Ser Lys			
	660	665	670	
	tcg gag tcc gag gag gat gac gat gag gag gag gag gac gac gag gag			2120

Ser Glu Ser Glu Glu Asp Asp Asp Glu Glu Glu Glu Asp Asp Glu Glu
 675 680 685 690
 gag gag gag gaa gag gaa gat gat gag aac ggt gac tct tct gag gat 2168
 Glu Glu Glu Glu Glu Glu Asp Asp Glu Asn Gly Asp Ser Ser Glu Asp
 695 700 705
 ggc ggc gac tct tct gag tcc agc agt gaa gat gaa agc gag gat ggc 2216
 Gly Gly Asp Ser Ser Glu Ser Ser Ser Glu Asp Glu Ser Glu Asp Gly
 710 715 720
 gat gag aat gat gat gac gac gac gat gaa gat gac gaa gat gac gac 2264
 Asp Glu Asn Asp Asp Asp Asp Asp Asp Glu Asp Asp Glu Asp Asp Asp
 725 730 735
 gat gag gat gaa gac aac gag tct gag ggc agt agc tcc agc tct tca 2312
 Asp Glu Asp Glu Asp Asn Glu Ser Glu Gly Ser Ser Ser Ser Ser Ser
 740 745 750
 tcc tca ggc gac tct tcg gat tct ggc tcc aac tga ggctcagcct 2358
 Ser Ser Gly Asp Ser Ser Asp Ser Gly Ser Asn
 755 760 765
 ccaccccagg caggcaggca ggcaggcagc caaggagaga gcccctgcag agctcatctc 2418
 cccaacagac aacctttgac aacctttgtc tctccctgtg ttctgtcccg taccctccgt 2478
 accctccaga ctcccactt tctttctttc tttctttttt tttttaaatc agtggggggg 2538
 aggaggctgc atgagcccaa gctaggactc tgcagccttg gagcctcagc tccagggttc 2598
 tccagggata gcaaccatca gactgagcca gcgctggacg ggcccaccct gcccctcttc 2658
 tgcattttgca gttccggcat ggacaatgga ctggggagtt tgggggtggg agagagtcct 2718
 aaagagtttg gtgagacctc cacacctgca gcctgcagca aggtggatgt tcggggggcc 2778
 tticcttccc agatgggctt gctacctgac cccacattga actggaggag acaagggtgc 2838
 tgccttcaag aaagcaggca gtggatccct gtccctctta accctgcccc tgcaggaagg 2898
 agctacctgg acccgttcgt gggggagggg cagagtgttt ttttatatat gtgtatatat 2958
 ttttttttta agctctgagc igtcaacgag acgtttccta ccgaaaaaaaa aaaaaaaaaa 3018
 aaaaaaaaaa aaa 3031

<210> 320

<211> 765

<212> PRT

<213> Mus musculus

<400> 320

Met Asn Gly Glu Ala Asp Cys Pro Thr Asp Leu Glu Met Ala Ala Pro

1 5 10 15

Lys Gly Gln Asp Arg Trp Ser Gln Glu Asp Met Leu Thr Leu Leu Glu

20 25 30

Cys Met Lys Asn Asn Leu Pro Ser Asn Asp Ser Ser Lys Phe Lys Thr

35 40 45

Thr Glu Ser His Met Asp Trp Glu Lys Val Ala Phe Lys Asp Phe Ser

50 55 60

Gly Asp Met Cys Lys Leu Lys Trp Val Glu Ile Ser Asn Glu Val Arg

65 70 75 80

Lys Phe Arg Thr Leu Thr Glu Leu Ile Leu Asp Ala Gln Glu His Val

85 90 95

Lys Asn Pro Tyr Lys Gly Lys Lys Leu Lys Lys His Pro Asp Phe Pro

100 105 110

Lys Lys Pro Leu Thr Pro Tyr Phe Arg Phe Phe Met Glu Lys Arg Ala

115 120 125

Lys Tyr Ala Lys Leu His Pro Glu Met Ser Asn Leu Asp Leu Thr Lys

130 135 140

Ile Leu Ser Lys Lys Tyr Lys Glu Leu Pro Glu Lys Lys Lys Met Lys

145 150 155 160

Tyr Ile Gln Asp Phe Gln Arg Glu Lys Gln Glu Phe Glu Arg Asn Leu

165 170 175

Ala Arg Phe Arg Glu Asp His Pro Asp Leu Ile Gln Asn Ala Lys Lys
 180 185 190
 Ser Asp Ile Pro Glu Lys Pro Lys Thr Pro Gln Gln Leu Trp Tyr Thr
 195 200 205
 His Glu Lys Lys Val Tyr Leu Lys Val Arg Pro Asp Ala Thr Thr Lys
 210 215 220
 Glu Val Lys Asp Ser Leu Gly Lys Gln Trp Ser Gln Leu Ser Asp Lys
 225 230 235 240
 Lys Thr Leu Lys Trp Ile His Lys Ala Leu Glu Gln Arg Lys Glu Tyr
 245 250 255
 Glu Glu Ile Met Arg Asp Tyr Ile Gln Lys His Pro Glu Leu Asn Ile
 260 265 270
 Ser Glu Glu Gly Ile Thr Lys Ser Thr Leu Thr Lys Ala Glu Arg Gln
 275 280 285
 Leu Lys Asp Lys Phe Asp Gly Arg Pro Thr Lys Pro Pro Pro Asn Ser
 290 295 300
 Tyr Ser Leu Tyr Cys Ala Glu Leu Met Ala Asn Met Lys Asp Val Pro
 305 310 315 320
 Ser Thr Glu Arg Met Val Leu Cys Ser Gln Gln Trp Lys Leu Leu Ser
 325 330 335
 Gln Lys Glu Lys Asp Ala Tyr His Lys Lys Cys Asp Gln Lys Lys Lys
 340 345 350
 Asp Tyr Glu Val Glu Leu Leu Arg Phe Leu Glu Ser Leu Pro Glu Glu
 355 360 365
 Glu Gln Gln Arg Val Leu Gly Glu Glu Lys Met Leu Asn Ile Asn Lys
 370 375 380
 Lys Gln Thr Thr Ser Pro Ala Ser Lys Lys Pro Ser Gln Glu Gly Gly
 385 390 395 400
 Lys Gly Gly Ser Glu Lys Pro Lys Arg Pro Val Ser Ala Met Phe Ile

	405	410	415
Phe Ser Glu Glu Lys Arg Arg Gln Leu Gln Glu Glu Arg Pro Glu Leu			
	420	425	430
Ser Glu Ser Glu Leu Thr Arg Leu Leu Ala Arg Met Trp Asn Asp Leu			
	435	440	445
Thr Glu Lys Lys Lys Ala Lys Tyr Lys Ala Arg Glu Ala Ala Leu Lys			
	450	455	460
Ala Gln Ser Glu Arg Lys Pro Gly Gly Glu Arg Glu Asp Arg Gly Lys			
465	470	475	480
Leu Pro Glu Ser Pro Lys Arg Ala Glu Glu Ile Trp Gln Gln Ser Val			
	485	490	495
Ile Gly Asp Tyr Leu Ala Arg Phe Lys Asn Asp Arg Val Lys Ala Leu			
	500	505	510
Lys Ala Met Glu Met Thr Trp Asn Asn Met Glu Lys Lys Glu Lys Leu			
	515	520	525
Met Trp Ile Lys Lys Ala Ala Glu Asp Gln Lys Arg Tyr Glu Arg Glu			
	530	535	540
Leu Ser Glu Met Arg Ala Pro Pro Ala Ala Thr Asn Ser Ser Lys Lys			
545	550	555	560
Met Lys Phe Gln Gly Glu Pro Lys Lys Pro Pro Met Asn Gly Tyr Gln			
	565	570	575
Lys Phe Ser Gln Glu Leu Leu Ser Asn Gly Glu Leu Asn His Leu Pro			
	580	585	590
Leu Lys Glu Arg Met Val Glu Ile Gly Ser Arg Trp Gln Arg Ile Ser			
	595	600	605
Gln Ser Gln Lys Glu His Tyr Lys Lys Leu Ala Glu Glu Gln Gln Arg			
	610	615	620
Gln Tyr Lys Val His Leu Asp Leu Trp Val Lys Ser Leu Ser Pro Gln			
625	630	635	640

Asp Arg Ala Ala Tyr Lys Glu Tyr Ile Ser Asn Lys Arg Lys Asn Met
 645 650 655
 Thr Lys Leu Arg Gly Pro Asn Pro Lys Ser Ser Arg Thr Thr Leu Gln
 660 665 670
 Ser Lys Ser Glu Ser Glu Glu Asp Asp Asp Glu Glu Glu Glu Asp Asp
 675 680 685
 Glu Glu Glu Glu Glu Glu Glu Glu Asp Asp Glu Asn Gly Asp Ser Ser
 690 695 700
 Glu Asp Gly Gly Asp Ser Ser Glu Ser Ser Ser Glu Asp Glu Ser Glu
 705 710 715 720
 Asp Gly Asp Glu Asn Asp Asp Asp Asp Asp Asp Glu Asp Asp Glu Asp
 725 730 735
 Asp Asp Asp Glu Asp Glu Asp Asn Glu Ser Glu Gly Ser Ser Ser Ser
 740 745 750
 Ser Ser Ser Ser Gly Asp Ser Ser Asp Ser Gly Ser Asn
 755 760 765

<210> 321

<211> 4479

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (94).. (3057)

<400> 321

gagtcggtgt gcacccgccc aggggaggggt cagacctggg ggggccaggg cccccaaac 60
 tcggatcgca ttcagccaaa gtgaggcggc gcc atg gag ctc cga gcg ctg ctg 114

	Met	Glu	Leu	Arg	Ala	Leu	Leu		
	1					5			
tgc tgg gct tcc ctc gcc act gct tta gaa gag acc ctg ttg aac aca								162	
Cys Trp Ala Ser Leu Ala Thr Ala Leu Glu Glu Thr Leu Leu Asn Thr									
10		15				20			
aaa ctg gaa acg gcg gat ctg aaa tgg gtg act tac cct cag gca gag								210	
Lys Leu Glu Thr Ala Asp Leu Lys Trp Val Thr Tyr Pro Gln Ala Glu									
25		30				35			
ggc cag tgg gag gag cta agc ggc ctg gat gag gaa cag cac agc gtc								258	
Gly Gln Trp Glu Glu Leu Ser Gly Leu Asp Glu Glu Gln His Ser Val									
40		45				50		55	
cgc acc tat gag gtg tgc gac atg aag cgt cca ggg ggc cag gct cac									306
Arg Thr Tyr Glu Val Cys Asp Met Lys Arg Pro Gly Gly Gln Ala His									
60		65				70			
tgg ctg cgc act ggc tgg gtc cca agg cga ggt gct gtc cac gtg tat								354	
Trp Leu Arg Thr Gly Trp Val Pro Arg Arg Gly Ala Val His Val Tyr									
75		80				85			
gcc acg ata cgc ttc acc atg atg gaa tgc ctg tcc ctg ccg agg gcc								402	
Ala Thr Ile Arg Phe Thr Met Met Glu Cys Leu Ser Leu Pro Arg Ala									
90		95				100			
agt cgc tcc tgc aag gag aca ttc act gtc ttc tat tac gag agc gaa								450	
Ser Arg Ser Cys Lys Glu Thr Phe Thr Val Phe Tyr Tyr Glu Ser Glu									
105		110				115			
cgt gat acg gcc acg gcc cat acg ccc gcc tgg atg gag aac ccc tac								498	
Arg Asp Thr Ala Thr Ala His Thr Pro Ala Trp Met Glu Asn Pro Tyr									
120		125				130		135	
atc aag gtg gac aca gtg gcc gca gaa cat ctg act cgg aag cgc cct								546	
Ile Lys Val Asp Thr Val Ala Ala Glu His Leu Thr Arg Lys Arg Pro									
140		145				150			

gga gct gaa gcc aca ggg aaa gtt aat atc aag acg ctg cgc ctg ggt 594
 Gly Ala Glu Ala Thr Gly Lys Val Asn Ile Lys Thr Leu Arg Leu Gly
 155 160 165
 cct ctc agc aaa gct ggc ttc tac ctg gct ttc cag gac caa gga gcc 642
 Pro Leu Ser Lys Ala Gly Phe Tyr Leu Ala Phe Gln Asp Gln Gly Ala
 170 175 180
 tgc atg gct ctg ctc tcc ctg cat ctc ttt tac aag aag tgc tcc tgg 690
 Cys Met Ala Leu Leu Ser Leu His Leu Phe Tyr Lys Lys Cys Ser Trp
 185 190 195
 ctg atc acg aac ttg acc tac ttc ccc gag acg gtg cct cgg gag ctc 738
 Leu Ile Thr Asn Leu Thr Tyr Phe Pro Glu Thr Val Pro Arg Glu Leu
 200 205 210 215
 gtg gtg ccg gtg gca ggt agc tgc gtg gcc aac gcg gtc cct acc gcc 786
 Val Val Pro Val Ala Gly Ser Cys Val Ala Asn Ala Val Pro Thr Ala
 220 225 230
 aac ccc agc ccc agc ctc tac tgc cgg gaa gat ggt caa tgg gct gag 834
 Asn Pro Ser Pro Ser Leu Tyr Cys Arg Glu Asp Gly Gln Trp Ala Glu
 235 240 245
 cag cag gtc acg ggc tgc agc tgc gcg cca ggg tac gag, gct gcg gaa 882
 Gln Gln Val Thr Gly Cys Ser Cys Ala Pro Gly Tyr Glu Ala Ala Glu
 250 255 260
 agc aac aaa gta tgc aga gcc tgt ggc cag gga acc ttc aag ccc caa 930
 Ser Asn Lys Val Cys Arg Ala Cys Gly Gln Gly Thr Phe Lys Pro Gln
 265 270 275
 ata gga gac gag tcc tgc ctg ccg tgc cca gcc aac agc cac tcg aat 978
 Ile Gly Asp Glu Ser Cys Leu Pro Cys Pro Ala Asn Ser His Ser Asn
 280 285 290 295
 aac att ggg tct cct gtc tgc ctg tgt cga att ggg tat tac cgg gcc 1026
 Asn Ile Gly Ser Pro Val Cys Leu Cys Arg Ile Gly Tyr Tyr Arg Ala

300	305	310	
cgc tca gac ccc cgg agt tca cct tgc act acc cca ccc tct gct cca	1074		
Arg Ser Asp Pro Arg Ser Ser Pro Cys Thr Thr Pro Pro Ser Ala Pro			
315	320	325	
aga agc gtg gtt cac cat ttg aat ggt tcc acc ctg cgc ctg gaa tgg	1122		
Arg Ser Val Val His His Leu Asn Gly Ser Thr Leu Arg Leu Glu Trp			
330	335	340	
agt gct ccc ctt gag tcc gga ggc cga gag gac ctc act tat gct gtt	1170		
Ser Ala Pro Leu Glu Ser Gly Gly Arg Glu Asp Leu Thr Tyr Ala Val			
345	350	355	
cgc tgc cga gag tgc cgt cct ggg ggt tcc tgc ttg ccc tgt ggg ggc	1218		
Arg Cys Arg Glu Cys Arg Pro Gly Gly Ser Cys Leu Pro Cys Gly Gly			
360	365	370	375
gac atg acc ttc gac ccc ggt cct cga gac ctg gtt gag ccc tgg gtg	1266		
Asp Met Thr Phe Asp Pro Gly Pro Arg Asp Leu Val Glu Pro Trp Val			
380	385	390	
gca atc cga ggg ctg cgt cct gat gtc acc tat acc ttt gag gtt gct	1314		
Ala Ile Arg Gly Leu Arg Pro Asp Val Thr Tyr Thr Phe Glu Val Ala			
395	400	405	
gct ttg aat ggt gtg tct acc tta gcc act gga cca cct cct ttt gag	1362		
Ala Leu Asn Gly Val Ser Thr Leu Ala Thr Gly Pro Pro Pro Phe Glu			
410	415	420	
cct gtc aat gtc acc act gac cgt gag gtg cct cct gca gtg tct gac	1410		
Pro Val Asn Val Thr Thr Asp Arg Glu Val Pro Pro Ala Val Ser Asp			
425	430	435	
atc cga gtg act cgg tgc tca ccc agc agc ttg atc ctg tca tgg gct	1458		
Ile Arg Val Thr Arg Ser Ser Pro Ser Ser Leu Ile Leu Ser Trp Ala			
440	445	450	455
atc ccc aga gca ccc agt ggg gcc gtg ctg gac tac gag gtc aag tat	1506		

Ile Pro Arg Ala Pro Ser Gly Ala Val Leu Asp Tyr Glu Val Lys Tyr	
460	465
470	
cat gag aag ggc gca gag ggc ccc agc agt gtt cgt ttc ctg aag aca	1554
His Glu Lys Gly Ala Glu Gly Pro Ser Ser Val Arg Phe Leu Lys Thr	
475	480
485	
tca gaa aac cga gct gag ctc cgg ggg ctg aag cgg gga gcc agc tat	1602
Ser Glu Asn Arg Ala Glu Leu Arg Gly Leu Lys Arg Gly Ala Ser Tyr	
490	495
500	
ctg gtc cag gta cgc gca cgg tcc gag gct ggc tac ggt ccc ttc ggc	1650
Leu Val Gln Val Arg Ala Arg Ser Glu Ala Gly Tyr Gly Pro Phe Gly	
505	510
515	
cag gag cat cac agt cag act caa ctg gat gag agc gag agc tgg cgg	1698
Gln Glu His His Ser Gln Thr Gln Leu Asp Glu Ser Glu Ser Trp Arg	
520	525
530	535
gag cag ctg gcc ctg att gca ggc act gcg gtt gtg ggt gtg gtc ctg	1746
Glu Gln Leu Ala Leu Ile Ala Gly Thr Ala Val Val Gly Val Val Leu	
540	545
550	
gtc ctg gtg gtc gtc atc att gca gtt ctc tgc ctc agg aag cag agc	1794
Val Leu Val Val Val Ile Ile Ala Val Leu Cys Leu Arg Lys Gln Ser	
555	560
565	
aat ggg agg gaa gtt gag tac tcg gat aag cat ggg cag tat ctc atc	1842
Asn Gly Arg Glu Val Glu Tyr Ser Asp Lys His Gly Gln Tyr Leu Ile	
570	575
580	
ggg cac ggt acc aag gtc tac att gat cct ttt act tac gaa gac cct	1890
Gly His Gly Thr Lys Val Tyr Ile Asp Pro Phe Thr Tyr Glu Asp Pro	
585	590
595	
aat gag gca gtg agg gaa ttt gcc aaa gag atc gat gtc tcc tat gtc	1938
Asn Glu Ala Val Arg Glu Phe Ala Lys Glu Ile Asp Val Ser Tyr Val	
600	605
610	615

aag att gaa gag gta att ggt gca ggt gag ttc ggc gag gtg tgc cgg 1986
Lys Ile Glu Glu Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Arg
620 625 630
ggg cgg ctg aag gca cca ggg aaa aag gag agc tgt gtg gcc atc aag 2034
Gly Arg Leu Lys Ala Pro Gly Lys Lys Glu Ser Cys Val Ala Ile Lys
635 640 645
act ctg aag ggt ggc tac acc gag cgc cag agg cgt gag ttc ctg agc 2082
Thr Leu Lys Gly Gly Tyr Thr Glu Arg Gln Arg Arg Glu Phe Leu Ser
650 655 660
gag gcc tcc atc atg ggc cag ttc gag cat ccc aac atc atc cgc ctc 2130
Glu Ala Ser Ile Met Gly Gln Phe Glu His Pro Asn Ile Ile Arg Leu
665 670 675
gag ggc gtg gtc acc aac agt gtg ccg gtt atg atc ctc acg gaa ttc 2178
Glu Gly Val Val Thr Asn Ser Val Pro Val Met Ile Leu Thr Glu Phe
680 685 690 695
atg gag aac gga gcc ctg gac tcc ttc ctg cgg ctg aac gac ggg cag 2226
Met Glu Asn Gly Ala Leu Asp Ser Phe Leu Arg Leu Asn Asp Gly Gln
700 705 710
ttc aca gtc atc cag ctg gtg ggc atg ctg agg ggc atc gcc tcg ggc 2274
Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly
715 720 725
atg cgg tac ctg gct gaa atg agc tat gtc cac cga gac ctg gct gct 2322
Met Arg Tyr Leu Ala Glu Met Ser Tyr Val His Arg Asp Leu Ala Ala
730 735 740
cgg aac atc ttg gtc aac agt aac ctg gtc tgc aag gtg tcc gac ttt 2370
Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe
745 750 755
ggc ctc tcc aga ttc ttg gag gag aac tcc tct gat ccc acc tac aca 2418
Gly Leu Ser Arg Phe Leu Glu Glu Asn Ser Ser Asp Pro Thr Tyr Thr

760	765	770	775	
agt tcc ctg gga ggc aag att tcc atc cga tgg acc gcc cct gaa gcc				2466
Ser Ser Leu Gly Gly Lys Ile Ser Ile Arg Trp Thr Ala Pro Glu Ala				
	780	785	790	
att gcc ttc agg aag ttc acc tct gcc agt gat gcc tgg agc tat ggg				2514
Ile Ala Phe Arg Lys Phe Thr Ser Ala Ser Asp Ala Trp Ser Tyr Gly				
	795	800	805	
atc gtc atg tgg gag gtc atg tct ttt ggg gaa cgg cca tac tgg gac				2562
Ile Val Met Trp Glu Val Met Ser Phe Gly Glu Arg Pro Tyr Trp Asp				
	810	815	820	
atg agc aac cag gat gtg atc aat gcc att gaa cag gac tac cgg ctg				2610
Met Ser Asn Gln Asp Val Ile Asn Ala Ile Glu Gln Asp Tyr Arg Leu				
	825	830	835	
cct cct cct cca gac tgc ccc acc tcc ctc cac cag ctc atg ctg gac				2658
Pro Pro Pro Pro Asp Cys Pro Thr Ser Leu His Gln Leu Met Leu Asp				
840	845	850	855	
tgt tgg cag aag gac cgg aat gcc cgg ccc cgc ttt ccc cag gtg gtc				2706
Cys Trp Gln Lys Asp Arg Asn Ala Arg Pro Arg Phe Pro Gln Val Val				
	860	865	870	
agc gct ctg gac aag atg atc cgg aat ccc gct agc ctc aaa atc gtg				2754
Ser Ala Leu Asp Lys Met Ile Arg Asn Pro Ala Ser Leu Lys Ile Val				
	875	880	885	
gcc agg gag aat ggc ggg gcc tca cat cca ctc ttg gac caa cgg cag				2802
Ala Arg Glu Asn Gly Gly Ala Ser His Pro Leu Leu Asp Gln Arg Gln				
	890	895	900	
cct cac tac tct gct ttc ggt tct gtg ggc gag tgg ctt cga gcc atc				2850
Pro His Tyr Ser Ala Phe Gly Ser Val Gly Glu Trp Leu Arg Ala Ile				
	905	910	915	
aag atg gga aga tac gag gaa agt ttt gca gcg gct gga ttc ggc tcc				2898

Lys Met Gly Arg Tyr Glu Glu Ser Phe Ala Ala Ala Gly Phe Gly Ser
 920 925 930 935
 ttt gag gtg gtc agt cag atc tct gcc gag gac ctt ctc cga att gga 2946
 Phe Glu Val Val Ser Gln Ile Ser Ala Glu Asp Leu Leu Arg Ile Gly
 940 945 950
 gtc act ctg gca gga cac cag aag aaa atc ttg gcc agt gtg cag cat 2994
 Val Thr Leu Ala Gly His Gln Lys Lys Ile Leu Ala Ser Val Gln His
 955 960 965
 atg aag tcc caa gct aag cca gga gcc cct ggt ggg aca ggg gga cca 3042
 Met Lys Ser Gln Ala Lys Pro Gly Ala Pro Gly Gly Thr Gly Gly Pro
 970 975 980
 gcc cag cag ttc tga cctccaagga ctcaccaccg tggcagattc ttctttccgg 3097
 Ala Gln Gln Phe
 985
 gaggcagagt tgggtgggga ctcacaagat gagccccctcc ccctcgtcac agccttccca 3157
 ttggattgca ctttgaacag aggggggtcgg agacacagga ttiggggaac cgtgccatat 3217
 gggatcatac atgtgccctc caggcgggga accccaaact cagagtgagt ctttccctca 3277
 agactgggca aagaaacatc cctacgtctc taacctccca tcttcccaga gggctctctc 3337
 cccaagcgcc ttccacctca acgggcatgt ccctgcagac caaagagaaa gggtgaccag 3397
 cctgccaaact tgggagtgga aaatgccgtc ccaggaggca ggaaggggct gtcaggaccc 3457
 ggtgatgtaa tcattgggtt ttgatgtcct gacttgcgtg caccaccaa ggcaatcatt 3517
 ttcccttgt aaatgcccct cccctcatct gccttcatat tgaaggttct gaagttttac 3577
 tgttttttat ttgttaatt ttttctctct tccccctcc ctcccttct tgtccagatt 3637
 ttgigtgtta aagggcacct ggttccacta tctcctgttg ggaacaagga cccatcgata 3697
 tgttctagaa cagtgccttg gaaatgccac agccttagac agttccccgg aattccggca 3757
 aggatcgcc gctatattaa gaatcctcga attgtgctat tggattcttc ttggagtac 3817
 aagaaaggag aaagccagac cgacatcgag attaccgggaggaggactt cacgcggatc 3877
 ctgcagattg gaggggggag tacatccatc agctgtgtga ggacatcatc cagctgaagc 3937
 ctgacgtggt catcacagag aagggcattc cagatttagc tcagcactac ctcatgcggg 3997

ccaatgtcac agccattcgt agagtccgga aaacagacaa taatcgcat t gctagagcct 4057
 gtggggcagc gatagtcagc cgacctgagg aactgagaga agatgatgtt ggtacagggg 4117
 caggcttatt ggaaatcaag aagattggag atgagtactt tacattcatc actgactgca 4177
 aagacccaaa ggccatgcacc attcttctta gaggagccag caaagagata ctctcggaag 4237
 tagaacgcaa cctccaggat gccatgcaag tgtgccgcaa tgttctactg gaccctcagc 4297
 tgggtgcctgg tgggtggagcc tctgtgatgg ctgtggctca tgccitgaca gaaaaatcta 4357
 aggccaatgac tgggtgtgaa caatggccat atagagctgt ggcccaggcg ttagagg tca 4417
 tccctcggac ctgatccag aattgtgggg ccagttacat tctctgtctt acctccttcg 4477
 gg 4479

<210> 322

<211> 987

<212> PRT

<213> Mus musculus

<400> 322

Met Glu Leu Arg Ala Leu Leu Cys Trp Ala Ser Leu Ala Thr Ala Leu
 1 5 10 15
 Glu Glu Thr Leu Leu Asn Thr Lys Leu Glu Thr Ala Asp Leu Lys Trp
 20 25 30
 Val Thr Tyr Pro Gln Ala Glu Gly Gln Trp Glu Glu Leu Ser Gly Leu
 35 40 45
 Asp Glu Glu Gln His Ser Val Arg Thr Tyr Glu Val Cys Asp Met Lys
 50 55 60
 Arg Pro Gly Gly Gln Ala His Trp Leu Arg Thr Gly Trp Val Pro Arg
 65 70 75 80
 Arg Gly Ala Val His Val Tyr Ala Thr Ile Arg Phe Thr Met Met Glu
 85 90 95
 Cys Leu Ser Leu Pro Arg Ala Ser Arg Ser Cys Lys Glu Thr Phe Thr

100	105	110
Val Phe Tyr Tyr Glu Ser Glu Arg Asp Thr Ala Thr Ala His Thr Pro		
115	120	125
Ala Trp Met Glu Asn Pro Tyr Ile Lys Val Asp Thr Val Ala Ala Glu		
130	135	140
His Leu Thr Arg Lys Arg Pro Gly Ala Glu Ala Thr Gly Lys Val Asn		
145	150	155
Ile Lys Thr Leu Arg Leu Gly Pro Leu Ser Lys Ala Gly Phe Tyr Leu		
165	170	175
Ala Phe Gln Asp Gln Gly Ala Cys Met Ala Leu Leu Ser Leu His Leu		
180	185	190
Phe Tyr Lys Lys Cys Ser Trp Leu Ile Thr Asn Leu Thr Tyr Phe Pro		
195	200	205
Glu Thr Val Pro Arg Glu Leu Val Val Pro Val Ala Gly Ser Cys Val		
210	215	220
Ala Asn Ala Val Pro Thr Ala Asn Pro Ser Pro Ser Leu Tyr Cys Arg		
225	230	235
Glu Asp Gly Gln Trp Ala Glu Gln Gln Val Thr Gly Cys Ser Cys Ala		
245	250	255
Pro Gly Tyr Glu Ala Ala Glu Ser Asn Lys Val Cys Arg Ala Cys Gly		
260	265	270
Gln Gly Thr Phe Lys Pro Gln Ile Gly Asp Glu Ser Cys Leu Pro Cys		
275	280	285
Pro Ala Asn Ser His Ser Asn Asn Ile Gly Ser Pro Val Cys Leu Cys		
290	295	300
Arg Ile Gly Tyr Tyr Arg Ala Arg Ser Asp Pro Arg Ser Ser Pro Cys		
305	310	315
Thr Thr Pro Pro Ser Ala Pro Arg Ser Val Val His His Leu Asn Gly		
325	330	335

Ser Thr Leu Arg Leu Glu Trp Ser Ala Pro Leu Glu Ser Gly Gly Arg
 340 345 350
 Glu Asp Leu Thr Tyr Ala Val Arg Cys Arg Glu Cys Arg Pro Gly Gly
 355 360 365
 Ser Cys Leu Pro Cys Gly Gly Asp Met Thr Phe Asp Pro Gly Pro Arg
 370 375 380
 Asp Leu Val Glu Pro Trp Val Ala Ile Arg Gly Leu Arg Pro Asp Val
 385 390 395 400
 Thr Tyr Thr Phe Glu Val Ala Ala Leu Asn Gly Val Ser Thr Leu Ala
 405 410 415
 Thr Gly Pro Pro Pro Phe Glu Pro Val Asn Val Thr Thr Asp Arg Glu
 420 425 430
 Val Pro Pro Ala Val Ser Asp Ile Arg Val Thr Arg Ser Ser Pro Ser
 435 440 445
 Ser Leu Ile Leu Ser Trp Ala Ile Pro Arg Ala Pro Ser Gly Ala Val
 450 455 460
 Leu Asp Tyr Glu Val Lys Tyr His Glu Lys Gly Ala Glu Gly Pro Ser
 465 470 475 480
 Ser Val Arg Phe Leu Lys Thr Ser Glu Asn Arg Ala Glu Leu Arg Gly
 485 490 495
 Leu Lys Arg Gly Ala Ser Tyr Leu Val Gln Val Arg Ala Arg Ser Glu
 500 505 510
 Ala Gly Tyr Gly Pro Phe Gly Gln Glu His His Ser Gln Thr Gln Leu
 515 520 525
 Asp Glu Ser Glu Ser Trp Arg Glu Gln Leu Ala Leu Ile Ala Gly Thr
 530 535 540
 Ala Val Val Gly Val Val Leu Val Leu Val Val Val Ile Ile Ala Val
 545 550 555 560
 Leu Cys Leu Arg Lys Gln Ser Asn Gly Arg Glu Val Glu Tyr Ser Asp

	565		570		575
Lys His Gly Gln Tyr Leu Ile Gly His Gly Thr Lys Val Tyr Ile Asp					
	580		585		590
Pro Phe Thr Tyr Glu Asp Pro Asn Glu Ala Val Arg Glu Phe Ala Lys					
	595		600		605
Glu Ile Asp Val Ser Tyr Val Lys Ile Glu Glu Val Ile Gly Ala Gly					
	610		615		620
Glu Phe Gly Glu Val Cys Arg Gly Arg Leu Lys Ala Pro Gly Lys Lys					
	625		630		635
					640
Glu Ser Cys Val Ala Ile Lys Thr Leu Lys Gly Gly Tyr Thr Glu Arg					
	645		650		655
Gln Arg Arg Glu Phe Leu Ser Glu Ala Ser Ile Met Gly Gln Phe Glu					
	660		665		670
His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Asn Ser Val Pro					
	675		680		685
Val Met Ile Leu Thr Glu Phe Met Glu Asn Gly Ala Leu Asp Ser Phe					
	690		695		700
Leu Arg Leu Asn Asp Gly Gln Phe Thr Val Ile Gln Leu Val Gly Met					
	705		710		715
					720
Leu Arg Gly Ile Ala Ser Gly Met Arg Tyr Leu Ala Glu Met Ser Tyr					
	725		730		735
Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu					
	740		745		750
Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Phe Leu Glu Glu Asn					
	755		760		765
Ser Ser Asp Pro Thr Tyr Thr Ser Ser Leu Gly Gly Lys Ile Ser Ile					
	770		775		780
Arg Trp Thr Ala Pro Glu Ala Ile Ala Phe Arg Lys Phe Thr Ser Ala					
	785		790		795
					800

Ser Asp Ala Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Phe
 805 810 815
 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Asn Ala
 820 825 830
 Ile Glu Gln Asp Tyr Arg Leu Pro Pro Pro Pro Asp Cys Pro Thr Ser
 835 840 845
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Asn Ala Arg
 850 855 860
 Pro Arg Phe Pro Gln Val Val Ser Ala Leu Asp Lys Met Ile Arg Asn
 865 870 875 880
 Pro Ala Ser Leu Lys Ile Val Ala Arg Glu Asn Gly Gly Ala Ser His
 885 890 895
 Pro Leu Leu Asp Gln Arg Gln Pro His Tyr Ser Ala Phe Gly Ser Val
 900 905 910
 Gly Glu Trp Leu Arg Ala Ile Lys Met Gly Arg Tyr Glu Glu Ser Phe
 915 920 925
 Ala Ala Ala Gly Phe Gly Ser Phe Glu Val Val Ser Gln Ile Ser Ala
 930 935 940
 Glu Asp Leu Leu Arg Ile Gly Val Thr Leu Ala Gly His Gln Lys Lys
 945 950 955 960
 Ile Leu Ala Ser Val Gln His Met Lys Ser Gln Ala Lys Pro Gly Ala
 965 970 975
 Pro Gly Gly Thr Gly Gly Pro Ala Gln Gln Phe
 980 985

<210> 323

<211> 5471

<212> DNA

<213> Mus musculus

<400> 323

cggatgaaga aaaaaaaaaa aagtagaggg agaagggcct cgtggagagg tgggaggggt 60
gtgtgtgata aagaacagcg gaccctacgg ccaaaagtaa ggaagaaaga gactaagagg 120
tagggggcca gacgaaagtc aggaagccag agaagagctg ctcagagggc cgagagtggc 180
gagacaaaga aagggcgctg ggaaagggca cttgcgcaa agctgtgaac tgcaaactgc 240
tggtgaaaaa gcagagaagg gctaagctac cgggtgacaa gaggtctgga actcaagggg 300
acgctaggaa aaggccggcc cggcgacacc caagtgtggg ggtccagtgt ggtgcgggcc 360
tacgtggacg gccgctgaat cagcaaggc tgtctgcccc cttccccca cccccggccg 420
gtaccgcgag tccccgcctc ctccggccgc gcctccacgg ggcggagccc tggccgggac 480
cagctgtctc gctataaagg ggctgcggcg aggcggcag aacgctgtga cagccacaca 540
cccaaggcc tccaagatga gctacacgt ggactcgctg ggcaaccgt cgcctaccg 600
gcgcgttcca accgagacce ggtccagctt cagccgcgtg agcggttccc cgtccagcgg 660
cttcgcctcg cagtcctggt cccgcggctc gccagcacc gtgtcctcct cctacacgcg 720
cagcgcggtc gccccgcgtc tcgcctacag ctccgctaig ctcagctcgg ccgagagcag 780
cctcgacttc agccagtcct cgtcgctgct caacggcggc tccggcggcg actacaaact 840
gtcccgtctt aacgagaaag agcagctgca ggggctgaac gaccgcttcg ccggtacat 900
cgagaaagtg cactacttgg aacaacagaa caaggagatc gaagcagaga tccaggcact 960
gcggcagaag caggcctcgc acgccagct gggatgatgt tacgaccagg agatccgaga 1020
gctgcgcgcc accctcgaga tggatgaacca cgagaaggct caagtgcagc tggactccga 1080
tcacttggag gaagacatcc accggctcaa ggagcgcttc gaggaggagg cgcggctgcg 1140
ggacgacacc gaggtgccca ttgcgcgct gcgcaaagac atcgaagagt cgtcgatggt 1200
taaggtggag ctggacaaga aggtgcagtc gctgcaggat gaggtggctt tcctgcggcg 1260
taatcacgaa gaggaggtgg ccgacctgt ggctcagatc caggcgtcgc acatcacggt 1320
agagcgcaaa gattacctga agacagacat ctccacggcg ctgaaggaga tccgtccca 1380
gctcgagtgt cactcagacc agaactgca ccaggccgaa gagtgggtca aatgccgcta 1440
cgccaagctc accgagggcg ccgagcagaa caaggaggcc attcgctctg ccaaggaaga 1500
gatcgccgag taccggcgcc agctgcagtc caagagcatc gagctcgagt cgggtcgagg 1560
cactaaggag tccctggaac ggcagctcag cgacatcgag gagcgccaca accacgacct 1620

cagcagctac caggtaggaa ccgcccggctg ggccggcctg cgcaggccag gccgcgcgcc 1680
ccgacacgac actcgagagc gcgcccagag gccctcttgg tcgcgctccc tggiggccgc 1740
atccagtg cgcacgagc ttgcgagacg cgggttagcc aaagcccaag gtctgtgctc 1800
gccctcctcc ttgccccacc cacttgccgc aactacttag aaattgccat ctgcttccga 1860
aaaacttgct ttcciatgat agatttactg taaaagtaaa aaggcacatt ctggtcgttg 1920
agaaacacac cgtttaataa gcaggagcat agatagctc ttgtattcct gcctcccttc 1980
ttcgctcccc ttccccctcc ccaccataat ctccacccct cctcctcacc cccttactct 2040
ccactccacc cccccgccc cgcctccagc cgcggatggg cgagctctca aagctggctt 2100
catccaaaat ttccgggggg ggggggcaaa gtccgctagg accttctca gattcctcag 2160
tgctccctta taggggccat ctaggcttgc cagtctccgt gtgtgttggt cctaggaact 2220
gtctgggtga tttttgttg tttgtttga attttactat cataaaagaa ggagggatac 2280
taggagggat gtctgcgagg ctcattgggac tggcggggaa gggggaattc cgggggtggg 2340
taggaaagg ctcggggcag ggaatagcaa gtgtcttggt aaggaagttt ctagagactc 2400
cctgtacctt tcaggacacc atccagcagt tggaaaatga acctcgggga accaagtggg 2460
aaatggctcg tcatttgcga gaataccagg atctccttaa cgtcaagatg gccctggaca 2520
tcgagatcgc cgcgtacagg tacaggatct ctgcagactt ggtccagacc ctacaggcac 2580
tgcagaggct gctgcgaaca ccttccccac attaaagcaa agctgacctt gtgagccagg 2640
ctcagagccc tgactcccca gctcagttac gaacagaatc ctaagtatta cagatacagg 2700
tttaccaacc tacttcagct ttaaagagtg actacggaga agatcgggga ggagggtgga 2760
actggggaag ggaacaaaa tatattgtat gaaaaagcc caaatatgca ccaaagaata 2820
gtacttttga gttgctgggg gcgtcagaat aggtttaaat tttgtttca agcatctgta 2880
tgtctgacaa gcagatgaag ttttcatttt taatatttca tctgatggtt ctcttttata 2940
aagccaagga caaacaccag gtcattgctt tctctctgt tacagcttat gttgccatcc 3000
tctggctgag actagatata ggcacactag aatatagctg cacttatatt aagcttatgg 3060
ataatataca tgcattcaat ctggctagaa atgtaaattt aatatatatt tatctacata 3120
tgtaaagigt gataccctca tatcgttaga tctacaaagg ctatcaggtc atgcgtgaga 3180
gtctggagca aaccaggaaa catatagaac tagacatata ggcaaatata gtttgtctct 3240
ttatctgtaa actgattcta tctaggctc ctgagtaatg ctgtctttct gttggccaga 3300
ctcaaagcat acagctcttg aggaggcagt cacttctgt aaggctgta tagcaagaat 3360

aaactgcact gtccttttta agggaaccaa acgattgtac caagagagca ttctgtcact 3420
gaacaaatta taatttgctt cacctatatt cgtatgtagc tataatttca aattcatcaa 3480
cattctgact taigctcaat agttttaatt ttaaattgaa catittatit gcttttaaaa 3540
ctcatagaaa tcttggcaat tcaaacgatg agggaggaca ccgtttgggg gacaaagtgg 3600
gttggccact agagaccatt ttagcacatt catactacac ctacaccaac tgcattgcctg 3660
ccgcagagct gcatttactg actgggtgtg gttagtgtc tactgggagt ggctaggcgc 3720
tgagcagagg actgtctggc actcttggag aatctgcccc aggataatgat aaacattgtt 3780
gatgaaatgg cagtaagcac tcactgccct ggtagaaaga gtatttcctt acgtggttct 3840
atttattcaa aagtgccac tacattaagc ttgtggtaat gaagattaga agaccaaaca 3900
agtctttctt gatgtctcat cctcttttgt tctctctta ggaaactcct agagggggaa 3960
gagaccagat ttagcacatt ttcaggaagc atcacgggc ctctgtacac acaccgacag 4020
ccctcagica caatatccag taagattcag aagaccaaag tcgaggcccc caagctcaag 4080
gtccaacaca aatttgtgga ggagatcatc gaagaaacta aagtgaaga tgagaagtca 4140
gaaatggaag aaaccctcac agccatcgca gaggagttag cagcctccgc caaagaggag 4200
aaggaagagg ccgaagaaaa ggaggaggaa ccagaagccg aaaagtctcc cgtgaagtct 4260
cctgaggcta aggaagagga ggaggaaggg gaaaaggagg aagaagagga aggccaggag 4320
gaagaagagg aggaagatga aggtgtcaag tcagaccagg cagaagaggg gggatctgag 4380
aaggaaggct ccagtgaata agatgaaggt gagcaggaag aagaagaagg agaaaccgag 4440
gcagaagggt aaggagagga agcagaagct aaggaggaaa agaaaattga gggaaaggtt 4500
gaggaagtgg ctgtcaagga ggaaatcaag gtcgagaagc ctgagaaagc caaatccctt 4560
atgcccataat caccgttga agaagtaaag ccaaaaccag aggccaaagg cgggaagggt 4620
gagcagaagg aggaagagaa agttgaggaa gagaagaagg aagtcaccaa agaatcacc 4680
aaggaagaga aggtggagaa aaaggaggag aagccaaaag atgttgacga taaaaagaag 4740
gccgagtcct cgtgaaaga gaaggctgtg gaggagggtg tcaccatcag caagtcggt 4800
aaggtgagcc tggagaaaga caccaaagag gagaagccgc agccgcagga gaaggtgaag 4860
gagaaggcag aggaggaggg gggcagttag gaggaaggga gtgaccgtag cccgcaggag 4920
tccaagaagg aagacatagc tatcaatggg gaggtggaag gaaaagagga ggaggagcag 4980
gaaactcagg agaagggcag tgggcgggag gaggagaaag ggggtgtcac taatggctta 5040
gatgtgagcc ctgcagagga gaagaaagga gaggatagca gtgatgataa agtgggtgtc 5100

accaagaagg tagaaaagat caccagcgag ggaggcgatg gtgctaccaa atacatcacc 5160
 aaatctgtaa ccgtcacica aaaggittgaa gagcatgagg agaccittga ggagaagctg 5220
 gtctcaacta aaaaggtaga aaaggtcact tcacacgcca tagtcaagga agtcaccag 5280
 ggtgactaag atcggagicc gtigcaaaag gttaagccat acgacaattt caaaatgcat 5340
 gtgattgaca gcttcaaaac agaatgggtt ctcccatggg ggctccagac attgtatttt 5400
 cctttgtgca atatgaggga actgcatgca agctcagggt gccccctcc tcagtccttg 5460
 gggggaattc c 5471

<210> 324

<211> 487

<212> DNA

<213> Mus musculus

<400> 324

gcggcctcct tacccaactt caggtaacaa tggggatccc agtggggaag tcgatgttgg 60
 tgcttctcat ctctttggcc ttgccttgt gctgcatcgc tgcctacggc tccggagaga 120
 ctctgtgctg agtggagcct gttagacagc ttcagtcgt ctgttcggat cgcggcttct 180
 atttcagcag gccttcaacc cgtgcaaacg gtcgcagcgg ttcatcgtgg gatgagtgc 240
 gcttccgaac tgccaccctg gccttctgt agacatactg tgtcaacccc ggccagtcct 300
 caaatggact ggctctcctt tagggccgta ctccggacc gattccctag ataccgcttg 360
 gtcaagtttt gccattttgt cccttgtagg tagtccgctg gacgttgcta taaggcctcc 420
 ttcaattctt gcgttgcacc ctgggttgta ttcttgtcaa ggactcaaga cattctggag 480
 cgccaaa 487

<210> 325

<211> 431

<212> DNA

<213> Mus musculus

<400> 325

accttcggca cttcgatccc gagtttaccg aggagccggt ccccagctcc atcggcaggt 60
 cccctgacag catccttgtc acggccagtg tgaaggaagc agcagaagcc ttcctcggct 120
 tctcctatgc acctcctgtg gattccttcc tctgagtgct cccgggatgg ttctgaagga 180
 cttcctcage gtttcctaaa gtgttttcgt tagcctttgg tggagttgcc agctgacaga 240
 acattttaaa agaatttgca cacctggaag ctgggcagtc tcgcctgccc ggcgtggcgc 300
 gacgcagccg gcnnitgcttg agtgggagct ttccgaagag cacaccctcc tctcaatgag 360
 cttgtgaggt cttcttttct tctcttccct ccaacgtggt gctagctcca ggcgagcgag 420
 cgtgagagtg c 431

<210> 326

<211> 2125

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (115).. (1434)

<400> 326

gcttttctaaa ctagcaagca tcgtgtgggt ccttcaggag tgggagtgc gacagacctg 60
 acagcgtccg ctaagcgaca ctgactgtac ttccactcct gaaggacceca cacg atg 117
 Met
 1
 ctt tct aaa cta gca agt ctg cag acc att gct gct ctg cgc cga gga 165
 Leu Ser Lys Leu Ala Ser Leu Gln Thr Ile Ala Ala Leu Arg Arg Gly
 5 10 15
 gtc cac acc tca gtc gcc tct gcc acg tct gtt gcc aca aag aag aca 213
 Val His Thr Ser Val Ala Ser Ala Thr Ser Val Ala Thr Lys Lys Thr

20	25	30	
gag caa ggc cca cca tcc tcc gag tac att ttt gaa cgg gaa tct aaa			261
Glu Gln Gly Pro Pro Ser Ser Glu Tyr Ile Phe Glu Arg Glu Ser Lys			
35	40	45	
tat ggt gca cac aat tac cat cct ttg cct gta gcc ctg gag aga gga			309
Tyr Gly Ala His Asn Tyr His Pro Leu Pro Val Ala Leu Glu Arg Gly			
50	55	60	65
aaa ggc att tat atg tgg gat gtg gaa ggc agg cag tac ttc gat ttc			357
Lys Gly Ile Tyr Met Trp Asp Val Glu Gly Arg Gln Tyr Phe Asp Phe			
	70	75	80
ctg agt gct tat ggt gct gtc agc caa gga cac tgc cac cca aag atc			405
Leu Ser Ala Tyr Gly Ala Val Ser Gln Gly His Cys His Pro Lys Ile			
85	90	95	
ata gat gcc atg aag agt cag gtg gac aag ctg aca tta aca tct cgg			453
Ile Asp Ala Met Lys Ser Gln Val Asp Lys Leu Thr Leu Thr Ser Arg			
100	105	110	
gct ttc tat aac aat gtc ctt ggt gaa tac gag gag tac atc acc aag			501
Ala Phe Tyr Asn Asn Val Leu Gly Glu Tyr Glu Glu Tyr Ile Thr Lys			
115	120	125	
ctt ttc aac tac aac aaa gtt ctc cct atg aat aca gga gtg gag gct			549
Leu Phe Asn Tyr Asn Lys Val Leu Pro Met Asn Thr Gly Val Glu Ala			
130	135	140	145
gga gag act gca tgt aag ctc gct cgt cgt tgg ggc tac acc gtg aaa			597
Gly Glu Thr Ala Cys Lys Leu Ala Arg Arg Trp Gly Tyr Thr Val Lys			
	150	155	160
ggc atc cag aaa tac aaa gca aag att gtt ttt gct gat ggg aac ttt			645
Gly Ile Gln Lys Tyr Lys Ala Lys Ile Val Phe Ala Asp Gly Asn Phe			
165	170	175	
tgg ggt cga aca cta tct gca atc tcc agt tcc aca gat ccg acc agt			693

Trp Gly Arg Thr Leu Ser Ala Ile Ser Ser Ser Thr Asp Pro Thr Ser	
180	185
190	
tat gat ggc ttt gga ccc ttc atg cca ggc ttt gaa acc atc cca tat	741
Tyr Asp Gly Phe Gly Pro Phe Met Pro Gly Phe Glu Thr Ile Pro Tyr	
195	200
205	
aac gat ctg ccc gca ctg gag cgt gct ctt cag gat cca aat gtt gct	789
Asn Asp Leu Pro Ala Leu Glu Arg Ala Leu Gln Asp Pro Asn Val Ala	
210	215
220	225
gcc ttc atg gtg gag ccc atc cag ggt gaa gca ggc gtt atc gtt ccg	837
Ala Phe Met Val Glu Pro Ile Gln Gly Glu Ala Gly Val Ile Val Pro	
230	235
240	
gat cca gga tac ctg aca gga gtt cgg gaa ctc tgc acc agg cac cag	885
Asp Pro Gly Tyr Leu Thr Gly Val Arg Glu Leu Cys Thr Arg His Gln	
245	250
255	
gtc ctg ttt att gct gat gaa ata cag aca gga ttg gcc aga act ggt	933
Val Leu Phe Ile Ala Asp Glu Ile Gln Thr Gly Leu Ala Arg Thr Gly	
260	265
270	
aga tgg ctg gct gtg gat cat gag aat gtc aga cct gat atg gtt ctt	981
Arg Trp Leu Ala Val Asp His Glu Asn Val Arg Pro Asp Met Val Leu	
275	280
285	
ctt ggg aag gcc ctt tct ggc ggt tta tac cct gtg tct gca gtg ctg	1029
Leu Gly Lys Ala Leu Ser Gly Gly Leu Tyr Pro Val Ser Ala Val Leu	
290	295
300	305
tgt gac gat gag ata atg ctg acc att aaa cca ggc gag cac ggc tcc	1077
Cys Asp Asp Glu Ile Met Leu Thr Ile Lys Pro Gly Glu His Gly Ser	
310	315
320	
aca tac ggc gga aac cca cta ggc tgc cga att gcc att gcg gct ctt	1125
Thr Tyr Gly Gly Asn Pro Leu Gly Cys Arg Ile Ala Ile Ala Ala Leu	
325	330
335	

gag gtt tta gaa gag gag aat ctt gct gag aat gca gac aag atg ggc 1173
 Glu Val Leu Glu Glu Glu Asn Leu Ala Glu Asn Ala Asp Lys Met Gly
 340 345 350
 gct atc ctg agg aag gag ctc atg aag ctg ccc tct gac gtt gtg acc 1221
 Ala Ile Leu Arg Lys Glu Leu Met Lys Leu Pro Ser Asp Val Val Thr
 355 360 365
 tca gtg aga ggg aaa ggg ttg cta aat gcc att gtc atc aga gaa acc 1269
 Ser Val Arg Gly Lys Gly Leu Leu Asn Ala Ile Val Ile Arg Glu Thr
 370 375 380 385
 aaa gac tgt gat gct tgg aag gtg tgc ctg cga ctt cga gat aac ggg 1317
 Lys Asp Cys Asp Ala Trp Lys Val Cys Leu Arg Leu Arg Asp Asn Gly
 390 395 400
 ctt ctg gcc aag cca acc cac ggt gat atc atc agg ctt gcc cct ccc 1365
 Leu Leu Ala Lys Pro Thr His Gly Asp Ile Ile Arg Leu Ala Pro Pro
 405 410 415
 ctt gtg atc aag gag gat gag atc cgg gag tcc gtg gag atc atc aac 1413
 Leu Val Ile Lys Glu Asp Glu Ile Arg Glu Ser Val Glu Ile Ile Asn
 420 425 430
 aag act atc ttg tcc ttc tga gtagtagaac tctggggagc catcttcaga 1464
 Lys Thr Ile Leu Ser Phe
 435 440
 cagggctctt gtgaaactct gcttgcagt gccagagcct gtctcctgaa aggcatatat 1524
 ttcagttgat gcataataga gtgacaccta ggaacctgca ggtggctgcg tgacagaaaa 1584
 gtgagagcga gaggcgaggc gtctctttgt tgaggtttga ctgtgtggga actttctaag 1644
 gaaaaacgga cccatctgcg tacagcctgc agatggaggc ctgcagtcac ttacgtgcgt 1704
 ctttacagtt tccttgctga tgtgaatggt ttgtatttag aagttatttc tgagatacta 1764
 cagaacagtt aaatcattat aatcaatgaa tgttaagttg attgaagggt aagcatatgt 1824
 aaaatactag tttaaagtaa acitttcatt ggccaacacc agaattgatt atatagattc 1884
 tgagaattca ttactaaatt acactttgct tgattgcaat ttgtaaaaca tttattttca 1944

gtatttcitt gaataaagct taatgtttct ttttacgcca acagagtatt ttgtatttcc 2004
 attttggtaa taatcagigt attatttcat cctgatgact ggcatttcat cacctattga 2064
 gatcactggg tgtgtttcag gccttttatt ctaaataaag ctatgaccag tttctgtctg 2124
 t 2125

<210> 327

<211> 439

<212> PRT

<213> Mus musculus

<400> 327

Met Leu Ser Lys Leu Ala Ser Leu Gln Thr Ile Ala Ala Leu Arg Arg
 1 5 10 15
 Gly Val His Thr Ser Val Ala Ser Ala Thr Ser Val Ala Thr Lys Lys
 20 25 30
 Thr Glu Gln Gly Pro Pro Ser Ser Glu Tyr Ile Phe Glu Arg Glu Ser
 35 40 45
 Lys Tyr Gly Ala His Asn Tyr His Pro Leu Pro Val Ala Leu Glu Arg
 50 55 60
 Gly Lys Gly Ile Tyr Met Trp Asp Val Glu Gly Arg Gln Tyr Phe Asp
 65 70 75 80
 Phe Leu Ser Ala Tyr Gly Ala Val Ser Gln Gly His Cys His Pro Lys
 85 90 95
 Ile Ile Asp Ala Met Lys Ser Gln Val Asp Lys Leu Thr Leu Thr Ser
 100 105 110
 Arg Ala Phe Tyr Asn Asn Val Leu Gly Glu Tyr Glu Glu Tyr Ile Thr
 115 120 125
 Lys Leu Phe Asn Tyr Asn Lys Val Leu Pro Met Asn Thr Gly Val Glu
 130 135 140

Ala Gly Glu Thr Ala Cys Lys Leu Ala Arg Arg Trp Gly Tyr Thr Val
 145 150 155 160
 Lys Gly Ile Gln Lys Tyr Lys Ala Lys Ile Val Phe Ala Asp Gly Asn
 165 170 175
 Phe Trp Gly Arg Thr Leu Ser Ala Ile Ser Ser Ser Thr Asp Pro Thr
 180 185 190
 Ser Tyr Asp Gly Phe Gly Pro Phe Met Pro Gly Phe Glu Thr Ile Pro
 195 200 205
 Tyr Asn Asp Leu Pro Ala Leu Glu Arg Ala Leu Gln Asp Pro Asn Val
 210 215 220
 Ala Ala Phe Met Val Glu Pro Ile Gln Gly Glu Ala Gly Val Ile Val
 225 230 235 240
 Pro Asp Pro Gly Tyr Leu Thr Gly Val Arg Glu Leu Cys Thr Arg His
 245 250 255
 Gln Val Leu Phe Ile Ala Asp Glu Ile Gln Thr Gly Leu Ala Arg Thr
 260 265 270
 Gly Arg Trp Leu Ala Val Asp His Glu Asn Val Arg Pro Asp Met Val
 275 280 285
 Leu Leu Gly Lys Ala Leu Ser Gly Gly Leu Tyr Pro Val Ser Ala Val
 290 295 300
 Leu Cys Asp Asp Glu Ile Met Leu Thr Ile Lys Pro Gly Glu His Gly
 305 310 315 320
 Ser Thr Tyr Gly Gly Asn Pro Leu Gly Cys Arg Ile Ala Ile Ala Ala
 325 330 335
 Leu Glu Val Leu Glu Glu Glu Asn Leu Ala Glu Asn Ala Asp Lys Met
 340 345 350
 Gly Ala Ile Leu Arg Lys Glu Leu Met Lys Leu Pro Ser Asp Val Val
 355 360 365
 Thr Ser Val Arg Gly Lys Gly Leu Leu Asn Ala Ile Val Ile Arg Glu

370	375	380	
Thr Lys Asp Cys Asp Ala Trp Lys Val Cys Leu Arg Leu Arg Asp Asn			
385	390	395	400
Gly Leu Leu Ala Lys Pro Thr His Gly Asp Ile Ile Arg Leu Ala Pro			
	405	410	415
Pro Leu Val Ile Lys Glu Asp Glu Ile Arg Glu Ser Val Glu Ile Ile			
	420	425	430
Asn Lys Thr Ile Leu Ser Phe			
435			

<210> 328

<211> 407

<212> DNA

<213> Mus musculus

<400> 328

```

cgctgtatcc ccgaggctta cagatcgccc agtaatgtca tccaagtcta tgggtctggg 60
ttactgggag atcctcgggc tggctcatgc tatccgcatg cttctggagt ggactgatgc 120
cagctatgag gagaaacggt acatctgttg ggaagctcct gactatgaga taagccaatg 180
gctgtacggt gaaattcaag ctagatctgg acttgcctaa cctgccctac ctcatggacg 240
ggaagaacaa gatcagccag actaaccgcc atcctgagat acatcgcatg gaagcacaac 300
atttgtggtg aactgtacg aggaagagag acgagtagac gtcatggaga agcagatcat 360
gggctttctg cagtcagctg gttcgccgct gctacaattc tagccac 407

```

<210> 329

<211> 474

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (16).. (204)

<400> 329

cggagtcagg ccaac atg agt gag aga caa agt gcc gga gcg acc aac gga 51

Met Ser Glu Arg Gln Ser Ala Gly Ala Thr Asn Gly

1

5

10

aaa gac aag acg tca gga gat aat gat ggg cag aag aaa gtc caa gaa 99

Lys Asp Lys Thr Ser Gly Asp Asn Asp Gly Gln Lys Lys Val Gln Glu

15

20

25

gaa ttt gat atc gac atg gat gca cca gag aca gag cgt gca gct gtg 147

Glu Phe Asp Ile Asp Met Asp Ala Pro Glu Thr Glu Arg Ala Ala Val

30

35

40

gcc att cag tct cag ttc aga aaa ttc cag aag aaa aag gca gga tca 195

Ala Ile Gln Ser Gln Phe Arg Lys Phe Gln Lys Lys Lys Ala Gly Ser

45

50

55

60

cag tcc tag tggatgaagct gcttcctggt ccacctgaag acaccaagtt 244

Gln Ser

caaccacccat ccatcaagaa atgaaaagaa caatacccta gagagaagtc atcctcactc 304

aatacacacc ctgctacaaa cctgaaatgc atgaagagaa acccatagta tttatgcccc 364

ctataggcag gtatccacag taaaattgtg agtagcttaa tctgtttatc tccattacaa 424

ttcctctgca actatatttcc ttgatgttgt aataaaaagg aggtaagatg 474

<210> 330

<211> 62

<212> PRT

<213> Mus musculus

<400> 330

Met Ser Glu Arg Gln Ser Ala Gly Ala Thr Asn Gly Lys Asp Lys Thr

1

5

10

15

Ser Gly Asp Asn Asp Gly Gln Lys Lys Val Gln Glu Glu Phe Asp Ile

20

25

30

Asp Met Asp Ala Pro Glu Thr Glu Arg Ala Ala Val Ala Ile Gln Ser

35

40

45

Gln Phe Arg Lys Phe Gln Lys Lys Lys Ala Gly Ser Gln Ser

50

55

60

<210> 331

<211> 2244

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (254).. (2164)

<400> 331

ccgccccgcc cgcggccccg cagctccaag caggaaccca gagaccgagg ccttcctgcc 60

gccccgaccc agcaccccca gcctcgtcc cccggttcca cggccgtiga gtacgcgtcg 120

attccggttg aattttgtcc ctctgcgtc gccccgctc cctcccccc ggctccgtcc 180

cccgccccg cactcgtctt cctccttca cgggaaaggt cgcggcctgc ggccccgagg 240

cagccgtgcc gag atg aac ccc agc gcc ccc agc tac ccc atg gcc tct 289

Met Asn Pro Ser Ala Pro Ser Tyr Pro Met Ala Ser

1

5

10

ctg tac gtg ggg gac ctg cac ccc gac gtg acc gag gcg atg ctc tac 337

Leu Tyr Val Gly Asp Leu His Pro Asp Val Thr Glu Ala Met Leu Tyr

15	20	25	
gag aag ttc agc ccg gcc ggg ccc atc ctc tcc atc cgg gtc tgc agg 385			
Glu Lys Phe Ser Pro Ala Gly Pro Ile Leu Ser Ile Arg Val Cys Arg			
30	35	40	
gac atg atc acc cgc cgc tcc ttg ggc tac gcg tac gtg aac ttc cag 433			
Asp Met Ile Thr Arg Arg Ser Leu Gly Tyr Ala Tyr Val Asn Phe Gln			
45	50	55	60
cag ccg gcg gac gcg gaa cgt gct ttg gac acc atg aat ttt gat gtt 481			
Gln Pro Ala Asp Ala Glu Arg Ala Leu Asp Thr Met Asn Phe Asp Val			
	65	70	75
ata aag ggc aag cca gta cgc atc atg tgg tct cag cgt gat cca tca 529			
Ile Lys Gly Lys Pro Val Arg Ile Met Trp Ser Gln Arg Asp Pro Ser			
80	85	90	
ctt cgc aaa agt gga gta ggc aac ata ttc att aaa aat ttg gac aaa 577			
Leu Arg Lys Ser Gly Val Gly Asn Ile Phe Ile Lys Asn Leu Asp Lys			
95	100	105	
tcc atc gac aat aaa gca cta tat gat acg ttt tct gcg ttt ggt aac 625			
Ser Ile Asp Asn Lys Ala Leu Tyr Asp Thr Phe Ser Ala Phe Gly Asn			
110	115	120	
atc ctt tca tgt aag gtg gtt tgt gat gaa aat ggc tcc aag ggc tat 673			
Ile Leu Ser Cys Lys Val Val Cys Asp Glu Asn Gly Ser Lys Gly Tyr			
125	130	135	140
gga ttt gta cac ttt gaa aca cag gaa gca gct gaa aga gct att gaa 721			
Gly Phe Val His Phe Glu Thr Gln Glu Ala Ala Glu Arg Ala Ile Glu			
	145	150	155
aaa atg aat ggg atg ctt cta aat gat cgt aaa gtg ttt gtt gga cga 769			
Lys Met Asn Gly Met Leu Leu Asn Asp Arg Lys Val Phe Val Gly Arg			
160	165	170	
ttt aaa tct cag aag gaa cga gaa gca gag ctt gga gcc agg gca aag 817			

Phe Lys Ser Gln Lys Glu Arg Glu Ala Glu Leu Gly Ala Arg Ala Lys
 175 180 185
 gag ttc acc aat gtt tac atc aag aac ttt gga gaa gac atg gat gat 865
 Glu Phe Thr Asn Val Tyr Ile Lys Asn Phe Gly Glu Asp Met Asp Asp
 190 195 200
 gag cgc ctt aag gaa ctc ttt ggc aag ttt ggg cct gcc tta agt gtg 913
 Glu Arg Leu Lys Glu Leu Phe Gly Lys Phe Gly Pro Ala Leu Ser Val
 205 210 215 220
 aaa gta atg aca gat gaa agt gga aaa tcc aaa gga ttt gga ttt gta 961
 Lys Val Met Thr Asp Glu Ser Gly Lys Ser Lys Gly Phe Gly Phe Val
 225 230 235
 agc ttt gaa agg cat gaa gat gcg cag aaa gct gtg gat gag atg aat 1009
 Ser Phe Glu Arg His Glu Asp Ala Gln Lys Ala Val Asp Glu Met Asn
 240 245 250
 ggg aag gag ctc aat gga aaa cag att tat gtt gga cga gct cag aaa 1057
 Gly Lys Glu Leu Asn Gly Lys Gln Ile Tyr Val Gly Arg Ala Gln Lys
 255 260 265
 aaa gtg gaa cgg cag acg gaa ctt aag cgc aaa ttt gag cag atg aag 1105
 Lys Val Glu Arg Gln Thr Glu Leu Lys Arg Lys Phe Glu Gln Met Lys
 270 275 280
 caa gat agg atc acc aga tat cag ggt gtg aac ctt tat gtg aaa aat 1153
 Gln Asp Arg Ile Thr Arg Tyr Gln Gly Val Asn Leu Tyr Val Lys Asn
 285 290 295 300
 ctt gat gac ggg att gat gat gag cgt ctc cgg aag gag ttt tct ccg 1201
 Leu Asp Asp Gly Ile Asp Asp Glu Arg Leu Arg Lys Glu Phe Ser Pro
 305 310 315
 ttt ggt aca atc acc agt gca aaa gta atg atg gag ggt ggg cgc agc 1249
 Phe Gly Thr Ile Thr Ser Ala Lys Val Met Met Glu Gly Gly Arg Ser
 320 325 330

aaa ggg ttt ggt ttt gta tgt ttc tca tcc cct gaa gaa gcc act aaa 1297
 Lys Gly Phe Gly Phe Val Cys Phe Ser Ser Pro Glu Glu Ala Thr Lys
 335 340 345
 gca gtt aca gag atg aat ggt aga att gtg gcc acg aag cca ctg tat 1345
 Ala Val Thr Glu Met Asn Gly Arg Ile Val Ala Thr Lys Pro Leu Tyr
 350 355 360
 gta gct tta gct cag cgc aaa gaa gag cgc cag gct cac ctc act aac 1393
 Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His Leu Thr Asn
 365 370 375 380
 cag tat atg cag agg atg gca agt gta cga gct gtg ccc aac ccc gtg 1441
 Gln Tyr Met Gln Arg Met Ala Ser Val Arg Ala Val Pro Asn Pro Val
 385 390 395
 atc aac ccc tac cag cca gca cct cct tca ggt tac ttc atg gca gct 1489
 Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe Met Ala Ala
 400 405 410
 atc cca cag act cag aac cgt gct gca tac tat cct cct agc caa att 1537
 Ile Pro Gln Thr Gln Asn Arg Ala Ala Tyr Tyr Pro Pro Ser Gln Ile
 415 420 425
 gct caa cta aga cca agt cct cgc tgg act gct cag ggt gcc aga cct 1585
 Ala Gln Leu Arg Pro Ser Pro Arg Trp Thr Ala Gln Gly Ala Arg Pro
 430 435 440
 cat cca ttc cag aat atg ccc ggt gct atc cgc cca gct gct cct aga 1633
 His Pro Phe Gln Asn Met Pro Gly Ala Ile Arg Pro Ala Ala Pro Arg
 445 450 455 460
 cca cca ttt agt acg atg aga cca gct tcc tca cag gtt cca cga gtc 1681
 Pro Pro Phe Ser Thr Met Arg Pro Ala Ser Ser Gln Val Pro Arg Val
 465 470 475
 atg tca aca cag cgt gtt gct aac aca tca aca cag aca atg ggt cca 1729
 Met Ser Thr Gln Arg Val Ala Asn Thr Ser Thr Gln Thr Met Gly Pro

480	485	490	
cgt cct gca gct gct gct gct gca gcc act cct gct gtc cgc acc gtt			1777
Arg Pro Ala Ala Ala Ala Ala Ala Ala Thr Pro Ala Val Arg Thr Val			
495	500	505	
ccc cag tat aaa tat gct gcg gga gtc cgc aat ccc cag caa cat ctt			1825
Pro Gln Tyr Lys Tyr Ala Ala Gly Val Arg Asn Pro Gln Gln His Leu			
510	515	520	
aat gca cag cca caa gtt acc atg caa cag cct gct gtt cat gtg caa			1873
Asn Ala Gln Pro Gln Val Thr Met Gln Gln Pro Ala Val His Val Gln			
525	530	535	540
ggt caa gaa cct tta act gct tcc atg ttg gca tct gcg ccc ccg caa			1921
Gly Gln Glu Pro Leu Thr Ala Ser Met Leu Ala Ser Ala Pro Pro Gln			
545	550	555	
gag cag aag caa atg ttg ggt gaa cgg ctg ttt cct ctt atc caa gcc			1969
Glu Gln Lys Gln Met Leu Gly Glu Arg Leu Phe Pro Leu Ile Gln Ala			
560	565	570	
atg cac cct tct ctt gct ggt aaa atc act ggc atg ctg ttg gag att			2017
Met His Pro Ser Leu Ala Gly Lys Ile Thr Gly Met Leu Leu Glu Ile			
575	580	585	
gat aac tca gaa tta ctt cac atg ctc gag tct cca gag tct ctc cgc			2065
Asp Asn Ser Glu Leu Leu His Met Leu Glu Ser Pro Glu Ser Leu Arg			
590	595	600	
tca aag gtt gat gaa gct gta gct gta cta caa gcc cac caa gcg aaa			2113
Ser Lys Val Asp Glu Ala Val Ala Val Leu Gln Ala His Gln Ala Lys			
605	610	615	620
gag gct gcc cag aaa gca gtg aac agt gcc act ggt gtt cca act gtc			2161
Glu Ala Ala Gln Lys Ala Val Asn Ser Ala Thr Gly Val Pro Thr Val			
625	630	635	
taa attgatcagg gaccacgaac agaaactcgt gcttcaccga agaaaaatat			2214

cttaaaccatc gaaaaattta aatattatga

2244

<210> 332

<211> 636

<212> PRT

<213> Mus musculus

<400> 332

Met Asn Pro Ser Ala Pro Ser Tyr Pro Met Ala Ser Leu Tyr Val Gly
 1 5 10 15
 Asp Leu His Pro Asp Val Thr Glu Ala Met Leu Tyr Glu Lys Phe Ser
 20 25 30
 Pro Ala Gly Pro Ile Leu Ser Ile Arg Val Cys Arg Asp Met Ile Thr
 35 40 45
 Arg Arg Ser Leu Gly Tyr Ala Tyr Val Asn Phe Gln Gln Pro Ala Asp
 50 55 60
 Ala Glu Arg Ala Leu Asp Thr Met Asn Phe Asp Val Ile Lys Gly Lys
 65 70 75 80
 Pro Val Arg Ile Met Trp Ser Gln Arg Asp Pro Ser Leu Arg Lys Ser
 85 90 95
 Gly Val Gly Asn Ile Phe Ile Lys Asn Leu Asp Lys Ser Ile Asp Asn
 100 105 110
 Lys Ala Leu Tyr Asp Thr Phe Ser Ala Phe Gly Asn Ile Leu Ser Cys
 115 120 125
 Lys Val Val Cys Asp Glu Asn Gly Ser Lys Gly Tyr Gly Phe Val His
 130 135 140
 Phe Glu Thr Gln Glu Ala Ala Glu Arg Ala Ile Glu Lys Met Asn Gly
 145 150 155 160
 Met Leu Leu Asn Asp Arg Lys Val Phe Val Gly Arg Phe Lys Ser Gln

	165		170		175										
Lys	Glu	Arg	Glu	Ala	Glu	Leu	Gly	Ala	Arg	Ala	Lys	Glu	Phe	Thr	Asn
	180		185		190										
Val	Tyr	Ile	Lys	Asn	Phe	Gly	Glu	Asp	Met	Asp	Asp	Glu	Arg	Leu	Lys
	195		200		205										
Glu	Leu	Phe	Gly	Lys	Phe	Gly	Pro	Ala	Leu	Ser	Val	Lys	Val	Met	Thr
	210		215		220										
Asp	Glu	Ser	Gly	Lys	Ser	Lys	Gly	Phe	Gly	Phe	Val	Ser	Phe	Glu	Arg
225			230		235									240	
His	Glu	Asp	Ala	Gln	Lys	Ala	Val	Asp	Glu	Met	Asn	Gly	Lys	Glu	Leu
	245		250		255										
Asn	Gly	Lys	Gln	Ile	Tyr	Val	Gly	Arg	Ala	Gln	Lys	Lys	Val	Glu	Arg
	260		265		270										
Gln	Thr	Glu	Leu	Lys	Arg	Lys	Phe	Glu	Gln	Met	Lys	Gln	Asp	Arg	Ile
	275		280		285										
Thr	Arg	Tyr	Gln	Gly	Val	Asn	Leu	Tyr	Val	Lys	Asn	Leu	Asp	Asp	Gly
	290		295		300										
Ile	Asp	Asp	Glu	Arg	Leu	Arg	Lys	Glu	Phe	Ser	Pro	Phe	Gly	Thr	Ile
305			310		315									320	
Thr	Ser	Ala	Lys	Val	Met	Met	Glu	Gly	Gly	Arg	Ser	Lys	Gly	Phe	Gly
	325		330		335										
Phe	Val	Cys	Phe	Ser	Ser	Pro	Glu	Glu	Ala	Thr	Lys	Ala	Val	Thr	Glu
	340		345		350										
Met	Asn	Gly	Arg	Ile	Val	Ala	Thr	Lys	Pro	Leu	Tyr	Val	Ala	Leu	Ala
	355		360		365										
Gln	Arg	Lys	Glu	Glu	Arg	Gln	Ala	His	Leu	Thr	Asn	Gln	Tyr	Met	Gln
	370		375		380										
Arg	Met	Ala	Ser	Val	Arg	Ala	Val	Pro	Asn	Pro	Val	Ile	Asn	Pro	Tyr
385			390		395									400	

Gln Pro Ala Pro Pro Ser Gly Tyr Phe Met Ala Ala Ile Pro Gln Thr
 405 410 415
 Gln Asn Arg Ala Ala Tyr Tyr Pro Pro Ser Gln Ile Ala Gln Leu Arg
 420 425 430
 Pro Ser Pro Arg Trp Thr Ala Gln Gly Ala Arg Pro His Pro Phe Gln
 435 440 445
 Asn Met Pro Gly Ala Ile Arg Pro Ala Ala Pro Arg Pro Pro Phe Ser
 450 455 460
 Thr Met Arg Pro Ala Ser Ser Gln Val Pro Arg Val Met Ser Thr Gln
 465 470 475 480
 Arg Val Ala Asn Thr Ser Thr Gln Thr Met Gly Pro Arg Pro Ala Ala
 485 490 495
 Ala Ala Ala Ala Ala Thr Pro Ala Val Arg Thr Val Pro Gln Tyr Lys
 500 505 510
 Tyr Ala Ala Gly Val Arg Asn Pro Gln Gln His Leu Asn Ala Gln Pro
 515 520 525
 Gln Val Thr Met Gln Gln Pro Ala Val His Val Gln Gly Gln Glu Pro
 530 535 540
 Leu Thr Ala Ser Met Leu Ala Ser Ala Pro Pro Gln Glu Gln Lys Gln
 545 550 555 560
 Met Leu Gly Glu Arg Leu Phe Pro Leu Ile Gln Ala Met His Pro Ser
 565 570 575
 Leu Ala Gly Lys Ile Thr Gly Met Leu Leu Glu Ile Asp Asn Ser Glu
 580 585 590
 Leu Leu His Met Leu Glu Ser Pro Glu Ser Leu Arg Ser Lys Val Asp
 595 600 605
 Glu Ala Val Ala Val Leu Gln Ala His Gln Ala Lys Glu Ala Ala Gln
 610 615 620
 Lys Ala Val Asn Ser Ala Thr Gly Val Pro Thr Val

625

630

635

<210> 333

<211> 2564

<212> DNA

<213> *Mus musculus*

<400> 333

tctagatgcc tctgccttc caactgtaca gagaaatgat ctgccagtc ctttaagcttt 60
cttgggtcaa gttctgaggc ttgttagatg atttctgaga ctgattccca gggctgtttc 120
caggtgccaa atgtaggctt tctttctccc cctccctcct gtgtgtgtgt gtgtgtgtct 180
gtctgtctgt ctatctgtct ctccagtggt tttcttttgt taaaatataa agataggccg 240
cttggacaaa gtgaggttcc ttacagctc aatttcatcc ctttttccct acaaggcttt 300
aagagatgga gggagagaat atagttcagt cctcttaatt gcaaattcat tctgagattg 360
tttcttagac agatcgtctt aagctcact cgccatacaa aaagttaaag gtgaatgcaa 420
gtccagtaat ctgggtacat tgacaggtac ccaactgagt gtgatgatgt attgctaacc 480
aaggactgag tgatctctgt gtaattaagt gtgctcctat gttggctgaa tatgggagcg 540
gcatgtcagc actgagtga ggtlaagattg ttgggtctct gttggcatgga gaatttcattg 600
tgcttgcgtg ggtgcaggct ttctttttct tttttttaa aaaataaacc acttttagatc 660
gtgtcgccct ccctcacttc tgtgattgat ttgctgaggc taatggtgctg taaaagcact 720
ggtgagatct ggggggcct cttggctga cgtcagagag agagttttaa aaggggagac 780
cgtggagagc tccatagcgg ctgaaggaga cgctaccgaa gccgtcgtg ctgcctgagg 840
acctgcgact agactgacc accgcgtcc agcttggctg cctgaggcaa ggaagatgct 900
gtcctgccgt ctccagtgcg ccttggctgc gctctgcatc gtcctggctt tgggcgggtgt 960
caccggcgcg cctcggacc ccagactccg tcagtttctg cagaagtctc tggcggctgc 1020
caccgggaaa caggtaagga ctgtccccct tacgaatccc ccagccttc tgcctgcagcc 1080
cctgcgacag gtgttttagcg ggcgttctc agatcgctc agcccctaag ctcccaggga 1140
aacttttgaa gttagggtcc cctcttactc tttcagaat tgatcagcgc aggtggtcac 1200
cttgcaggta agttcctccc tggctttcaa gaaaattcag aaagcaggta ggagagactg 1260

ggctctatcc ctgggtgctgg caagagggtt gctgaccccg gtgctgaaac gcaatgtttg 1320
 ttcacaaaac gattctgggg caagaggctc ttcagtttat gggaagggtt gcttttacct 1380
 ttcaaaaaat ctggcaagaa ctgagctcca ctcatatct catcacagga aaatggacgt 1440
 gcgcaaaacta ttggcattct atgtagttaa aaacgacttc ttaatcatct gtgatttctc 1500
 tgtgttttaa ggcagagcac tttctgaaag acttgcgttt gggaagctt tttttctcct 1560
 gcataatcta atgaatacat acagcaatca cccatgatgt gtgaaaact gggttttgag 1620
 tgattaaatc ttactttcaa accacatttt cccccctctc ccattcctcc cttttgttct 1680
 tctcactgcc ctatccagga actggccaag tacttcttgg cagagctgct gtccgagccc 1740
 aaccagacag agaatgatgc cctggagccc gaggatttgc ccaggcagc tgagcaggac 1800
 gagatgaggc tggagctgca gaggctgcc aactcgaacc cagcaatggc accccgggaa 1860
 cgcaaagctg gctgcaagaa cttcttcttg aagacattca catcctgtta gctttaatat 1920
 tgttgtccta gccagacctc tgatccctct ccccaaacc ccatactct tccttaactc 1980
 ctggcccccg atgctcaact tgaccctgca ttagaaattg aagactgtaa atacaaaata 2040
 aaattatggt gagattatga agagcaagcg ttgacttct tattgagtaa attgttttgt 2100
 tcagaaatac atgatgagca tgggttgttg ttccgtaaa catattttag gtgtacatac 2160
 ccacatacac aaagggtgat tgaaaattcc ctgcggtaat aaaagttaga ctttaaaaaat 2220
 gactgttctt ttaaaacttg aataactttg aatgtctata aattgaacca tgtatccgaa 2280
 tgatggctat tgggaacagc tgccataaac atcctttgca tgttaaagac atttgggaat 2340
 agctgtagga tiaccaaaat gtgtttttaga atttatgggc agtcaggctg aagcgcttaa 2400
 cactgtacta tgctgattca caaaacataa aacatattta aaatggaaag aaaataatca 2460
 aaaaagtggg aaagaacttg gtttaaagag gtgaaacaaa ctttcagctt ttaaattttg 2520
 ttttggtttg gttttttgtt tgtttgtgaa catttacctc taga 2564

<210> 334

<211> 756

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (60).. (482)

<400> 334

```

gctaccgcgcg accccgcgcac cccagcaaca gcccgiagag cagccccagt agcagcgcc 59
atg gcc ggg tgg aac gcc tac atc gac agc ctt atg gcg gac ggg acc 107
Met Ala Gly Trp Asn Ala Tyr Ile Asp Ser Leu Met Ala Asp Gly Thr
      1             5             10             15
tgt cag gac gcg gcc atc gta ggc tac aag gac tcg ccc tcc gtc tgg 155
Cys Gln Asp Ala Ala Ile Val Gly Tyr Lys Asp Ser Pro Ser Val Trp
              20             25             30
gcc gcc gtc ccc ggg aag acc ttc gtt agc att acg cca gct gag gtt 203
Ala Ala Val Pro Gly Lys Thr Phe Val Ser Ile Thr Pro Ala Glu Val
              35             40             45
ggc gtc cta gta ggc aaa gac cgg tca agt ttt ttc gtc aat ggg ctg 251
Gly Val Leu Val Gly Lys Asp Arg Ser Ser Phe Phe Val Asn Gly Leu
      50             55             60
aca ctt ggg ggc cag aaa tgt tct gtg atc cgg gac tca ctg ctg caa 299
Thr Leu Gly Gly Gln Lys Cys Ser Val Ile Arg Asp Ser Leu Leu Gln
      65             70             75             80
gac ggg gaa ttt aca atg gat ctt cgt acc aag agc acc gga gga gcc 347
Asp Gly Glu Phe Thr Met Asp Leu Arg Thr Lys Ser Thr Gly Gly Ala
              85             90             95
ccc acc ttc aat gtc act gtc acc atg act gcc aag acg cta gtc ctg 395
Pro Thr Phe Asn Val Thr Val Thr Met Thr Ala Lys Thr Leu Val Leu
              100            105            110
ctg atg ggc aaa gaa ggt gtc cac ggt ggt ttg atc aac aag aaa tgt 443
Leu Met Gly Lys Glu Gly Val His Gly Gly Leu Ile Asn Lys Lys Cys
              115            120            125

```

tat gaa atg gcc tct cac ctg cgg cgt tcc cag tac tga cctcgtctgt 492
 Tyr Glu Met Ala Ser His Leu Arg Arg Ser Gln Tyr
 130 135 140
 cccttccccc caccgttccc ttiggtttt gcacccctt cttccatac acacacatac 552
 cattatTTTT tgggccatta ccccatTTcc cttattgctg ccaaaaccac atgggctggg 612
 ggctggggct ggatggacag acacctcccc ctaccatac cccctcctgt gtgtgtttgg 672
 aaaatttttg tttttgggtt taattttttg ttttttggtc tttttttttt ttttttctg 732
 aataaaaaag gatttacta accg 756

<210> 335

<211> 140

<212> PRT

<213> Mus musculus

<400> 335

Met Ala Gly Trp Asn Ala Tyr Ile Asp Ser Leu Met Ala Asp Gly Thr
 1 5 10 15
 Cys Gln Asp Ala Ala Ile Val Gly Tyr Lys Asp Ser Pro Ser Val Trp
 20 25 30
 Ala Ala Val Pro Gly Lys Thr Phe Val Ser Ile Thr Pro Ala Glu Val
 35 40 45
 Gly Val Leu Val Gly Lys Asp Arg Ser Ser Phe Phe Val Asn Gly Leu
 50 55 60
 Thr Leu Gly Gly Gln Lys Cys Ser Val Ile Arg Asp Ser Leu Leu Gln
 65 70 75 80
 Asp Gly Glu Phe Thr Met Asp Leu Arg Thr Lys Ser Thr Gly Gly Ala
 85 90 95
 Pro Thr Phe Asn Val Thr Val Thr Met Thr Ala Lys Thr Leu Val Leu
 100 105 110

Leu Met Gly Lys Glu Gly Val His Gly Gly Leu Ile Asn Lys Lys Cys

115

120

125

Tyr Glu Met Ala Ser His Leu Arg Arg Ser Gln Tyr

130

135

140

<210> 336

<211> 478

<212> DNA

<213> Mus musculus

<400> 336

```

agcaagtacc tcatttacc agtgcactcc aatatcccca tgatggacca gaaggccata 60
ttccaacagc ctccacttgg ggtacgcaag attgtatigg ccaccaacat tgctgaaacc 120
tccatcacag ttaacgacat tgtacatgtc gtggacagcg gtctgcacaa ggaggaacgc 180
tatgacctga agaccaaggt gtcctgcctg gagactgtgt ggggtgtcgag agcaaattgtc 240
attcagcgcc ggggcagggc aggccgtgc cagtcagggt ttgcctacca ctgttcccg 300
aggagccggc tggagaaaat ggttcctttc caagtgccag agatcctgcg cacacctctt 360
gagaacctgg tgctgcaacc aaaatccata tgcctgagaa gacggcagtg gagttcctct 420
ctaaggctgt ggacagtcca aatatcaagg cagtggatga ggccgtgac ctgctcca 478

```

<210> 337

<211> 1008

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (208).. (846)

<400> 337

ggcgggctgt tattgttccg aagctgggcg ctgtgtccgc gctcgggtgt cagttcgtcc 60
 cgctgccctt cggccittgc tgcgtgctct gacggcgacc gacggcgggc ggggcccggg 120
 ttgcgggccg agcggcgccg gtgaggcgcg ggaggaggcg cacagcgga ggaggagccg 180
 tgagcctggc acggagcggc cgcggcc atg gcg tac gcc tat ctc ttc aag tac 234

Met Ala Tyr Ala Tyr Leu Phe Lys Tyr

1

5

atc atc atc ggc gac aca ggt gtt gga aaa tcg tgc tta ttg cta cag 282
 Ile Ile Ile Gly Asp Thr Gly Val Gly Lys Ser Cys Leu Leu Leu Gln
 10 15 20 25

ttt aca gac aag agg ttt cag ccg gtg cat gac ctc aca att ggt gta 330
 Phe Thr Asp Lys Arg Phe Gln Pro Val His Asp Leu Thr Ile Gly Val
 30 35 40

gag ttt ggt gct cgg atg ata acg att gat ggg aaa cag ata aaa ctc 378
 Glu Phe Gly Ala Arg Met Ile Thr Ile Asp Gly Lys Gln Ile Lys Leu
 45 50 55

cag atc tgg gat aca gca ggg cag gag tcc ttt cgt tct atc aca cgg 426
 Gln Ile Trp Asp Thr Ala Gly Gln Glu Ser Phe Arg Ser Ile Thr Arg
 60 65 70

tca tat tac aga ggt gca gcg ggg gct tta cta gtg tat gat att aca 474
 Ser Tyr Tyr Arg Gly Ala Ala Gly Ala Leu Leu Val Tyr Asp Ile Thr
 75 80 85

agg aga gac acg ttc aac cac ttg aca acc tgg tta gaa gat gcc cgt 522
 Arg Arg Asp Thr Phe Asn His Leu Thr Thr Trp Leu Glu Asp Ala Arg.
 90 95 100 105

cag cat tcc aat tcc aac atg gtc atc atg ctt att gga aat aaa agt 570
 Gln His Ser Asn Ser Asn Met Val Ile Met Leu Ile Gly Asn Lys Ser
 110 115 120

gac tta gaa tct agg aga gaa gtg aaa aag gaa gaa ggt gaa gct ttt 618

Asp Leu Glu Ser Arg Arg Glu Val Lys Lys Glu Glu Gly Glu Ala Phe
 125 130 135
 gca cga gag cat gga ctt atc ttc atg gaa act tct gcc aag act gcg 666
 Ala Arg Glu His Gly Leu Ile Phe Met Glu Thr Ser Ala Lys Thr Ala
 140 145 150
 tct aat gta gag gag gca ttt att aac aca gca aaa gaa att tat gaa 714
 Ser Asn Val Glu Glu Ala Phe Ile Asn Thr Ala Lys Glu Ile Tyr Glu
 155 160 165
 aaa atc caa gaa ggg gtc ttt gac att aat aat gag gca aac ggc att 762
 Lys Ile Gln Glu Gly Val Phe Asp Ile Asn Asn Glu Ala Asn Gly Ile
 170 175 180 185
 aaa att ggc cct cag cac gct gct acc aac gca tct cat gga agc aac 810
 Lys Ile Gly Pro Gln His Ala Ala Thr Asn Ala Ser His Gly Ser Asn
 190 195 200
 caa ggc gga cag cag gca ggg gga ggc tgc tgt tga ggctgggtgtt 856
 Gln Gly Gly Gln Gln Ala Gly Gly Gly Cys Cys
 205 210
 accggctagc tgcccagtg agccacgcac tctgtcaccc tctttcctca tgctcagctg 916
 agacatgaaa ctattgaaat ggctttatgt cacaggagac tttaatcctt cagattcttg 976
 tataactttg aataaatggt taatgttcac tt 1008

<210> 338

<211> 212

<212> PRT

<213> Mus musculus

<400> 338

Met Ala Tyr Ala Tyr Leu Phe Lys Tyr Ile Ile Ile Gly Asp Thr Gly

1

5

10

15

Val Gly Lys Ser Cys Leu Leu Leu Gln Phe Thr Asp Lys Arg Phe Gln
 20 25 30
 Pro Val His Asp Leu Thr Ile Gly Val Glu Phe Gly Ala Arg Met Ile
 35 40 45
 Thr Ile Asp Gly Lys Gln Ile Lys Leu Gln Ile Trp Asp Thr Ala Gly
 50 55 60
 Gln Glu Ser Phe Arg Ser Ile Thr Arg Ser Tyr Tyr Arg Gly Ala Ala
 65 70 75 80
 Gly Ala Leu Leu Val Tyr Asp Ile Thr Arg Arg Asp Thr Phe Asn His
 85 90 95
 Leu Thr Thr Trp Leu Glu Asp Ala Arg Gln His Ser Asn Ser Asn Met
 100 105 110
 Val Ile Met Leu Ile Gly Asn Lys Ser Asp Leu Glu Ser Arg Arg Glu
 115 120 125
 Val Lys Lys Glu Glu Gly Glu Ala Phe Ala Arg Glu His Gly Leu Ile
 130 135 140
 Phe Met Glu Thr Ser Ala Lys Thr Ala Ser Asn Val Glu Glu Ala Phe
 145 150 155 160
 Ile Asn Thr Ala Lys Glu Ile Tyr Glu Lys Ile Gln Glu Gly Val Phe
 165 170 175
 Asp Ile Asn Asn Glu Ala Asn Gly Ile Lys Ile Gly Pro Gln His Ala
 180 185 190
 Ala Thr Asn Ala Ser His Gly Ser Asn Gln Gly Gly Gln Gln Ala Gly
 195 200 205
 Gly Gly Cys Cys
 210

<210> 339

<211> 398

<212> DNA

<213> Mus musculus

<400> 339

aattcggatc catggatgtg gtgagcccat ctgagttcaa gaccagatc cagagatatg 60
cgccacgctt catgggctat aatcagcagg atgtcaggaa ttccttcgtt tccttctgga 120
tggtctccac aatgaggiga accgggtggc agcaaggcct aaggcagccc tgagaccctt 180
gatcatctcc ctgatgaaga aaaggggcga cagatgtgga ggaagtaict ggaaaggga 240
gacagtcgga ttggggatct ctctgttggg cagctgaaga gctccctcac atgcaccgat 300
tgtggctact gctctacagt ctctgatccc ttctgggata tctcgttgcc catcgcaaag 360
agaggttacc ctgaggtagc gttaatggat tgtatgag 398

<210> 340

<211> 886

<212> DNA

<213> Mus musculus

<400> 340

ggggcccggc ggcgtggaca gcagtcctgg cactcggcgc cccgccgccc gcagcctcgc 60
ccagcgcttc ccgagccgcg cgcttcgcgc ctccagccacc ggccgcccgc gccgccgccc 120
ccgccaccga gcggcccgag atgcaggcca tcaagtgtgt ggtgggtgga gacggagctg 180
ttggtaaaac ctgcctgctc atcagttaca cgaccaatgc atttcctgga gatlacatcc 240
ccaccgtctt tgacaactat tccgccaatg ttatggtaga tggaaaacca gtgaatctgg 300
gcctatggga cacagctgga caagaagatt atgacagatt gcgtcccttc tcctaccgcg 360
agacagacgt gttcttaatt tgcttttccc ttgtgagtcg tgcatcattt gaaaatgtcc 420
gtgcaaagtg gtatcctgaa gtgcgacacc actgtcccaa tactcctatc atcctcgtgg 480
ggacgaagct tgatcttagg gatgataagg acaccattga gaagctgaag gagaagaagc 540
tgaccccatc cacctaccgc caggggctgg ccatggcgaa agagatcggt gcigtcaaat 600
acctggagtg ctccagctctc acacagcgag gactcaagac agtgtttgac gaagctatcc 660

gagcggttct ctgtccccc cctgtcaaga agaggaagag aaaatgcctg ctgttgtaaa 720
 tgteggagcc cctcgttctc ggicctgcct ggaacctttg tagctttgct caaaaatcag 780
 cgagcccttcg catttgatgc caagtttttg ttacagatta atttttccat aaaaccattt 840
 tgaaccaatg aaccagtcaa taattttaag gticigtittt aaatgt 886

<210> 341

<211> 1808

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (181).. (1278)

<400> 341

aagagggtgg gaggcgaggt cgaatgtctgt ggccggagcg gacgggtgcag attgcgagcc 60
 ggcctaaaag cgtgctcttt ggcgtaaatt gcaatcgatt agggatcggt tctcagactc 120
 aagttagaag tgagagttca gataagtgag gccgacattg ctgccttgaa gaaggggaga 180
 atg gat tta tca gga gtg aaa aag aag agc ttg cta gga gtc aaa gag 228
 Met Asp Leu Ser Gly Val Lys Lys Lys Ser Leu Leu Gly Val Lys Glu
 1 5 10 15
 aat aat aaa aag tcc agc act agg gct cct tct cct acc aaa cgc aag 276
 Asn Asn Lys Lys Ser Ser Thr Arg Ala Pro Ser Pro Thr Lys Arg Lys
 20 25 30
 gac cga tct gat gag aag tcc aag gat cga tct aaa gat aaa ggg gcc 324
 Asp Arg Ser Asp Glu Lys Ser Lys Asp Arg Ser Lys Asp Lys Gly Ala
 35 40 45
 act aaa gag tca agt gag aag gat cgt ggc aga gat aag act cgg aag 372
 Thr Lys Glu Ser Ser Glu Lys Asp Arg Gly Arg Asp Lys Thr Arg Lys

50	55	60	
aac gca tgg ctt caa gcg gac aag gca gta cca ggt cta ggt cca gct	420		
Asn Ala Trp Leu Gln Ala Asp Lys Ala Val Pro Gly Leu Gly Pro Ala			
65	70	75	80
caa cct cca gct cgg gct cca gca cca gca cag gct caa gca gtg gct	468		
Gln Pro Pro Ala Arg Ala Pro Ala Pro Ala Gln Ala Gln Ala Val Ala			
85	90	95	
cca gct cgt cct ctg cat cca gcc gct cag gaa gct cca gca cgt ccc	516		
Pro Ala Arg Pro Leu His Pro Ala Ala Gln Glu Ala Pro Ala Arg Pro			
100	105	110	
gga gct cca gtt cta gca gct cct ccg gct ccc caa gcc ctt ctc ggc	564		
Gly Ala Pro Val Leu Ala Ala Pro Pro Ala Pro Gln Ala Leu Leu Gly			
115	120	125	
gca ggc atg aca aca ggc gcg tcc cgc tcc aaa tcc aaa cca cct aaa	612		
Ala Gly Met Thr Thr Gly Ala Ser Arg Ser Lys Ser Lys Pro Pro Lys			
130	135	140	
aga gat gaa aaa gag agg aaa agg cgg cac gtt cac cta aac caa cca	660		
Arg Asp Glu Lys Glu Arg Lys Arg Arg His Val His Leu Asn Gln Pro			
145	150	155	160
aag tgc aca ttg gga ggc tca cca ggg aat gtg acc aag gat cat atc	708		
Lys Cys Thr Leu Gly Gly Ser Pro Gly Asn Val Thr Lys Asp His Ile			
165	170	175	
atg gaa ata ttt tct act tac ggg aaa atc aaa atg att gac atg cct	756		
Met Glu Ile Phe Ser Thr Tyr Gly Lys Ile Lys Met Ile Asp Met Pro			
180	185	190	
gtc gag agg atg cat cct cac ctc tcc aaa ggc tat gca tat gtg gag	804		
Val Glu Arg Met His Pro His Leu Ser Lys Gly Tyr Ala Tyr Val Glu			
195	200	205	
ttt gag aat ccc gat gaa gca gag aag gct ctg aaa cac atg gat gga	852		

Phe Glu Asn Pro Asp Glu Ala Glu Lys Ala Leu Lys His Met Asp Gly
 210 215 220
 gga caa att gat ggc caa gag atc act gct act gct gtg ttg gca ccc 900
 Gly Gln Ile Asp Gly Gln Glu Ile Thr Ala Thr Ala Val Leu Ala Pro
 225 230 235 240
 tgg cct cgg cca cca cct cgg cga ttc agc cct cct agg agg atg ctt 948
 Trp Pro Arg Pro Pro Pro Arg Arg Phe Ser Pro Pro Arg Arg Met Leu
 245 250 255
 cca cca cct ccc atg tgg cgt agg tca ccc cca cgg atg agg aga agg 996
 Pro Pro Pro Pro Met Trp Arg Arg Ser Pro Pro Arg Met Arg Arg Arg
 260 265 270
 tct cga tcc cca aga cgc agg tcc cct gtg cgt agg agg tct cgc tct 1044
 Ser Arg Ser Pro Arg Arg Arg Ser Pro Val Arg Arg Arg Ser Arg Ser
 275 280 285
 cct ggg ccg ccg ccg cca cag gag ccg atc cag ctc caa ctc ctc ccg 1092
 Pro Gly Pro Pro Pro Pro Gln Glu Pro Ile Gln Leu Gln Leu Leu Pro
 290 295 300
 ata agc agg gac att gat tgc tac ctc tgt aac tta tgt tgc ccc aga 1140
 Ile Ser Arg Asp Ile Asp Ser Tyr Leu Cys Asn Leu Cys Cys Pro Arg
 305 310 315 320
 ctc tgt ttt gtc ctt ttc tct agc caa gtg agg gtc tgt aga gaa agg 1188
 Leu Cys Phe Val Leu Phe Ser Ser Gln Val Arg Val Cys Arg Glu Arg
 325 330 335
 atc cct tac tgg gta cag cag ttg aga tat ctc ctc tac aga agg gtt 1236
 Ile Pro Tyr Trp Val Gln Gln Leu Arg Tyr Leu Leu Tyr Arg Arg Val
 340 345 350
 ctg gct tgt aga gct act gtt ggt tca cgg ctg ctc cca tag 1278
 Leu Ala Cys Arg Ala Thr Val Gly Ser Arg Leu Leu Pro
 355 360 365

aggtgccctg tagttttctg gctagaaagt tcatcccttc agttcttgat aggctggtag 1338
 cagagccagc tggaacctat ggcagcacac ggatttccac agatgaccca gaaccagaca 1398
 gcctgggtcta gccccgctg tgccacacct gtgcaaagga ccacactgct gtctctgttg 1458
 gccgaccatg ccttgctgag tacgcttcaa ctiagagggc taaaaccttt gaaggattcc 1518
 tccacaaatg gttacctttc tgtccccgtg tctctgttac tttctagaat ttgtgagcca 1578
 gttctacagg gtcctcatga aacctacccc acccgttgt cacctgcat tcatggtgat 1638
 gttgcagggt aaccttggca gtgtgtacat tgcccccttt tgcttttatt gtacagtcag 1698
 tactataaaa ttgttttga gttttataac ttgttagcat tttagataag gttgtgtttg 1758
 tacttgtgta gagtgaaagg actgttgaat aaaacctagg attagaatgc 1808

<210> 342

<211> 365

<212> PRT

<213> Mus musculus

<400> 342

Met	Asp	Leu	Ser	Gly	Val	Lys	Lys	Lys	Ser	Leu	Leu	Gly	Val	Lys	Glu
1					5				10					15	
Asn	Asn	Lys	Lys	Ser	Ser	Thr	Arg	Ala	Pro	Ser	Pro	Thr	Lys	Arg	Lys
				20				25					30		
Asp	Arg	Ser	Asp	Glu	Lys	Ser	Lys	Asp	Arg	Ser	Lys	Asp	Lys	Gly	Ala
			35				40					45			
Thr	Lys	Glu	Ser	Ser	Glu	Lys	Asp	Arg	Gly	Arg	Asp	Lys	Thr	Arg	Lys
	50					55					60				
Asn	Ala	Trp	Leu	Gln	Ala	Asp	Lys	Ala	Val	Pro	Gly	Leu	Gly	Pro	Ala
65				70				75					80		
Gln	Pro	Pro	Ala	Arg	Ala	Pro	Ala	Pro	Ala	Gln	Ala	Gln	Ala	Val	Ala
			85				90					95			
Pro	Ala	Arg	Pro	Leu	His	Pro	Ala	Ala	Gln	Glu	Ala	Pro	Ala	Arg	Pro

100	105	110
Gly Ala Pro Val Leu Ala Ala Pro Pro Ala Pro Gln Ala Leu Leu Gly		
115	120	125
Ala Gly Met Thr Thr Gly Ala Ser Arg Ser Lys Ser Lys Pro Pro Lys		
130	135	140
Arg Asp Glu Lys Glu Arg Lys Arg Arg His Val His Leu Asn Gln Pro		
145	150	155
Lys Cys Thr Leu Gly Gly Ser Pro Gly Asn Val Thr Lys Asp His Ile		
165	170	175
Met Glu Ile Phe Ser Thr Tyr Gly Lys Ile Lys Met Ile Asp Met Pro		
180	185	190
Val Glu Arg Met His Pro His Leu Ser Lys Gly Tyr Ala Tyr Val Glu		
195	200	205
Phe Glu Asn Pro Asp Glu Ala Glu Lys Ala Leu Lys His Met Asp Gly		
210	215	220
Gly Gln Ile Asp Gly Gln Glu Ile Thr Ala Thr Ala Val Leu Ala Pro		
225	230	235
Trp Pro Arg Pro Pro Pro Arg Arg Phe Ser Pro Pro Arg Arg Met Leu		
245	250	255
Pro Pro Pro Pro Met Trp Arg Arg Ser Pro Pro Arg Met Arg Arg Arg		
260	265	270
Ser Arg Ser Pro Arg Arg Arg Ser Pro Val Arg Arg Arg Ser Arg Ser		
275	280	285
Pro Gly Pro Pro Pro Pro Gln Glu Pro Ile Gln Leu Gln Leu Leu Pro		
290	295	300
Ile Ser Arg Asp Ile Asp Ser Tyr Leu Cys Asn Leu Cys Cys Pro Arg		
305	310	315
Leu Cys Phe Val Leu Phe Ser Ser Gln Val Arg Val Cys Arg Glu Arg		
325	330	335

Ile Pro Tyr Trp Val Gln Gln Leu Arg Tyr Leu Leu Tyr Arg Arg Val

340

345

350

Leu Ala Cys Arg Ala Thr Val Gly Ser Arg Leu Leu Pro

355

360

365

<210> 343

<211> 7292

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (507).. (5282)

<400> 343

gggccaaatg accagattca tcatagcacg aaacttcaca agttacaccc actccctcgc 60
 cggcagcggg gaaggctaca gcttcctgat ttcagttact ggaagttgga gagatggaaa 120
 ggcgcccggg agtgtgagcc tcgctgagca gcgggtagaa ccattgtgga ctgaaaccca 180
 cctttccaga tctgaaagga agactgagga agaggaaggg aggggacagt cccggagaca 240
 attctagtcc ctcactcagg acttgagcag cgccttcaga tggcaccttt ggagatcttg 300
 accaaggctc ttctgtttgg cctgggggtt ctggcacatt ctcccagact caggtgagac 360
 cccgatgggc accccgtggg gcaggtcctg acacacgtcc cgactccagc cactgacacc 420
 attgccagcc tcagtctcta aatgccacac cgctcctggg gccagttggg ctgggcacca 480
 ctgttgccctt tgaagaccat aaaacc atg gga aac gca gaa agc caa aat gta 533

Met Gly Asn Ala Glu Ser Gln Asn Val

1

5

gac cac gag ttt tat gga gaa aag cat gcc agc ctg ggg cgg aag cac 581

Asp His Glu Phe Tyr Gly Glu Lys His Ala Ser Leu Gly Arg Lys His

10

15

20

25

act tca cgc tcc ctg cgg ctg tca cac aag acc cgg agg aca cgg cat 629
 Thr Ser Arg Ser Leu Arg Leu Ser His Lys Thr Arg Arg Thr Arg His
 30 35 40
 gct tcc tcc ggg aag gcg atc cac agg aac tct gaa gtg agc acc cgg 677
 Ala Ser Ser Gly Lys Ala Ile His Arg Asn Ser Glu Val Ser Thr Arg
 45 50 55
 tcc agc agc acg ccc agc atc ccc cag tcc ctg gct gaa aat ggc ctg 725
 Ser Ser Ser Thr Pro Ser Ile Pro Gln Ser Leu Ala Glu Asn Gly Leu
 60 65 70
 gag ccc ttc tcc caa gaa ggc gcc cta gac gac ttc ggg gac ccc atc 773
 Glu Pro Phe Ser Gln Glu Gly Ala Leu Asp Asp Phe Gly Asp Pro Ile
 75 80 85
 tgg gtg gac cga gta gat atg ggc ttg aga ccc gta tct tac acc gat 821
 Trp Val Asp Arg Val Asp Met Gly Leu Arg Pro Val Ser Tyr Thr Asp
 90 95 100 105
 tct tcc gtc act ccc agc gta gat ggc agc atc gtc ctc act gca gcc 869
 Ser Ser Val Thr Pro Ser Val Asp Gly Ser Ile Val Leu Thr Ala Ala
 110 115 120
 tct gtg cag agc atg cca gac tca gag gag agc cgg ctt tac ggg gat 917
 Ser Val Gln Ser Met Pro Asp Ser Glu Glu Ser Arg Leu Tyr Gly Asp
 125 130 135
 gac gct acg tac ttg gct gag gga ggc agg agg cag tgt ccc tat aca 965
 Asp Ala Thr Tyr Leu Ala Glu Gly Gly Arg Arg Gln Cys Pro Tyr Thr
 140 145 150
 tcc aat ggg ccc aca ttc atg gag aca gcg agc ttt aag aag aag cgc 1013
 Ser Asn Gly Pro Thr Phe Met Glu Thr Ala Ser Phe Lys Lys Lys Arg
 155 160 165
 tcc aaa tct gca gac atc tgg cgg gag gac agc ctg gaa ttc tca ctc 1061
 Ser Lys Ser Ala Asp Ile Trp Arg Glu Asp Ser Leu Glu Phe Ser Leu

170	175	180	185	
tca gat ctg agc caa gaa cat tta aca agc aac gaa gaa atc ttg ggt	1109			
Ser Asp Leu Ser Gln Glu His Leu Thr Ser Asn Glu Glu Ile Leu Gly				
190	195	200		
tcc gcg gaa gag aag gat tgc gag gag gct cgg ggg atg gaa aca gag	1157			
Ser Ala Glu Glu Lys Asp Cys Glu Glu Ala Arg Gly Met Glu Thr Glu				
205	210	215		
gcg agt ccc cgg cag ctc agc acc tgt cag cga gcc aac tcc ctg ggt	1205			
Ala Ser Pro Arg Gln Leu Ser Thr Cys Gln Arg Ala Asn Ser Leu Gly				
220	225	230		
gac ttg tat gct cag aaa aac tct ggg gtg aag gct aat gga gga ccg	1253			
Asp Leu Tyr Ala Gln Lys Asn Ser Gly Val Lys Ala Asn Gly Gly Pro				
235	240	245		
agg aac aga ttc tca agc tac tgc cgg aat ttg gtg tcg gat att ccc	1301			
Arg Asn Arg Phe Ser Ser Tyr Cys Arg Asn Leu Val Ser Asp Ile Pro				
250	255	260	265	
gat ctt gca aag cat aag atg cca ccg gct gct gcc gaa gag act cct	1349			
Asp Leu Ala Lys His Lys Met Pro Pro Ala Ala Ala Glu Glu Thr Pro				
270	275	280		
ccg tac agt aat tac aac acg ctt ccc tgt agg aag tcg cac tgt ctt	1397			
Pro Tyr Ser Asn Tyr Asn Thr Leu Pro Cys Arg Lys Ser His Cys Leu				
285	290	295		
tcc gag ggt gcc acc aac cca caa att agc ctt agc aag agc atg caa	1445			
Ser Glu Gly Ala Thr Asn Pro Gln Ile Ser Leu Ser Lys Ser Met Gln				
300	305	310		
ggc aga aga gca aaa acc acc cag gat gtt aac aca ggc gag ggc agc	1493			
Gly Arg Arg Ala Lys Thr Thr Gln Asp Val Asn Thr Gly Glu Gly Ser				
315	320	325		
gag ttt gcg gac agt ggg atc gaa ggg gcc acc acc gac acg gac ctc	1541			

Glu Phe Ala Asp Ser Gly Ile Glu Gly Ala Thr Thr Asp Thr Asp Leu
 330 335 340 345
 ttg tcc agg aga tcc aat gcc acc aac tca agc tac tcg ccc ccc aca 1589
 Leu Ser Arg Arg Ser Asn Ala Thr Asn Ser Ser Tyr Ser Pro Pro Thr
 350 355 360
 ggc cga gcc ttt gtg ggc agc gac agc ggc agc agt tca aca ggg gat 1637
 Gly Arg Ala Phe Val Gly Ser Asp Ser Gly Ser Ser Ser Thr Gly Asp
 365 370 375
 cgt gcg cgc cag ggg gtg tac gag aac ttc agg cgg gaa ctg gag atg 1685
 Arg Ala Arg Gln Gly Val Tyr Glu Asn Phe Arg Arg Glu Leu Glu Met
 380 385 390
 agt acc acc aac agt gag agc ctg gag gag gct ggc tct gcg cac agc 1733
 Ser Thr Thr Asn Ser Glu Ser Leu Glu Glu Ala Gly Ser Ala His Ser
 395 400 405
 gat gag cag agc agc gga acc ctc agt tcc ccg ggc cag tcg gac atc 1781
 Asp Glu Gln Ser Ser Gly Thr Leu Ser Ser Pro Gly Gln Ser Asp Ile
 410 415 420 425
 ctg cta acg gct gcg cag ggc act gtg cgg aag gct gga gcg ctg gca 1829
 Leu Leu Thr Ala Ala Gln Gly Thr Val Arg Lys Ala Gly Ala Leu Ala
 430 435 440
 gtc aag aac ttc ctg gtc cac aag aag aat aag aag gtg gag tcg gct 1877
 Val Lys Asn Phe Leu Val His Lys Lys Asn Lys Lys Val Glu Ser Ala
 445 450 455
 acc cgg agg aag tgg aag cac tac tgg gtg tcc ctg aaa ggt tgc acg 1925
 Thr Arg Arg Lys Trp Lys His Tyr Trp Val Ser Leu Lys Gly Cys Thr
 460 465 470
 ctc ttt ttc tat gag act gat ggc agg tct ggg ata gac cac aac agt 1973
 Leu Phe Phe Tyr Glu Thr Asp Gly Arg Ser Gly Ile Asp His Asn Ser
 475 480 485

gtc ccc aag cac gcc gtc tgg gtg gag aac agc atc gtg cag gct gtg	2021
Val Pro Lys His Ala Val Trp Val Glu Asn Ser Ile Val Gln Ala Val	
490 495 500 505	
cct gag cac ccc aag aaa gac ttc gtc ttc tgc ctc agc aac tcc ctg	2069
Pro Glu His Pro Lys Lys Asp Phe Val Phe Cys Leu Ser Asn Ser Leu	
510 515 520	
ggt gac gcc ttc ctc ttc cag acc acg agc cag aca gag ctg gag aac	2117
Gly Asp Ala Phe Leu Phe Gln Thr Thr Ser Gln Thr Glu Leu Glu Asn	
525 530 535	
tgg atc acc gcc atc cac tct gcc tgc gca gct gcc gtc gca agg cac	2165
Trp Ile Thr Ala Ile His Ser Ala Cys Ala Ala Ala Val Ala Arg His	
540 545 550	
cac cac aag gag gac acg ctc cgc ctc ctc aag tcg gaa atc aag aag	2213
His His Lys Glu Asp Thr Leu Arg Leu Leu Lys Ser Glu Ile Lys Lys	
555 560 565	
ctg gag cag aag atc gac atg gac gag aag atg aag aag atg ggg gag	2261
Leu Glu Gln Lys Ile Asp Met Asp Glu Lys Met Lys Lys Met Gly Glu	
570 575 580 585	
atg cag ctg tct tcc gtc acc gac tcg aag aag aag aag acc atc cta	2309
Met Gln Leu Ser Ser Val Thr Asp Ser Lys Lys Lys Lys Thr Ile Leu	
590 595 600	
gac cag atc ttc gtt tgg gag cag aac ctc gaa cag ttc cag atg gac	2357
Asp Gln Ile Phe Val Trp Glu Gln Asn Leu Glu Gln Phe Gln Met Asp	
605 610 615	
ctg ttc cga ttc cgc tgt tac ctc gcc agc ctc cag ggc ggg gag ctg	2405
Leu Phe Arg Phe Arg Cys Tyr Leu Ala Ser Leu Gln Gly Gly Glu Leu	
620 625 630	
cca aac ccc aaa agg ctg ctt gct ttt gcg agc cgg ccc acg aag gtg	2453
Pro Asn Pro Lys Arg Leu Leu Ala Phe Ala Ser Arg Pro Thr Lys Val	

635	640	645	
gcc atg ggc cgc ctg ggg atc ttc tcc gtg tca tct ttt cat gcc ctg	2501		
Ala Met Gly Arg Leu Gly Ile Phe Ser Val Ser Ser Phe His Ala Leu			
650	655	660	665
gtg gca gcc cgg act ggt gag atc gga gtg aga agg cgt act cag gcc	2549		
Val Ala Ala Arg Thr Gly Glu Ile Gly Val Arg Arg Arg Thr Gln Ala			
670	675	680	
atg tcc agg tct gca agc aag cga agg agc agg ttt tct tct ctg tgg	2597		
Met Ser Arg Ser Ala Ser Lys Arg Arg Ser Arg Phe Ser Ser Leu Trp			
685	690	695	
ggc cta gac act acc tcc aaa aag aag cag gga cgc cca acc atc aac	2645		
Gly Leu Asp Thr Thr Ser Lys Lys Lys Gln Gly Arg Pro Thr Ile Asn			
700	705	710	
cag gtg ttt gga gag ggg act gat gct gta aag aga tct tta gag gga	2693		
Gln Val Phe Gly Glu Gly Thr Asp Ala Val Lys Arg Ser Leu Glu Gly			
715	720	725	
ata ttt gat gac act gtt cca gat ggc aag agg gag aag gaa gtg gtc	2741		
Ile Phe Asp Asp Thr Val Pro Asp Gly Lys Arg Glu Lys Glu Val Val			
730	735	740	745
tta ccc agt gtc cac cag cac aac ccc gac tgt gac att tgg gtc cat	2789		
Leu Pro Ser Val His Gln His Asn Pro Asp Cys Asp Ile Trp Val His			
750	755	760	
gaa tat ttc act cca tcc tgg ttc tgt cta ccc aac aac cag cca gcc	2837		
Glu Tyr Phe Thr Pro Ser Trp Phe Cys Leu Pro Asn Asn Gln Pro Ala			
765	770	775	
ttg acg gtt gtc cgg cca ggg gac act gcg agg gac acc ttg gag ctg	2885		
Leu Thr Val Val Arg Pro Gly Asp Thr Ala Arg Asp Thr Leu Glu Leu			
780	785	790	
att tgc aag aca cat caa ctg gat cat tcc gcc cat tac ctg cgc ctg	2933		

Ile Cys Lys Thr His Gln Leu Asp His Ser Ala His Tyr Leu Arg Leu
 795 800 805
 aaa ttc cta atg gag aac aga gtg cag ttc tac atc ccg cag ccc gag 2981
 Lys Phe Leu Met Glu Asn Arg Val Gln Phe Tyr Ile Pro Gln Pro Glu
 810 815 820 825
 gag gac att tac gag ctg ctt tac aaa gaa att gaa atc tgt cca aaa 3029
 Glu Asp Ile Tyr Glu Leu Leu Tyr Lys Glu Ile Glu Ile Cys Pro Lys
 830 835 840
 gtc acc cag aat atc cac att gag aag tca gac gcg gcc gct gat aat 3077
 Val Thr Gln Asn Ile His Ile Glu Lys Ser Asp Ala Ala Ala Asp Asn
 845 850 855
 tac ggg ttt ttg ctt tct tct gtg gat gaa gat ggc att cga agg ctc 3125
 Tyr Gly Phe Leu Leu Ser Ser Val Asp Glu Asp Gly Ile Arg Arg Leu
 860 865 870
 tac gtg aac agt gtc aag gaa acc ggg tta gct tcc aag aaa ggc ctg 3173
 Tyr Val Asn Ser Val Lys Glu Thr Gly Leu Ala Ser Lys Lys Gly Leu
 875 880 885
 aag gcg ggg gat gag att ctc gag atc aat aat cgt gct gct ggt acc 3221
 Lys Ala Gly Asp Glu Ile Leu Glu Ile Asn Asn Arg Ala Ala Gly Thr
 890 895 900 905
 ctg aac tca tct atg ctc aaa gat ttc ctc tca cag ccc tcc ctg ggc 3269
 Leu Asn Ser Ser Met Leu Lys Asp Phe Leu Ser Gln Pro Ser Leu Gly
 910 915 920
 ctc ctg gtg agg acc tac cct gag cca gag gga ggc gtg gag ctg ctg 3317
 Leu Leu Val Arg Thr Tyr Pro Glu Pro Glu Gly Gly Val Glu Leu Leu
 925 930 935
 gag aac cct ccg cac cga gtg gac ggc cct gtg gac ctt ggc gag agc 3365
 Glu Asn Pro Pro His Arg Val Asp Gly Pro Val Asp Leu Gly Glu Ser
 940 945 950

ccc ctc gcc ttc ctc acc agc aac cca ggg cac agc ctc tcc agt gag 3413
 Pro Leu Ala Phe Leu Thr Ser Asn Pro Gly His Ser Leu Ser Ser Glu
 955 960 965
 cag ggc agc agt gct gag aca gct cca gaa gag ggc gaa gga ccg gac 3461
 Gln Gly Ser Ser Ala Glu Thr Ala Pro Glu Glu Gly Glu Gly Pro Asp
 970 975 980 985
 ttg gag tct tct gat gag aca gat cac agc agc aag agc aca gaa cag 3509
 Leu Glu Ser Ser Asp Glu Thr Asp His Ser Ser Lys Ser Thr Glu Gln
 990 995 1000
 gtt gca gcg ttt tgc cgg agt ctg cac gag atg agc ccc tct gac tca 3557
 Val Ala Ala Phe Cys Arg Ser Leu His Glu Met Ser Pro Ser Asp Ser
 1005 1010 1015
 agc ccg tcc cct cag gat gcc aca agc cct cag ctg gca acc aca cga 3605
 Ser Pro Ser Pro Gln Asp Ala Thr Ser Pro Gln Leu Ala Thr Thr Arg
 1020 1025 1030
 cag ctg tcg gat gcg gat aag ctg cgc aag gtg atc tgt gaa ctg ctg 3653
 Gln Leu Ser Asp Ala Asp Lys Leu Arg Lys Val Ile Cys Glu Leu Leu
 1035 1040 1045
 gag act gaa cgc acc tat gtg aaa gac tta aac tgc ctc atg gag aga 3701
 Glu Thr Glu Arg Thr Tyr Val Lys Asp Leu Asn Cys Leu Met Glu Arg
 1050 1055 1060 1065
 tac ctg aag ccc ctt cag aag gag acc ttt ctc acc cag gat gag ctt 3749
 Tyr Leu Lys Pro Leu Gln Lys Glu Thr Phe Leu Thr Gln Asp Glu Leu
 1070 1075 1080
 gat gta ctt ttt gga aat tta acc gaa atg gtg gag ttt caa gtc gag 3797
 Asp Val Leu Phe Gly Asn Leu Thr Glu Met Val Glu Phe Gln Val Glu
 1085 1090 1095
 ttc ctt aag act cta gaa gat gga gta aga ctg gtc cct gac ttg gaa 3845
 Phe Leu Lys Thr Leu Glu Asp Gly Val Arg Leu Val Pro Asp Leu Glu

1100	1105	1110	
aag ctg gag aag gtt gac cag ttc aag aaa gtg ctc ttc tct ctg ggg			3893
Lys Leu Glu Lys Val Asp Gln Phe Lys Lys Val Leu Phe Ser Leu Gly			
1115	1120	1125	
gga tcc ttc ctg tac tac gcg gac cgc ttc aag ctc tac agt gcc ttc			3941
Gly Ser Phe Leu Tyr Tyr Ala Asp Arg Phe Lys Leu Tyr Ser Ala Phe			
1130	1135	1140	1145
tgt gcg agc cac aca aaa gtc ccc aag gtc ctg gtg aaa gcc aag acg			3989
Cys Ala Ser His Thr Lys Val Pro Lys Val Leu Val Lys Ala Lys Thr			
1150	1155	1160	
gac aca gcc ttc aag gcg ttc ctc gat gcc cag aac ccg agg cag cag			4037
Asp Thr Ala Phe Lys Ala Phe Leu Asp Ala Gln Asn Pro Arg Gln Gln			
1165	1170	1175	
cac tca tcc acg ctg gag tct tac ctc atc aag ccc atc cag agg gtc			4085
His Ser Ser Thr Leu Glu Ser Tyr Leu Ile Lys Pro Ile Gln Arg Val			
1180	1185	1190	
ctc aag tac ccg ctt ctg ctc agg gag ctg ttt gcg ctg acc gat gcg			4133
Leu Lys Tyr Pro Leu Leu Leu Arg Glu Leu Phe Ala Leu Thr Asp Ala			
1195	1200	1205	
gag agc gag gaa cac tac cac ctg gac gtg gcc atc aag act atg aac			4181
Glu Ser Glu Glu His Tyr His Leu Asp Val Ala Ile Lys Thr Met Asn			
1210	1215	1220	1225
aag gtc gcc agt cac atc aat gag atg cag aag atc cac gaa gag ttt			4229
Lys Val Ala Ser His Ile Asn Glu Met Gln Lys Ile His Glu Glu Phe			
1230	1235	1240	
ggt gct gtg ttt gac cag ctg att gct gag cag acg gga gag aag aaa			4277
Gly Ala Val Phe Asp Gln Leu Ile Ala Glu Gln Thr Gly Glu Lys Lys			
1245	1250	1255	
gag gtt gca gat ctg agc atg ggt gac ctg ctc ttg cac acc agc gtc			4325

Glu Val Ala Asp Leu Ser Met Gly Asp Leu Leu Leu His Thr Ser Val
 1260 1265 1270
 atc tgg ctg aac cca ccc gcc tca ctg gga aag tgg aaa aag gag cca 4373
 Ile Trp Leu Asn Pro Pro Ala Ser Leu Gly Lys Trp Lys Lys Glu Pro
 1275 1280 1285
 gaa tta gca gcc ttc gtc ttc aaa acg gcc gtg gtc ctt gta tat aaa 4421
 Glu Leu Ala Ala Phe Val Phe Lys Thr Ala Val Val Leu Val Tyr Lys
 1290 1295 1300 1305
 gac ggt tcc aag cag aag aag aaa ctt gtt ggc tct cac agg ctg tca 4469
 Asp Gly Ser Lys Gln Lys Lys Lys Leu Val Gly Ser His Arg Leu Ser
 1310 1315 1320
 atc tac gag gag tgg gac cct ttc cgg ttt cgc cac atg atc cct acc 4517
 Ile Tyr Glu Glu Trp Asp Pro Phe Arg Phe Arg His Met Ile Pro Thr
 1325 1330 1335
 gaa gct ttg cag gtc cga gct ctg ccc agt gca gat gca gag gca aat 4565
 Glu Ala Leu Gln Val Arg Ala Leu Pro Ser Ala Asp Ala Glu Ala Asn
 1340 1345 1350
 gcg gta tgc gaa att gtc cac gtg aaa tca gag tca gaa ggg agg ccc 4613
 Ala Val Cys Glu Ile Val His Val Lys Ser Glu Ser Glu Gly Arg Pro
 1355 1360 1365
 gag cgg gtt ttc cac ctc tgc tgc agt tcc cca gag agc aga aag gac 4661
 Glu Arg Val Phe His Leu Cys Cys Ser Ser Pro Glu Ser Arg Lys Asp
 1370 1375 1380 1385
 ttt ctg aag tct gtg cat tcg atc ctg cga gat aaa cac aga aga cag 4709
 Phe Leu Lys Ser Val His Ser Ile Leu Arg Asp Lys His Arg Arg Gln
 1390 1395 1400
 ctc ctc aaa acg gaa agc ctt ccg tca gcc cag cag tat gtc ccc ttt 4757
 Leu Leu Lys Thr Glu Ser Leu Pro Ser Ala Gln Gln Tyr Val Pro Phe
 1405 1410 1415

gga ggc aag aga ttg tgt gcg ctt aaa ggc gcc agg ccg gcc atg agc 4805
 Gly Gly Lys Arg Leu Cys Ala Leu Lys Gly Ala Arg Pro Ala Met Ser
 1420 1425 1430
 agg gca gtg tct gcc cca agc aag tct ctt ggg agg agg agg cgg cga 4853
 Arg Ala Val Ser Ala Pro Ser Lys Ser Leu Gly Arg Arg Arg Arg Arg
 1435 1440 1445
 ctg gcc cga aac agg ttt acc atc gat tca gac gcc atc tca gcc agc 4901
 Leu Ala Arg Asn Arg Phe Thr Ile Asp Ser Asp Ala Ile Ser Ala Ser
 1450 1455 1460 1465
 agc ccg gag aaa gag ccc cag cag ccc gcc ggt ggt ggg gac act gac 4949
 Ser Pro Glu Lys Glu Pro Gln Gln Pro Ala Gly Gly Gly Asp Thr Asp
 1470 1475 1480
 cga tgg gta gag gaa cag ttc gat ctt gct cag tac gag gag cag gat 4997
 Arg Trp Val Glu Glu Gln Phe Asp Leu Ala Gln Tyr Glu Glu Gln Asp
 1485 1490 1495
 gac atc aag gag aca gac atc ctc agt gac gat gac gaa ttc tgt gag 5045
 Asp Ile Lys Glu Thr Asp Ile Leu Ser Asp Asp Asp Glu Phe Cys Glu
 1500 1505 1510
 tcc ctg aag ggc gcc tca gtg gac aga gac ctt cag gag cag ctt cag 5093
 Ser Leu Lys Gly Ala Ser Val Asp Arg Asp Leu Gln Glu Gln Leu Gln
 1515 1520 1525
 gct gcc tcc atc agt cag cgg gcc cga ggc cgg aga acc ctc gat agc 5141
 Ala Ala Ser Ile Ser Gln Arg Ala Arg Gly Arg Arg Thr Leu Asp Ser
 1530 1535 1540 1545
 cac gcc tcc cgc atg aca cag ctc aag aag caa gcg gcc ctc tcg ggc 5189
 His Ala Ser Arg Met Thr Gln Leu Lys Lys Gln Ala Ala Leu Ser Gly
 1550 1555 1560
 atc aac ggg ggc ctg gag agt gcg agc gag gaa gtc att tgg gtc agg 5237
 Ile Asn Gly Gly Leu Glu Ser Ala Ser Glu Glu Val Ile Trp Val Arg

1565	1570	1575	
cgc gaa gac ttt gcc ccc tcc agg aaa ctg aac acg gag ata tga			5282
Arg Glu Asp Phe Ala Pro Ser Arg Lys Leu Asn Thr Glu Ile			
1580	1585	1590	
cttccttgct ccgtagaga atatgtgtgt agatatgatg ccggccccac cctcactccg			5342
cccaccctcc tgtgccgtcc acgagaatgt ccccttaggt cgcactcttg acacagattt			5402
tggcagctga ctgggtctg aagccaatgta gccaccacc ttcatcattc ttaatgacac			5462
cagagagaat cgttcagaat cccagacaaa caagcttgag tcccttcctc tgtgccaaagg			5522
gctttctttt atttattctc aattcatcgg ggcctgaaga tttagaacga aggaccgata			5582
gcgctagaaa tcaaaccgtc cccaccccag cagtcaaac agggacagga cggigtgcac			5642
agattgtccc agctccacct ctctaaatcc agtctcgcag ctgaggaaca accaccttca			5702
aacacacata gagaacgga acagaatgaa acacctgtac agcgtgcagt gttctgactc			5762
ctccctcttt cagcgtccga gaatatctgt gtatcttaag aatgtgtgag gaaagggtag			5822
tcgtctctgt acgatgagcc ttattcttta tttttttttt ctctctgttca tgtctatagc			5882
tggctcttact ctgtgtcagt gtctggaagc tctagttttg cagagaatta taaagatgcc			5942
aaactcttgg aaaagagatc caaatctatc acttagaggg agagagaaga aaaaaaagaa			6002
acaciatttt ttgtattttc ctgagatgc aggggcacaa atagatgaga attttacagt			6062
gttaggtgta actcagtcctg aaaatgagga tataaccttt tgcagagcaa gcggggcacg			6122
atgactttat atttatacac aaacggccaa caagaagctc atgctaagaa taactttttc			6182
tgagaaacag attttttttt taaatgtatg aatctatatt tgagatggga gtttggttgg			6242
attacaggga caggaaatgg ggcagtgtgt gcgtgtgtct gttgttcatg gtgggggagg			6302
ggagcctcct catggggttg ccatggcaat cattggtttt cccatcaaac ttgcatcttc			6362
atccacagat gacctccct tccctgagag tccacggcag aatcttagaa cctcttcaga			6422
gacgcccttt gtggttaata tticctccat gccaatgaga cagggtaaac tcgctacggg			6482
gcctaacctt ctaaattgat gccagacag gaagaacaaa accattcta gcactttcat			6542
ttttaaaaaa aaaaaagggt tatagctttt tggctcgcc cctcctcccc atttcacaat			6602
gtccattcct taagaagggt ttaaataata tgaaaacttt gtttttgaa ataaaaaaat			6662
atctatatat ctatatatct atatatctat ttgggtgttg atacatcgtt aggtacttta			6722
aagacctgaa ttttatagta gctttagcaa ttatatatta taagaatcag ttatgacttt			6782

atatttccag atagagagtt cagaacacca tgctctaaag cctccccac cccggcttgc 6842
 tticctgctt tccgacctc tcccccccc cccctttcg ggtttccagg gctttgagct 6902
 tgatcttttg aaagtittat tctattacag tttttgctat taccttctgg ttttcttaag 6962
 aagcittaga gttgtttcta tgccttttgt accactgcac tgttcgtaac atctcggggg 7022
 cgattgcgtc cggatgggaa actgaagcag aggtgtcgga tagtcacatt ttctggctctc 7082
 cctgcaacac gtccatcgga aaaaaaata ctggaaagtc tgggtgcttag agagggtgcc 7142
 attgtctctt gtatatcgg tcatgaigtg tctatgtcaa aagttcttat atatttcttt 7202
 tataagctga aagaaggctt atttttatgt ttttaggtct atgaatggaa cgttgtaaat 7262
 gccgtgccaa caataaaagt actgaaaagg 7292

<210> 344

<211> 1591

<212> PRT

<213> Mus musculus

<400> 344

Met	Gly	Asn	Ala	Glu	Ser	Gln	Asn	Val	Asp	His	Glu	Phe	Tyr	Gly	Glu
1				5				10						15	
Lys	His	Ala	Ser	Leu	Gly	Arg	Lys	His	Thr	Ser	Arg	Ser	Leu	Arg	Leu
				20				25						30	
Ser	His	Lys	Thr	Arg	Arg	Thr	Arg	His	Ala	Ser	Ser	Gly	Lys	Ala	Ile
				35				40						45	
His	Arg	Asn	Ser	Glu	Val	Ser	Thr	Arg	Ser	Ser	Ser	Thr	Pro	Ser	Ile
				50				55						60	
Pro	Gln	Ser	Leu	Ala	Glu	Asn	Gly	Leu	Glu	Pro	Phe	Ser	Gln	Glu	Gly
				65				70						75	
Ala	Leu	Asp	Asp	Phe	Gly	Asp	Pro	Ile	Trp	Val	Asp	Arg	Val	Asp	Met
				85				90						95	
Gly	Leu	Arg	Pro	Val	Ser	Tyr	Thr	Asp	Ser	Ser	Val	Thr	Pro	Ser	Val

100	105	110
Asp Gly Ser Ile Val Leu Thr	Ala Ala Ser Val Gln Ser Met Pro Asp	
115	120	125
Ser Glu Glu Ser Arg Leu Tyr Gly Asp Asp Ala Thr Tyr Leu Ala Glu		
130	135	140
Gly Gly Arg Arg Gln Cys Pro Tyr Thr Ser Asn Gly Pro Thr Phe Met		
145	150	155
Glu Thr Ala Ser Phe Lys Lys Lys Arg Ser Lys Ser Ala Asp Ile Trp		
165	170	175
Arg Glu Asp Ser Leu Glu Phe Ser Leu Ser Asp Leu Ser Gln Glu His		
180	185	190
Leu Thr Ser Asn Glu Glu Ile Leu Gly Ser Ala Glu Glu Lys Asp Cys		
195	200	205
Glu Glu Ala Arg Gly Met Glu Thr Glu Ala Ser Pro Arg Gln Leu Ser		
210	215	220
Thr Cys Gln Arg Ala Asn Ser Leu Gly Asp Leu Tyr Ala Gln Lys Asn		
225	230	235
Ser Gly Val Lys Ala Asn Gly Gly Pro Arg Asn Arg Phe Ser Ser Tyr		
245	250	255
Cys Arg Asn Leu Val Ser Asp Ile Pro Asp Leu Ala Lys His Lys Met		
260	265	270
Pro Pro Ala Ala Ala Glu Glu Thr Pro Pro Tyr Ser Asn Tyr Asn Thr		
275	280	285
Leu Pro Cys Arg Lys Ser His Cys Leu Ser Glu Gly Ala Thr Asn Pro		
290	295	300
Gln Ile Ser Leu Ser Lys Ser Met Gln Gly Arg Arg Ala Lys Thr Thr		
305	310	315
Gln Asp Val Asn Thr Gly Glu Gly Ser Glu Phe Ala Asp Ser Gly Ile		
325	330	335

Glu Gly Ala Thr Thr Asp Thr Asp Leu Leu Ser Arg Arg Ser Asn Ala
 340 345 350
 Thr Asn Ser Ser Tyr Ser Pro Pro Thr Gly Arg Ala Phe Val Gly Ser
 355 360 365
 Asp Ser Gly Ser Ser Ser Thr Gly Asp Arg Ala Arg Gln Gly Val Tyr
 370 375 380
 Glu Asn Phe Arg Arg Glu Leu Glu Met Ser Thr Thr Asn Ser Glu Ser
 385 390 395 400
 Leu Glu Glu Ala Gly Ser Ala His Ser Asp Glu Gln Ser Ser Gly Thr
 405 410 415
 Leu Ser Ser Pro Gly Gln Ser Asp Ile Leu Leu Thr Ala Ala Gln Gly
 420 425 430
 Thr Val Arg Lys Ala Gly Ala Leu Ala Val Lys Asn Phe Leu Val His
 435 440 445
 Lys Lys Asn Lys Lys Val Glu Ser Ala Thr Arg Arg Lys Trp Lys His
 450 455 460
 Tyr Trp Val Ser Leu Lys Gly Cys Thr Leu Phe Phe Tyr Glu Thr Asp
 465 470 475 480
 Gly Arg Ser Gly Ile Asp His Asn Ser Val Pro Lys His Ala Val Trp
 485 490 495
 Val Glu Asn Ser Ile Val Gln Ala Val Pro Glu His Pro Lys Lys Asp
 500 505 510
 Phe Val Phe Cys Leu Ser Asn Ser Leu Gly Asp Ala Phe Leu Phe Gln
 515 520 525
 Thr Thr Ser Gln Thr Glu Leu Glu Asn Trp Ile Thr Ala Ile His Ser
 530 535 540
 Ala Cys Ala Ala Ala Val Ala Arg His His His Lys Glu Asp Thr Leu
 545 550 555 560
 Arg Leu Leu Lys Ser Glu Ile Lys Lys Leu Glu Gln Lys Ile Asp Met

	565		570		575										
Asp	Glu	Lys	Met	Lys	Lys	Met	Gly	Glu	Met	Gln	Leu	Ser	Ser	Val	Thr
	580		585		590										
Asp	Ser	Lys	Lys	Lys	Lys	Thr	Ile	Leu	Asp	Gln	Ile	Phe	Val	Trp	Glu
	595		600		605										
Gln	Asn	Leu	Glu	Gln	Phe	Gln	Met	Asp	Leu	Phe	Arg	Phe	Arg	Cys	Tyr
	610		615		620										
Leu	Ala	Ser	Leu	Gln	Gly	Gly	Glu	Leu	Pro	Asn	Pro	Lys	Arg	Leu	Leu
625			630		635									640	
Ala	Phe	Ala	Ser	Arg	Pro	Thr	Lys	Val	Ala	Met	Gly	Arg	Leu	Gly	Ile
	645		650		655										
Phe	Ser	Val	Ser	Ser	Phe	His	Ala	Leu	Val	Ala	Ala	Arg	Thr	Gly	Glu
	660		665		670										
Ile	Gly	Val	Arg	Arg	Arg	Thr	Gln	Ala	Met	Ser	Arg	Ser	Ala	Ser	Lys
	675		680		685										
Arg	Arg	Ser	Arg	Phe	Ser	Ser	Leu	Trp	Gly	Leu	Asp	Thr	Thr	Ser	Lys
	690		695		700										
Lys	Lys	Gln	Gly	Arg	Pro	Thr	Ile	Asn	Gln	Val	Phe	Gly	Glu	Gly	Thr
705			710		715									720	
Asp	Ala	Val	Lys	Arg	Ser	Leu	Glu	Gly	Ile	Phe	Asp	Asp	Thr	Val	Pro
	725		730		735										
Asp	Gly	Lys	Arg	Glu	Lys	Glu	Val	Val	Leu	Pro	Ser	Val	His	Gln	His
	740		745		750										
Asn	Pro	Asp	Cys	Asp	Ile	Trp	Val	His	Glu	Tyr	Phe	Thr	Pro	Ser	Trp
	755		760		765										
Phe	Cys	Leu	Pro	Asn	Asn	Gln	Pro	Ala	Leu	Thr	Val	Val	Arg	Pro	Gly
	770		775		780										
Asp	Thr	Ala	Arg	Asp	Thr	Leu	Glu	Leu	Ile	Cys	Lys	Thr	His	Gln	Leu
785			790		795									800	

Asp His Ser Ala His Tyr Leu Arg Leu Lys Phe Leu Met Glu Asn Arg
 805 810 815
 Val Gln Phe Tyr Ile Pro Gln Pro Glu Glu Asp Ile Tyr Glu Leu Leu
 820 825 830
 Tyr Lys Glu Ile Glu Ile Cys Pro Lys Val Thr Gln Asn Ile His Ile
 835 840 845
 Glu Lys Ser Asp Ala Ala Ala Asp Asn Tyr Gly Phe Leu Leu Ser Ser
 850 855 860
 Val Asp Glu Asp Gly Ile Arg Arg Leu Tyr Val Asn Ser Val Lys Glu
 865 870 875 880
 Thr Gly Leu Ala Ser Lys Lys Gly Leu Lys Ala Gly Asp Glu Ile Leu
 885 890 895
 Glu Ile Asn Asn Arg Ala Ala Gly Thr Leu Asn Ser Ser Met Leu Lys
 900 905 910
 Asp Phe Leu Ser Gln Pro Ser Leu Gly Leu Leu Val Arg Thr Tyr Pro
 915 920 925
 Glu Pro Glu Gly Gly Val Glu Leu Leu Glu Asn Pro Pro His Arg Val
 930 935 940
 Asp Gly Pro Val Asp Leu Gly Glu Ser Pro Leu Ala Phe Leu Thr Ser
 945 950 955 960
 Asn Pro Gly His Ser Leu Ser Ser Glu Gln Gly Ser Ser Ala Glu Thr
 965 970 975
 Ala Pro Glu Glu Gly Glu Gly Pro Asp Leu Glu Ser Ser Asp Glu Thr
 980 985 990
 Asp His Ser Ser Lys Ser Thr Glu Gln Val Ala Ala Phe Cys Arg Ser
 995 1000 1005
 Leu His Glu Met Ser Pro Ser Asp Ser Ser Pro Ser Pro Gln Asp Ala
 1010 1015 1020
 Thr Ser Pro Gln Leu Ala Thr Thr Arg Gln Leu Ser Asp Ala Asp Lys

025	1030	1035	1040
Leu Arg Lys Val Ile Cys Glu Leu Leu Glu Thr Glu Arg Thr Tyr Val			
1045	1050	1055	
Lys Asp Leu Asn Cys Leu Met Glu Arg Tyr Leu Lys Pro Leu Gln Lys			
1060	1065	1070	
Glu Thr Phe Leu Thr Gln Asp Glu Leu Asp Val Leu Phe Gly Asn Leu			
1075	1080	1085	
Thr Glu Met Val Glu Phe Gln Val Glu Phe Leu Lys Thr Leu Glu Asp			
1090	1095	1100	
Gly Val Arg Leu Val Pro Asp Leu Glu Lys Leu Glu Lys Val Asp Gln			
1105	1110	1115	1120
Phe Lys Lys Val Leu Phe Ser Leu Gly Gly Ser Phe Leu Tyr Tyr Ala			
1125	1130	1135	
Asp Arg Phe Lys Leu Tyr Ser Ala Phe Cys Ala Ser His Thr Lys Val			
1140	1145	1150	
Pro Lys Val Leu Val Lys Ala Lys Thr Asp Thr Ala Phe Lys Ala Phe			
1155	1160	1165	
Leu Asp Ala Gln Asn Pro Arg Gln Gln His Ser Ser Thr Leu Glu Ser			
1170	1175	1180	
Tyr Leu Ile Lys Pro Ile Gln Arg Val Leu Lys Tyr Pro Leu Leu Leu			
1185	1190	1195	1200
Arg Glu Leu Phe Ala Leu Thr Asp Ala Glu Ser Glu Glu His Tyr His			
1205	1210	1215	
Leu Asp Val Ala Ile Lys Thr Met Asn Lys Val Ala Ser His Ile Asn			
1220	1225	1230	
Glu Met Gln Lys Ile His Glu Glu Phe Gly Ala Val Phe Asp Gln Leu			
1235	1240	1245	
Ile Ala Glu Gln Thr Gly Glu Lys Lys Glu Val Ala Asp Leu Ser Met			
1250	1255	1260	

Gly Asp Leu Leu Leu His Thr Ser Val Ile Trp Leu Asn Pro Pro Ala
 265 1270 1275 1280
 Ser Leu Gly Lys Trp Lys Lys Glu Pro Glu Leu Ala Ala Phe Val Phe
 1285 1290 1295
 Lys Thr Ala Val Val Leu Val Tyr Lys Asp Gly Ser Lys Gln Lys Lys
 1300 1305 1310
 Lys Leu Val Gly Ser His Arg Leu Ser Ile Tyr Glu Glu Trp Asp Pro
 1315 1320 1325
 Phe Arg Phe Arg His Met Ile Pro Thr Glu Ala Leu Gln Val Arg Ala
 1330 1335 1340
 Leu Pro Ser Ala Asp Ala Glu Ala Asn Ala Val Cys Glu Ile Val His
 345 1350 1355 1360
 Val Lys Ser Glu Ser Glu Gly Arg Pro Glu Arg Val Phe His Leu Cys
 1365 1370 1375
 Cys Ser Ser Pro Glu Ser Arg Lys Asp Phe Leu Lys Ser Val His Ser
 1380 1385 1390
 Ile Leu Arg Asp Lys His Arg Arg Gln Leu Leu Lys Thr Glu Ser Leu
 1395 1400 1405
 Pro Ser Ala Gln Gln Tyr Val Pro Phe Gly Gly Lys Arg Leu Cys Ala
 1410 1415 1420
 Leu Lys Gly Ala Arg Pro Ala Met Ser Arg Ala Val Ser Ala Pro Ser
 425 1430 1435 1440
 Lys Ser Leu Gly Arg Arg Arg Arg Arg Leu Ala Arg Asn Arg Phe Thr
 1445 1450 1455
 Ile Asp Ser Asp Ala Ile Ser Ala Ser Ser Pro Glu Lys Glu Pro Gln
 1460 1465 1470
 Gln Pro Ala Gly Gly Gly Asp Thr Asp Arg Trp Val Glu Glu Gln Phe
 1475 1480 1485
 Asp Leu Ala Gln Tyr Glu Glu Gln Asp Asp Ile Lys Glu Thr Asp Ile

1490	1495	1500
Leu Ser Asp Asp Asp Glu Phe Cys Glu Ser Leu Lys Gly Ala Ser Val		
505	1510	1515
Asp Arg Asp Leu Gln Glu Gln Leu Gln Ala Ala Ser Ile Ser Gln Arg		1520
	1525	1530
Ala Arg Gly Arg Arg Thr Leu Asp Ser His Ala Ser Arg Met Thr Gln		1535
	1540	1545
Leu Lys Lys Gln Ala Ala Leu Ser Gly Ile Asn Gly Gly Leu Glu Ser		1550
	1555	1560
Ala Ser Glu Glu Val Ile Trp Val Arg Arg Glu Asp Phe Ala Pro Ser		1565
	1570	1575
Arg Lys Leu Asn Thr Glu Ile		1580
585	1590	

<210> 345

<211> 462

<212> DNA

<213> Mus musculus

<400> 345

```

tttatccaac gtatgacttt gcctgcccta tagtggacag cattgaaggt gttactcatg 60
ccttgaggac aacagagtac caccgaccgag atgaacaatt ttattggatc gttgaagcitt 120
taggcataag gaaaccatac atctgggagt acagtcgctt aaatctcaac aacaccgtgc 180
tgtccaaaag aaagctcacg tggtttgtca atgaaggact ggtagatgga tgggatgacc 240
cacggtttcc tacagttcgt ggagttctga gaagagggat gacagttgag gtgctgaggc 300
agttcattgc tgctcagggc tcctcaaggt ctgttgtgaa catggaatgg gacgaaatgt 360
gggcgttcag caagagggtt agtgaccagt ggctcacggt acgttgcatt ctgaagaaga 420
agtcgtccag tgagtgtcgt gatgccagga ggagataagg aa 462

```

<210> 346

<211> 384

<212> DNA

<213> Mus musculus

<400> 346

```
cacaggtcgt gcctactcaa gaactctaca acaagctgct gtgcctctgt tacccaagag 60
gttttgtaaa gagaggtaca agggactatt tactgggaga atgctctgtg ctgggaacct 120
ccaagaagac aaccgtgtgg acagctgcc a gggagacagt ggaggaccac tcatgtgtga 180
aaagcc t gat g agtcctggg ttgtgtatgg ggtgacttcc tgggggtatg gatgtggagt 240
caaagacact cctggagitt ataccagagt ccccgccitt gtaccttgga taaaaagtgt 300
caccagtctg taactta tgg aaagctcaag aaaatagtaa aacagtaacc attcagtcctt 360
catacttggc accatgccag aaaa 384
```

<210> 347

<211> 628

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (49).. (618)

<400> 347

```
tgccacattg ctggcatcag gccagggcac ctgctctgct ctgagcaa atg gct gct 57
Met Ala Ala
```

1

```
ctt cgc atg ctg tgg atg ggt ttg gtc ctc ctg ggt ctc ttg gga ttc 105
Leu Arg Met Leu Trp Met Gly Leu Val Leu Leu Gly Leu Leu Gly Phe
```

5	10	15	
cca cag acc cca gcc cag ggc cat gac aca gtg cag ccc aac ttt caa	153		
Pro Gln Thr Pro Ala Gln Gly His Asp Thr Val Gln Pro Asn Phe Gln			
20	25	30	35
caa gac aag ttc ctg ggg cgc tgg tac agc gcg ggc ctc gcc tcc aac	201		
Gln Asp Lys Phe Leu Gly Arg Trp Tyr Ser Ala Gly Leu Ala Ser Asn			
40	45	50	
tca agc tgg ttc cgg gag aag aaa gct gta ttg tat atg tgc aag aca	249		
Ser Ser Trp Phe Arg Glu Lys Lys Ala Val Leu Tyr Met Cys Lys Thr			
55	60	65	
gtg gta gcc ccc tcc aca gaa ggc ggc ctc aat ctc acc tct acc ttc	297		
Val Val Ala Pro Ser Thr Glu Gly Gly Leu Asn Leu Thr Ser Thr Phe			
70	75	80	
ctc agg aaa aac cag tgt gag acc aag atc atg gta ctg cag cct gcg	345		
Leu Arg Lys Asn Gln Cys Glu Thr Lys Ile Met Val Leu Gln Pro Ala			
85	90	95	
ggg gct cct gga cac tac acc tac agc agc ccc cac tcg ggc agc atc	393		
Gly Ala Pro Gly His Tyr Thr Tyr Ser Ser Pro His Ser Gly Ser Ile			
100	105	110	115
cac tcc gtg tca gtg gtg gag gcc aac tat gac gag tac gct ctg cta	441		
His Ser Val Ser Val Val Glu Ala Asn Tyr Asp Glu Tyr Ala Leu Leu			
120	125	130	
ttc agc aga ggc acc aag ggc cca ggc cag gac ttc cgc atg gcc acc	489		
Phe Ser Arg Gly Thr Lys Gly Pro Gly Gln Asp Phe Arg Met Ala Thr			
135	140	145	
ctc tac agc aga acc cag act ctg aag gac gag ctg aag gag aaa ttc	537		
Leu Tyr Ser Arg Thr Gln Thr Leu Lys Asp Glu Leu Lys Glu Lys Phe			
150	155	160	
acc acc ttt agc aag gcc cag ggc ctc aca gag gag gac att gtt ttc	585		

Thr Thr Phe Ser Lys Ala Gln Gly Leu Thr Glu Glu Asp Ile Val Phe

165

170

175

ctg ccc caa ccg gat aag tgc att caa gag taa acgcaggtga

628

Leu Pro Gln Pro Asp Lys Cys Ile Gln Glu

180

185

190

<210> 348

<211> 189

<212> PRT

<213> Mus musculus

<400> 348

Met Ala Ala Leu Arg Met Leu Trp Met Gly Leu Val Leu Leu Gly Leu

1

5

10

15

Leu Gly Phe Pro Gln Thr Pro Ala Gln Gly His Asp Thr Val Gln Pro

20

25

30

Asn Phe Gln Gln Asp Lys Phe Leu Gly Arg Trp Tyr Ser Ala Gly Leu

35

40

45

Ala Ser Asn Ser Ser Trp Phe Arg Glu Lys Lys Ala Val Leu Tyr Met

50

55

60

Cys Lys Thr Val Val Ala Pro Ser Thr Glu Gly Gly Leu Asn Leu Thr

65

70

75

80

Ser Thr Phe Leu Arg Lys Asn Gln Cys Glu Thr Lys Ile Met Val Leu

85

90

95

Gln Pro Ala Gly Ala Pro Gly His Tyr Thr Tyr Ser Ser Pro His Ser

100

105

110

Gly Ser Ile His Ser Val Ser Val Val Glu Ala Asn Tyr Asp Glu Tyr

115

120

125

Ala Leu Leu Phe Ser Arg Gly Thr Lys Gly Pro Gly Gln Asp Phe Arg

130	135	140
Met Ala Thr Leu Tyr Ser Arg Thr Gln Thr Leu Lys Asp Glu Leu Lys		
145	150	155
Glu Lys Phe Thr Thr Phe Ser Lys Ala Gln Gly Leu Thr Glu Glu Asp		160
	165	170
Ile Val Phe Leu Pro Gln Pro Asp Lys Cys Ile Gln Glu		175
	180	185

<210> 349

<211> 359

<212> DNA

<213> Mus musculus

<400> 349

```

ggagtcaatg gaggcatcca tgcacccgat gtaacaaatg catgcagaac gatgcttttt 60
aacatccact ctttggaatg ggataaagat ctctgtgact tttttgaaat tccaatgagc 120
atccctccaa atgtatgcag ttctgctgag atctatggcc tgatgacatc acggggcctt 180
ggaaggcgtg ccaatatctg gatgtttggg ggatcagctt gctgcttttag tgtgacaaat 240
gtgtttcatg aagggtcaacc aaaaacacat accgaacagg ctgttttgta ctatgtaata 300
caggccacga aatgtgtggt ttctgaacat tggcttctga gcacaattgc cttacaaac 359

```

<210> 350

<211> 650

<212> DNA

<213> Mus musculus

<400> 350

```

tgggtgtgaaa gttggcctga caaattatgc tgcagcctat tgcactggcc tgctgctggc 60
ccgcagcttc tgaatagggt tggcatggac aagatctatg aaggccaagt ggaggatgaat 120

```


ggaggtgaat acaatgtgga aagcattgac ggtcagcctg gtgccttcac ttgctatctg 180
 gatgcaggtc ttgccgaac tacaactggc aataaagttt ttggggccct gaaggagct 240
 gtggatggag gcttgtctat ccctcatagt accaaacgat tccctggta tgactctgaa 300
 agcaaggagt tcaatgcaga ggtacatcgg aagcacatca tgggtcagaa tgtggcagac 360
 tacatgcgct acctaattgga ggaagatgaa gatgcgtata agaaacagtt ctctcagtac 420
 atcaagaaca acgtaacctc agacatgatg gaggagatgt ataagaaagc tcatgctgct 480
 atccgagaga atccagtcta tgagaagaag cccaagagag aagtgaagaa gaagaggttg 540
 aatcgtccca aatgtctctt gcccagaag aagatcgggt ttgctcaaag aagcaagctt 600
 ctccagagctc aggaaggct gctgaactan agcagtgtct atgagatttt 650

<210> 351

<211> 482

<212> DNA

<213> Mus musculus

<400> 351

atcaagaaag ttctacagga caagcgattt aagaaccgag agctccagat catgagaaag 60
 ctagaccact gtaacatagt ccgactgcgg tatttcttct actcgagtgg tgagaagaaa 120
 gatgaggctt accttaacct ggtgctggac tatgttccgg agacagtgtc cagagtcgcc 180
 agaactatag tcgagccaag cagacactcc ctgtgatcta tgtcaagtig tataatgtatc 240
 agctgttcag aagtctagcc tataatccatt cctttggaat ctgccatga gacattaaac 300
 cacagaacct ctgtttggat cctgatacag ctgtattaaa actctgtgac tttggaagtg 360
 caaagcagct ggtccgagga gagcccaatg ttccatatat ctgttctcgg tactacaggg 420
 caccagagtt gatctttgga gcactgatta cacgtccagt atagatgtat ggtctgcagg 480
 ct 482

<210> 352

<211> 2461

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (46).. (1899)

<400> 352

ctgtgataat ttgtattttc tatgttttca ggaaatcttt aagac atg gct gga gct 57

Met Ala Gly Ala

1

aag gcg tac cga ctt gga gca gtt ctg ctt ctt atc cac tta att ttc 105

Lys Ala Tyr Arg Leu Gly Ala Val Leu Leu Leu Ile His Leu Ile Phe

5 10 15 20

ctc atc tct gga gcc gaa gca gct tcc ttc cag cga aac cag ctg ctt 153

Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg Asn Gln Leu Leu

25 30 35

cag aaa gaa cca gac ctc aga ttg gag aat gtc caa aag ttt cct agt 201

Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln Lys Phe Pro Ser

40 45 50

cca gaa atg atc agg gct ttg gag tac ata gaa aag ctc agg cag caa 249

Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Lys Leu Arg Gln Gln

55 60 65

gct cac aga gaa gaa agc agc cca gac tac aat ccc tac caa ggc gtc 297

Ala His Arg Glu Glu Ser Ser Pro Asp Tyr Asn Pro Tyr Gln Gly Val

70 75 80

tct gtt cct ctt caa ctc aaa gaa aac gga gaa gaa agc cac ttg gca 345

Ser Val Pro Leu Gln Leu Lys Glu Asn Gly Glu Glu Ser His Leu Ala

85 90 95 100

gag agc tca agg gat gca ctg agt gaa gac gag tgg atg cgg ata ata 393

Glu Ser Ser Arg Asp Ala Leu Ser Glu Asp Glu Trp Met Arg Ile Ile
 105 110 115
 ctc gag gct ctg agg cag gct gaa aat gag ccg cca tct gcc ccc aaa 441
 Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Pro Ser Ala Pro Lys
 120 125 130
 gag aac aag ccc tat gcc ttg aat ctg gag aag aac ttc cca gtg gac 489
 Glu Asn Lys Pro Tyr Ala Leu Asn Leu Glu Lys Asn Phe Pro Val Asp
 135 140 145
 acg cct gat gac tat gag act caa cag tgg cct gag agg aaa ctc aag 537
 Thr Pro Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu Arg Lys Leu Lys
 150 155 160
 cac atg cgg ttc cct ctc atg tat gaa gag aat tcc aga gaa aac ccc 585
 His Met Arg Phe Pro Leu Met Tyr Glu Glu Asn Ser Arg Glu Asn Pro
 165 170 175 180
 ttc aaa cgc aca aat gaa ata gtc gag gaa caa tac aca ccc caa agt 633
 Phe Lys Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr Thr Pro Gln Ser
 185 190 195
 ctt gct acc ctg gag tct gtg ttc caa gag ctt ggg aaa ctg aca ggg 681
 Leu Ala Thr Leu Glu Ser Val Phe Gln Glu Leu Gly Lys Leu Thr Gly
 200 205 210
 cca agc aac cag aag cgt gag agg gtt gac gag gaa caa aag ctg tac 729
 Pro Ser Asn Gln Lys Arg Glu Arg Val Asp Glu Glu Gln Lys Leu Tyr
 215 220 225
 aca gat gat gaa gac gac gtg tac aag acc aac aac att gcc tat gaa 777
 Thr Asp Asp Glu Asp Asp Val Tyr Lys Thr Asn Asn Ile Ala Tyr Glu
 230 235 240
 gat gtc gtg ggg gga gaa gac tgg agc ccc ata gag gag aaa ata gag 825
 Asp Val Val Gly Gly Glu Asp Trp Ser Pro Ile Glu Glu Lys Ile Glu
 245 250 255 260

act caa acc cag gaa gag gtg aga gac agc aaa gag aac aca gaa aaa 873
 Thr Gln Thr Gln Glu Glu Val Arg Asp Ser Lys Glu Asn Thr Glu Lys
 265 270 275
 aat gaa caa atc aat gaa gag atg aaa cgt tca ggg cag ttg ggg ctc 921
 Asn Glu Gln Ile Asn Glu Glu Met Lys Arg Ser Gly Gln Leu Gly Leu
 280 285 290
 cca gat gaa gaa aac cgg aga gag agt aaa gac caa ctc tca gag gat 969
 Pro Asp Glu Glu Asn Arg Arg Glu Ser Lys Asp Gln Leu Ser Glu Asp
 295 300 305
 gcc tcc aaa gtt atc acc tac ctg aga agg tia gtg aat gct gtg ggc 1017
 Ala Ser Lys Val Ile Thr Tyr Leu Arg Arg Leu Val Asn Ala Val Gly
 310 315 320
 agt ggg agg tca cag agt ggg cca aat ggg gac agg gca gcc cgg ctt 1065
 Ser Gly Arg Ser Gln Ser Gly Pro Asn Gly Asp Arg Ala Ala Arg Leu
 325 330 335 340
 ctt cag aag ccc ctt gat tct cag tct att tat cag ctg att gaa atc 1113
 Leu Gln Lys Pro Leu Asp Ser Gln Ser Ile Tyr Gln Leu Ile Glu Ile
 345 350 355
 tcc agg aat ttg cag ata ccc cct gaa gat tta att gag atg ctc aaa 1161
 Ser Arg Asn Leu Gln Ile Pro Pro Glu Asp Leu Ile Glu Met Leu Lys
 360 365 370
 gct gga gag aag cca aat ggg ttg gtg gag cca gag cag gat ctg gag 1209
 Ala Gly Glu Lys Pro Asn Gly Leu Val Glu Pro Glu Gln Asp Leu Glu
 375 380 385
 ctt gct gtt gac cta gat gac atc cca gag gct gac cta gac cgt cca 1257
 Leu Ala Val Asp Leu Asp Asp Ile Pro Glu Ala Asp Leu Asp Arg Pro
 390 395 400
 gac atg ttt caa agt aag atg ctc tcc aag ggt ggg tat ccc aag gca 1305
 Asp Met Phe Gln Ser Lys Met Leu Ser Lys Gly Gly Tyr Pro Lys Ala

405	410	415	420	
cct ggt cgt ggt atg gta gag gcc ttg cct gat ggg ctg agt gtc gag	1353			
Pro Gly Arg Gly Met Val Glu Ala Leu Pro Asp Gly Leu Ser Val Glu				
425	430	435		
gac att tta aat gtt tta ggg atg gag aat gta gta aat cag aag tcc	1401			
Asp Ile Leu Asn Val Leu Gly Met Glu Asn Val Val Asn Gln Lys Ser				
440	445	450		
cca tat ttt ccc aac caa tat agc caa gac aag gct ctg atg agg ctc	1449			
Pro Tyr Phe Pro Asn Gln Tyr Ser Gln Asp Lys Ala Leu Met Arg Leu				
455	460	465		
cct tat ggt cct ggg aaa tct aga gcc aac cag att ccc aaa gta gcc	1497			
Pro Tyr Gly Pro Gly Lys Ser Arg Ala Asn Gln Ile Pro Lys Val Ala				
470	475	480		
tgg atc cct gat gtt gaa agc aga caa gca cct tat gaa aat ctg aat	1545			
Trp Ile Pro Asp Val Glu Ser Arg Gln Ala Pro Tyr Glu Asn Leu Asn				
485	490	495	500	
gac caa gaa ttg gga gag tac tta gcc agg atg cta gtt aag tac cct	1593			
Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu Val Lys Tyr Pro				
505	510	515		
gag ctc ctg aat acc aac cag ctg aag aga gtg ccc agt cca gtc tcc	1641			
Glu Leu Leu Asn Thr Asn Gln Leu Lys Arg Val Pro Ser Pro Val Ser				
520	525	530		
tca gag gat gac ctc caa gaa gaa gag cag ctc gag cag gcc atc aag	1689			
Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Leu Glu Gln Ala Ile Lys				
535	540	545		
gaa cat ctg ggg cca gga agc tcc cag gaa atg gag aga ctg gcc aag	1737			
Glu His Leu Gly Pro Gly Ser Ser Gln Glu Met Glu Arg Leu Ala Lys				
550	555	560		
gtg agc aaa agg atc ccc gta gga tcc ctg aag aat gag gac acc cca	1785			

Val Ser Lys Arg Ile Pro Val Gly Ser Leu Lys Asn Glu Asp Thr Pro
 565 570 575 580
 aac aga cag tac ctg gat gaa gat atg ctc ctg aaa gtg ctg gag tac 1833
 Asn Arg Gln Tyr Leu Asp Glu Asp Met Leu Leu Lys Val Leu Glu Tyr
 585 590 595
 ctc aac caa gag cag gca gag cag ggg agg gag cat ctt gcc aag cgg 1881
 Leu Asn Gln Glu Gln Ala Glu Gln Gly Arg Glu His Leu Ala Lys Arg
 600 605 610
 gcc atg gaa aac atg taa acagctttaa tgcccaattt cctttctttc 1929
 Ala Met Glu Asn Met
 615
 ccccaagtaa gccccctaca tttctcttaa gtgtgtgat ctcctatcctg ttgacagtgt 1989
 aatatcttta aagtgatgta taggcagatg actccaggtc attttggggg atctgcttca 2049
 cttattctga gcigtgtacgt tgtgtgtgga tgtgtgtaaa tgttatgatt cccagattga 2109
 aaaaaaatgt tcittattca agaaagatat ctatgatagt gttggctaata gttatctaatg 2169
 gtcatggaat tgatgatgct cacataatgat aaagagtatc ctataattat ctiggaagtt 2229
 ttttaacattt attgaattat tttgttactg tctgtagtgt ttgttgaggat tctggagcaa 2289
 aaccaataaa gcattataaa tatatagttt tacttataag gccitttcta ttgtgtgttt 2349
 tattgttgat taataaatgt tatttctgga tacctttgga cttttttattc tggaaccag 2409
 agacaactgg tatggatcaa gcagcatgga gccagaggag aaaattatta cc 2461

<210> 353

<211> 617

<212> PRT

<213> Mus musculus

<400> 353

Met Ala Gly Ala Lys Ala Tyr Arg Leu Gly Ala Val Leu Leu Leu Ile

1

5

10

15

His Leu Ile Phe Leu Ile Ser Gly Ala Glu Ala Ala Ser Phe Gln Arg
 20 25 30
 Asn Gln Leu Leu Gln Lys Glu Pro Asp Leu Arg Leu Glu Asn Val Gln
 35 40 45
 Lys Phe Pro Ser Pro Glu Met Ile Arg Ala Leu Glu Tyr Ile Glu Lys
 50 55 60
 Leu Arg Gln Gln Ala His Arg Glu Glu Ser Ser Pro Asp Tyr Asn Pro
 65 70 75 80
 Tyr Gln Gly Val Ser Val Pro Leu Gln Leu Lys Glu Asn Gly Glu Glu
 85 90 95
 Ser His Leu Ala Glu Ser Ser Arg Asp Ala Leu Ser Glu Asp Glu Trp
 100 105 110
 Met Arg Ile Ile Leu Glu Ala Leu Arg Gln Ala Glu Asn Glu Pro Pro
 115 120 125
 Ser Ala Pro Lys Glu Asn Lys Pro Tyr Ala Leu Asn Leu Glu Lys Asn
 130 135 140
 Phe Pro Val Asp Thr Pro Asp Asp Tyr Glu Thr Gln Gln Trp Pro Glu
 145 150 155 160
 Arg Lys Leu Lys His Met Arg Phe Pro Leu Met Tyr Glu Glu Asn Ser
 165 170 175
 Arg Glu Asn Pro Phe Lys Arg Thr Asn Glu Ile Val Glu Glu Gln Tyr
 180 185 190
 Thr Pro Gln Ser Leu Ala Thr Leu Glu Ser Val Phe Gln Glu Leu Gly
 195 200 205
 Lys Leu Thr Gly Pro Ser Asn Gln Lys Arg Glu Arg Val Asp Glu Glu
 210 215 220
 Gln Lys Leu Tyr Thr Asp Asp Glu Asp Asp Val Tyr Lys Thr Asn Asn
 225 230 235 240
 Ile Ala Tyr Glu Asp Val Val Gly Gly Glu Asp Trp Ser Pro Ile Glu

	245	250	255
Glu Lys Ile Glu Thr Gln Thr Gln Glu Glu Val Arg Asp Ser Lys Glu			
260	265	270	
Asn Thr Glu Lys Asn Glu Gln Ile Asn Glu Glu Met Lys Arg Ser Gly			
275	280	285	
Gln Leu Gly Leu Pro Asp Glu Glu Asn Arg Arg Glu Ser Lys Asp Gln			
290	295	300	
Leu Ser Glu Asp Ala Ser Lys Val Ile Thr Tyr Leu Arg Arg Leu Val			
305	310	315	320
Asn Ala Val Gly Ser Gly Arg Ser Gln Ser Gly Pro Asn Gly Asp Arg			
325	330	335	
Ala Ala Arg Leu Leu Gln Lys Pro Leu Asp Ser Gln Ser Ile Tyr Gln			
340	345	350	
Leu Ile Glu Ile Ser Arg Asn Leu Gln Ile Pro Pro Glu Asp Leu Ile			
355	360	365	
Glu Met Leu Lys Ala Gly Glu Lys Pro Asn Gly Leu Val Glu Pro Glu			
370	375	380	
Gln Asp Leu Glu Leu Ala Val Asp Leu Asp Asp Ile Pro Glu Ala Asp			
385	390	395	400
Leu Asp Arg Pro Asp Met Phe Gln Ser Lys Met Leu Ser Lys Gly Gly			
405	410	415	
Tyr Pro Lys Ala Pro Gly Arg Gly Met Val Glu Ala Leu Pro Asp Gly			
420	425	430	
Leu Ser Val Glu Asp Ile Leu Asn Val Leu Gly Met Glu Asn Val Val			
435	440	445	
Asn Gln Lys Ser Pro Tyr Phe Pro Asn Gln Tyr Ser Gln Asp Lys Ala			
450	455	460	
Leu Met Arg Leu Pro Tyr Gly Pro Gly Lys Ser Arg Ala Asn Gln Ile			
465	470	475	480

Pro Lys Val Ala Trp Ile Pro Asp Val Glu Ser Arg Gln Ala Pro Tyr
 485 490 495
 Glu Asn Leu Asn Asp Gln Glu Leu Gly Glu Tyr Leu Ala Arg Met Leu
 500 505 510
 Val Lys Tyr Pro Glu Leu Leu Asn Thr Asn Gln Leu Lys Arg Val Pro
 515 520 525
 Ser Pro Val Ser Ser Glu Asp Asp Leu Gln Glu Glu Glu Gln Leu Glu
 530 535 540
 Gln Ala Ile Lys Glu His Leu Gly Pro Gly Ser Ser Gln Glu Met Glu
 545 550 555 560
 Arg Leu Ala Lys Val Ser Lys Arg Ile Pro Val Gly Ser Leu Lys Asn
 565 570 575
 Glu Asp Thr Pro Asn Arg Gln Tyr Leu Asp Glu Asp Met Leu Leu Lys
 580 585 590
 Val Leu Glu Tyr Leu Asn Gln Glu Gln Ala Glu Gln Gly Arg Glu His
 595 600 605
 Leu Ala Lys Arg Ala Met Glu Asn Met
 610 615

<210> 354

<211> 1968

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (121).. (969)

<400> 354

gtggagcgcg ggcccgcggt ggcggcggtg acggtggcgg tggcgggtggc ggcggcgga 60
 gctggcgacc gggcgcggtta gacggggccg gggctccgcgg cgcgctctcc gccacagag 120
 atg agc cgc cag act gct aca gca tta ccc act ggc acc tca aag tgt 168
 Met Ser Arg Gln Thr Ala Thr Ala Leu Pro Thr Gly Thr Ser Lys Cys
 1 5 10 15
 cca cca tcc cag agg gta cct gcc ttg acc ggc aca act gca tcc aac 216
 Pro Pro Ser Gln Arg Val Pro Ala Leu Thr Gly Thr Thr Ala Ser Asn
 20 25 30
 aat gac ttg gcg agt ctt ttt gag tgt cct gtc tgc ttt gac tat gtg 264
 Asn Asp Leu Ala Ser Leu Phe Glu Cys Pro Val Cys Phe Asp Tyr Val
 35 40 45
 ttg cca cct att ctt cag tgt cag agt ggc cat ctt gtt tgt agc aac 312
 Leu Pro Pro Ile Leu Gln Cys Gln Ser Gly His Leu Val Cys Ser Asn
 50 55 60
 tgt cgc ccc aaa ctt aca tgt tgt ccc act tgc cgg ggc cca ttg gga 360
 Cys Arg Pro Lys Leu Thr Cys Cys Pro Thr Cys Arg Gly Pro Leu Gly
 65 70 75 80
 tcc att cgc aac ttg gct atg gag aaa gtg gcc aac tca gta ctc ttc 408
 Ser Ile Arg Asn Leu Ala Met Glu Lys Val Ala Asn Ser Val Leu Phe
 85 90 95
 cct tgt aaa tat gcc tct tct gga tgt gaa ata act ctg cca cac acc 456
 Pro Cys Lys Tyr Ala Ser Ser Gly Cys Glu Ile Thr Leu Pro His Thr
 100 105 110
 gaa aag gca gag cac gag gag ctc tgt gag ttc agg cct tac tcc tgc 504
 Glu Lys Ala Glu His Glu Glu Leu Cys Glu Phe Arg Pro Tyr Ser Cys
 115 120 125
 ccc tgc cct ggt gct tcc tgt aag tgg caa ggc tcc ttg gat gcc gtc 552
 Pro Cys Pro Gly Ala Ser Cys Lys Trp Gln Gly Ser Leu Asp Ala Val
 130 135 140

atg ccc cac ctg atg cat cag cac aag tcc att acc acc ctg caa gga 600
 Met Pro His Leu Met His Gln His Lys Ser Ile Thr Thr Leu Gln Gly
 145 150 155 160
 gaa gat ata gtt ttc ctt gct aca gac att aac ctt cct ggt gct gtt 648
 Glu Asp Ile Val Phe Leu Ala Thr Asp Ile Asn Leu Pro Gly Ala Val
 165 170 175
 gac tgg gtg atg atg cag tct tgt ttt ggc ttt cat ttc atg tta gtc 696
 Asp Trp Val Met Met Gln Ser Cys Phe Gly Phe His Phe Met Leu Val
 180 185 190
 ttg gag aaa caa gaa aaa tat gat ggt cat cag cag ttc ttt gca att 744
 Leu Glu Lys Gln Glu Lys Tyr Asp Gly His Gln Gln Phe Phe Ala Ile
 195 200 205
 gta caa ctg ata gga aca cgc aag caa gct gaa aat ttt gca tat cga 792
 Val Gln Leu Ile Gly Thr Arg Lys Gln Ala Glu Asn Phe Ala Tyr Arg
 210 215 220
 ctt gag cta aat ggt cat agg cgg cga ttg act tgg gaa gcg act cct 840
 Leu Glu Leu Asn Gly His Arg Arg Arg Leu Thr Trp Glu Ala Thr Pro
 225 230 235 240
 cgg tct att cat gag gga att gca aca gcc att atg aat agt gac tgc 888
 Arg Ser Ile His Glu Gly Ile Ala Thr Ala Ile Met Asn Ser Asp Cys
 245 250 255
 cta gtg ttt gac acc agc att gca cag ctt ttt gca gaa aat ggc aat 936
 Leu Val Phe Asp Thr Ser Ile Ala Gln Leu Phe Ala Glu Asn Gly Asn
 260 265 270
 tta ggc atc aat gta act att tcc atg tgt tga aacggcaatc aaatatttct 989
 Leu Gly Ile Asn Val Thr Ile Ser Met Cys
 275 280
 ggccagtgtt taaaatttgc atttgacttc acagagaata aggcacccat ctgcttgcca 1049
 acctaaaact ttcttggtag gtagaagcta gacatgaagg taaataaaaa gaaaagctgt 1109

taatacagga aacagttgca tgtagtaaca ctaatatatt taaaaataat tcaacagtaa 1169
 accactgaaa aaaatatata tacccaagat gggcatcttt tgtattaaga aaggaaacat 1229
 tgtaaaatat ttctgaactt tgtgtttgtt gtagattgat tgtattgttg acaatitttt 1289
 ggggtgtgt gtctgtgcac gcatgcgtgc acgtgtgtgg ttggttttct ttttaactgac 1349
 aagccatctg cgtggtcata gaccactgtt ttcccttgt gagtcaacac atagtgtctg 1409
 tgtgggtttg tttttgtttt tctgttttgt tttgtttttt tgatgtgtgt atttgctaata 1469
 ttttattcta gtttttcatt aaataaatit gactttcttt tctgtaattc aggtttttct 1529
 cacttttgta ccttttaagt tagtgtcttt ttgatattca taattgctta atgtcaaaaag 1589
 tttgtgttca gtacatactt tcttttcctt caatcaattt attagaaata tttttaattt 1649
 agcccttttg tgaaaatagg aattccagaa aggcaaggta gcagagcagc agtcaaggct 1709
 gaagtgagtg caggatgctc ttgtctctct cggtagctgt cccatggagc cacacgtcag 1769
 gtcaggctga ctcttagaaa gggtaggtta gggagtaaac tctgatitatt ataaatttaa 1829
 aaaaaaatca ggcttttcct ctcttcaaata gtctggggca aatcacatgt ttttaattggt 1889
 tcttgtattt attggttttg caaaagagtg cagcatcata cacagtattt gtaattaaag 1949
 taaatcattt gttttttta 1968

<210> 355

<211> 282

<212> PRT

<213> Mus musculus

<400> 355

Met	Ser	Arg	Gln	Thr	Ala	Thr	Ala	Leu	Pro	Thr	Gly	Thr	Ser	Lys	Cys
1				5					10					15	
Pro	Pro	Ser	Gln	Arg	Val	Pro	Ala	Leu	Thr	Gly	Thr	Thr	Ala	Ser	Asn
			20						25					30	
Asn	Asp	Leu	Ala	Ser	Leu	Phe	Glu	Cys	Pro	Val	Cys	Phe	Asp	Tyr	Val
			35						40					45	
Leu	Pro	Pro	Ile	Leu	Gln	Cys	Gln	Ser	Gly	His	Leu	Val	Cys	Ser	Asn

50	55	60
Cys Arg Pro Lys Leu Thr	Cys Cys Pro Thr	Cys Arg Gly Pro Leu Gly
65	70	75
Ser Ile Arg Asn Leu Ala Met Glu Lys Val	Ala Asn Ser Val	Leu Phe
85	90	95
Pro Cys Lys Tyr Ala Ser Ser Gly Cys Glu Ile Thr	Leu Pro His Thr	
100	105	110
Glu Lys Ala Glu His Glu Glu Leu Cys Glu Phe Arg	Pro Tyr Ser Cys	
115	120	125
Pro Cys Pro Gly Ala Ser Cys Lys Trp Gln Gly Ser	Leu Asp Ala Val	
130	135	140
Met Pro His Leu Met His Gln His Lys Ser Ile Thr Thr	Leu Gln Gly	
145	150	155
Glu Asp Ile Val Phe Leu Ala Thr Asp Ile Asn Leu Pro Gly	Ala Val	
165	170	175
Asp Trp Val Met Met Gln Ser Cys Phe Gly Phe His Phe Met	Leu Val	
180	185	190
Leu Glu Lys Gln Glu Lys Tyr Asp Gly His Gln Gln Phe Phe	Ala Ile	
195	200	205
Val Gln Leu Ile Gly Thr Arg Lys Gln Ala Glu Asn Phe Ala Tyr	Arg	
210	215	220
Leu Glu Leu Asn Gly His Arg Arg Arg Leu Thr Trp Glu Ala Thr	Pro	
225	230	235
Arg Ser Ile His Glu Gly Ile Ala Thr Ala Ile Met Asn Ser Asp	Cys	
245	250	255
Leu Val Phe Asp Thr Ser Ile Ala Gln Leu Phe Ala Glu Asn Gly	Asn	
260	265	270
Leu Gly Ile Asn Val Thr Ile Ser Met Cys		
275	280	

<210> 356

<211> 2198

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (290).. (1267)

<400> 356

.tgccgctcct gaagcgagtg ggccagggct ctgcgcacca gaacgccgcc ggaggagggc 60
 accgcacggc cgcgagcccc gagagcgacg accactccgg gtgccgccga gaggatcggc 120
 gcggtccggc ccccgccctc ccggtgccgg tcgggtccgc gctgggtccc ccgggctggg 180
 cgccgtggcg ttgccccgga gcccgccacc cgcggggcgc gcaccgcctt aacccgggcg 240
 gccccgcggc aggcagacgc ccgcaggtcc atggtgggct cggagcgcg atg agc cgc 298

Met Ser Arg

1

ccg tcc tcc acc ggc ccc agc gct aac aaa ccc tgc agc aag cag ccg 346
 Pro Ser Ser Thr Gly Pro Ser Ala Asn Lys Pro Cys Ser Lys Gln Pro

5

10

15

ccg ccg cct cag acc ccg cac gcc ccg tcc ccg gct gcg ccc ccg gcc 394
 Pro Pro Pro Gln Thr Pro His Ala Pro Ser Pro Ala Ala Pro Pro Ala

20

25

30

35

gcc gcc acc atc tcg gca gcg ggc ccc ggc tcg tcc gcg gtg ccc gcc 442
 Ala Ala Thr Ile Ser Ala Ala Gly Pro Gly Ser Ser Ala Val Pro Ala

40

45

50

gcg gca gcg gtg atc tca ggc ccc gga gcc ggc ggc ggg gcc gac ccg 490
 Ala Ala Ala Val Ile Ser Gly Pro Gly Ala Gly Gly Gly Ala Asp Pro

55	60	65	
gtg tcc ccg cag cac cac gag ctg acc tcg ctc ttc gag tgc ccg gtc	538		
Val Ser Pro Gln His His Glu Leu Thr Ser Leu Phe Glu Cys Pro Val			
70	75	80	
tgc ttt gac tat gtc ctg ccc ccc att ctg cag tgc cag gcc ggg cac	586		
Cys Phe Asp Tyr Val Leu Pro Pro Ile Leu Gln Cys Gln Ala Gly His			
85	90	95	
ctg gtg tgt aac caa tgc cgc cag aag tta agc tgc tgc ccg acg tgc	634		
Leu Val Cys Asn Gln Cys Arg Gln Lys Leu Ser Cys Cys Pro Thr Cys			
100	105	110	115
agg ggc gcc cta acg ccc agc atc agg aac ctg gct atg gag aag gtc	682		
Arg Gly Ala Leu Thr Pro Ser Ile Arg Asn Leu Ala Met Glu Lys Val			
120	125	130	
gcc tcg gca gtt ctg ttt ccc tgt aag tat gct acc acg ggc tgt tcc	730		
Ala Ser Ala Val Leu Phe Pro Cys Lys Tyr Ala Thr Thr Gly Cys Ser			
135	140	145	
ctg act cta cac cat aca gag aaa cca gag cat gaa gac atc tgt gaa	778		
Leu Thr Leu His His Thr Glu Lys Pro Glu His Glu Asp Ile Cys Glu			
150	155	160	
tac cgt cct tat tcc tgt cct tgt cct ggt gca tcc tgc aag tgg cag	826		
Tyr Arg Pro Tyr Ser Cys Pro Cys Pro Gly Ala Ser Cys Lys Trp Gln			
165	170	175	
gga tcc ctg gaa gct gtg atg tcc cat ctc atg cat gcc cac aag agt	874		
Gly Ser Leu Glu Ala Val Met Ser His Leu Met His Ala His Lys Ser			
180	185	190	195
atc act acc ctt cag gga gag gag aca gtc ttt cta gct aca gac att	922		
Ile Thr Thr Leu Gln Gly Glu Glu Thr Val Phe Leu Ala Thr Asp Ile			
200	205	210	
aac ctg cca ggg gct gtg gac tgg gtg atg atg cag tcc tgt ttt ggc	970		

Asn Leu Pro Gly Ala Val Asp Trp Val Met Met Gln Ser Cys Phe Gly
 215 220 225
 cac cac ttc atg ctg gta ctt gaa aag caa gag aag tac gaa ggc cac 1018
 His His Phe Met Leu Val Leu Glu Lys Gln Glu Lys Tyr Glu Gly His
 230 235 240
 cag cag ttc ttt gcc atc gtc ctc ctc att ggc acc cga aag caa gct 1066
 Gln Gln Phe Phe Ala Ile Val Leu Leu Ile Gly Thr Arg Lys Gln Ala
 245 250 255
 gag aac ttt gcc tac aga ctg gag ttg aat ggg aac cgg agg aga ctg 1114
 Glu Asn Phe Ala Tyr Arg Leu Glu Leu Asn Gly Asn Arg Arg Arg Leu
 260 265 270 275
 acc tgg gag gcc aca cct cgg tcc att cat gat ggc gtg gct gca gcc 1162
 Thr Trp Glu Ala Thr Pro Arg Ser Ile His Asp Gly Val Ala Ala Ala
 280 285 290
 atc atg aac agt gac tgt ctt gtt ttt gac aca gcc ata gca cat ctc 1210
 Ile Met Asn Ser Asp Cys Leu Val Phe Asp Thr Ala Ile Ala His Leu
 295 300 305
 ttt gca gat aat ggg aac ctt gga atc aat gtc acg ata tct aca tgc 1258
 Phe Ala Asp Asn Gly Asn Leu Gly Ile Asn Val Thr Ile Ser Thr Cys
 310 315 320
 tgt cag tga ggctccagga ggctttccta accctgggaa gttatttggg 1307
 Cys Gln
 325
 catagcgctc tatgtttaat aaagggtttt taatagatgt tttattcagt acatcttccc 1367
 gaggcgagac ccacaactgt cctatgtttt atttaaacga tagcttcctg tctggcactg 1427
 atgaatctaa gttcaccgaa ctgtgataat cggagttggc ctgttagtaa tttggaggtg 1487
 gttcgggtgat ctcaaataaa ctctattcta tttccttccct gaacagctct tgacagatcg 1547
 ctcagggtcg cctccctctg cctcaccctg agccaacaaa agcacagtga ctttcttgag 1607
 agtcccgtaa tttctaggag gtagcagttg ctttaataacc tttcaggctg ggtatttaca 1667

cagaatcacc tgtagtactc atctccaaca cagagctaga gaatcaacag agttgagcaa 1727
 cctcctcatc tcagagtttg aggattactg gcttgaattg tgggcaaggg tccaggatct 1787
 aaaggtgctt taaggcgctc tctgctgaca ctgttggtct ctactgtccg tcctcagcct 1847
 ctgcacacac cacatggaga ccagaactct aaatccatgg ggatgcaacc cctggggttg 1907
 gcctgccttc aggcgctcag tgagttgaga gtcttcacag ttagttgttg ctaccatag 1967
 tacggatgac ttgtttacat atggcttccc ttggaagccc tccttgactg taactgatgt 2027
 gagagactag atcagtgtt gggagaactt gataaccagt gtcacatgct tgccatttta 2087
 aaagcatgtg tcagtttgtt gggtttagtt ttgtttgttt ttgtttttat cttacatac 2147
 gcgcacacac atacacatac actttaattt ttttaataaaa ttttttcaat a 2198

<210> 357

<211> 325

<212> PRT

<213> Mus musculus

<400> 357

Met	Ser	Arg	Pro	Ser	Ser	Thr	Gly	Pro	Ser	Ala	Asn	Lys	Pro	Cys	Ser
1				5				10					15		
Lys	Gln	Pro	Pro	Pro	Pro	Gln	Thr	Pro	His	Ala	Pro	Ser	Pro	Ala	Ala
				20				25					30		
Pro	Pro	Ala	Ala	Ala	Thr	Ile	Ser	Ala	Ala	Gly	Pro	Gly	Ser	Ser	Ala
				35				40					45		
Val	Pro	Ala	Ala	Ala	Ala	Val	Ile	Ser	Gly	Pro	Gly	Ala	Gly	Gly	Gly
				50				55					60		
Ala	Asp	Pro	Val	Ser	Pro	Gln	His	His	Glu	Leu	Thr	Ser	Leu	Phe	Glu
				65				70					75		80
Cys	Pro	Val	Cys	Phe	Asp	Tyr	Val	Leu	Pro	Pro	Ile	Leu	Gln	Cys	Gln
				85				90					95		
Ala	Gly	His	Leu	Val	Cys	Asn	Gln	Cys	Arg	Gln	Lys	Leu	Ser	Cys	Cys

100	105	110
Pro Thr Cys Arg Gly Ala Leu Thr	Pro Ser Ile Arg Asn Leu Ala Met	
115	120	125
Glu Lys Val Ala Ser Ala Val Leu Phe	Pro Cys Lys Tyr Ala Thr Thr	
130	135	140
Gly Cys Ser Leu Thr Leu His His Thr	Glu Lys Pro Glu His Glu Asp	
145	150	155
Ile Cys Glu Tyr Arg Pro Tyr Ser Cys	Pro Cys Pro Gly Ala Ser Cys	
165	170	175
Lys Trp Gln Gly Ser Leu Glu Ala Val	Met Ser His Leu Met His Ala	
180	185	190
His Lys Ser Ile Thr Thr Leu Gln Gly	Glu Glu Thr Val Phe Leu Ala	
195	200	205
Thr Asp Ile Asn Leu Pro Gly Ala Val	Asp Trp Val Met Met Gln Ser	
210	215	220
Cys Phe Gly His His Phe Met Leu Val	Leu Glu Lys Gln Glu Lys Tyr	
225	230	235
Glu Gly His Gln Gln Phe Phe Ala Ile	Val Leu Leu Ile Gly Thr Arg	
245	250	255
Lys Gln Ala Glu Asn Phe Ala Tyr Arg	Leu Glu Leu Asn Gly Asn Arg	
260	265	270
Arg Arg Leu Thr Trp Glu Ala Thr Pro	Arg Ser Ile His Asp Gly Val	
275	280	285
Ala Ala Ala Ile Met Asn Ser Asp Cys	Leu Val Phe Asp Thr Ala Ile	
290	295	300
Ala His Leu Phe Ala Asp Asn Gly Asn	Leu Gly Ile Asn Val Thr Ile	
305	310	315
Ser Thr Cys Cys Gln		320
325		

<210> 358

<211> 1644

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (99).. (1277)

<400> 358

gcagttcitta tgaagcctct ttcttcagcg tacatgatac gtcctccctt gctcgcccca 60
 gaggtgaccc ttaccctggt cagctgatcc caaccact atg gca gct gct gct gca 116

Met Ala Ala Ala Ala Ala

1

5

gca aca cca ggc tta ggc cca ctc cag ctg cag gat gaa gtg gcc cag 164
 Ala Thr Pro Gly Leu Gly Pro Leu Gln Leu Gln Asp Glu Val Ala Gln

10

15

20

cca ctg aac cta tca gct aag ccc aag acc tct gat ggc aaa tca cct 212
 Pro Leu Asn Leu Ser Ala Lys Pro Lys Thr Ser Asp Gly Lys Ser Pro

25

30

35

gca tca ccc acc tct cct cac atg cca gct ctg aga ata aac agt ggg 260
 Ala Ser Pro Thr Ser Pro His Met Pro Ala Leu Arg Ile Asn Ser Gly

40

45

50

gct ggc ccc ctc aaa gcc tct gtc ccg gca gca tta gct agt cct tct 308
 Ala Gly Pro Leu Lys Ala Ser Val Pro Ala Ala Leu Ala Ser Pro Ser

55

60

65

70

gca aga gtt agc aca ata ggc tat tta aat gac cac gat gct gtc acc 356
 Ala Arg Val Ser Thr Ile Gly Tyr Leu Asn Asp His Asp Ala Val Thr

75	80	85	
aag gca atc caa gaa gct cgc cag atg aaa gag caa ctc agg cga gag			404
Lys Ala Ile Gln Glu Ala Arg Gln Met Lys Glu Gln Leu Arg Arg Glu			
90	95	100	
cag caa gcg ttg gac ggg aag gtg gcc gtg gtg aac agc ata ggt ctc			452
Gln Gln Ala Leu Asp Gly Lys Val Ala Val Val Asn Ser Ile Gly Leu			
105	110	115	
agc aac tgc cgg aca gaa aag gaa aaa aca aca ctg gag agc ctg act			500
Ser Asn Cys Arg Thr Glu Lys Glu Lys Thr Thr Leu Glu Ser Leu Thr			
120	125	130	
cag cag ttg gca gtt aaa cag aat gaa gaa ggg aaa ttt agc cat gga			548
Gln Gln Leu Ala Val Lys Gln Asn Glu Glu Gly Lys Phe Ser His Gly			
135	140	145	150
atg atg gat ttc aat atg agt gga gat tct gac gga agc gct gga gtc			596
Met Met Asp Phe Asn Met Ser Gly Asp Ser Asp Gly Ser Ala Gly Val			
155	160	165	
tca gag tca aga att tac agg gaa tcc agg gga cgt ggt agc aac gag			644
Ser Glu Ser Arg Ile Tyr Arg Glu Ser Arg Gly Arg Gly Ser Asn Glu			
170	175	180	
ccc cac ata aag cgt cca atg aat gcc ttc atg gtg tgg gcg aaa gat			692
Pro His Ile Lys Arg Pro Met Asn Ala Phe Met Val Trp Ala Lys Asp			
185	190	195	
gaa cgg agg aaa atc ctt cag gcc ttt ccc gac atg cac aat tcc aac			740
Glu Arg Arg Lys Ile Leu Gln Ala Phe Pro Asp Met His Asn Ser Asn			
200	205	210	
atc agc aag ata ctg gga tct cgc tgg aaa gct atg acc aac cta gag			788
Ile Ser Lys Ile Leu Gly Ser Arg Trp Lys Ala Met Thr Asn Leu Glu			
215	220	225	230
aaa cag cca tac tat gag gag cag gcc cgc ctc agc aaa cag cac ctg			836

Lys Gln Pro Tyr Tyr Glu Glu Gln Ala Arg Leu Ser Lys Gln His Leu
 235 240 245
 gag aag tac ccg gac tat aag tac aag cct agg ccg aag cgc acc tgt 884
 Glu Lys Tyr Pro Asp Tyr Lys Tyr Lys Pro Arg Pro Lys Arg Thr Cys
 250 255 260
 ctg gtg gac ggc aag aaa ctg cgt atc ggg gag tac aag gcc atc atg 932
 Leu Val Asp Gly Lys Lys Leu Arg Ile Gly Glu Tyr Lys Ala Ile Met
 265 270 275
 cgg aac cgg agg cag gaa atg cga cag tac ttc aat gtt ggg caa caa 980
 Arg Asn Arg Arg Gln Glu Met Arg Gln Tyr Phe Asn Val Gly Gln Gln
 280 285 290
 gca cag atc ccc atc gcg acg gcc gga gtt gta tac ccc ggc gcc atc 1028
 Ala Gln Ile Pro Ile Ala Thr Ala Gly Val Val Tyr Pro Gly Ala Ile
 295 300 305 310
 gcc atg gca gga atg ccg tcc cct cac ctg ccc tcc gag cac tcg agc 1076
 Ala Met Ala Gly Met Pro Ser Pro His Leu Pro Ser Glu His Ser Ser
 315 320 325
 gtg tcc agc agc ccg gag ccc ggg atg ccc gtg atc cag agc act tac 1124
 Val Ser Ser Ser Pro Glu Pro Gly Met Pro Val Ile Gln Ser Thr Tyr
 330 335 340
 ggc gcc aag gga gag gag ccc cac atc aag gaa gag atc cag gct gag 1172
 Gly Ala Lys Gly Glu Glu Pro His Ile Lys Glu Glu Ile Gln Ala Glu
 345 350 355
 gac atc aac gga gag att tac gag gag tac gat gag gag gag gag gac 1220
 Asp Ile Asn Gly Glu Ile Tyr Glu Glu Tyr Asp Glu Glu Glu Glu Asp
 360 365 370
 ccg gat gtg gat tat ggg agt gac agc gaa aac cac att gcg gga caa 1268
 Pro Asp Val Asp Tyr Gly Ser Asp Ser Glu Asn His Ile Ala Gly Gln
 375 380 385 390

gcc aac tga taagggccaa cagactgtgg tgagccgagg acttgaagaa 1317

Ala Asn

gccctgtccg gttcattcctt cccagtggcc aagcacatta actctctcat acactgactg 1377

ttatitttaac tgttagtctt atatagtgg gacatcagct gacaaataga cctcagcctc 1437

aaaaggctcg gaaagaaaag aaagaaagaa agaaagaaag aaaaaaaaaat tacaagcaaa 1497

aacgtcatca agaagaagag atcgaaataa gctatgggtt aaacagtgcc agtaactcag 1557

ctgctacacc ccagcactga agcttcaccc gtcaactttt tttttttttt taataaactt 1617

tatggctggtt tgttctaaaa aaaaaaa 1644

<210> 359

<211> 392

<212> PRT

<213> Mus musculus

<400> 359

Met Ala Ala Ala Ala Ala Thr Pro Gly Leu Gly Pro Leu Gln Leu

1 5 10 15

Gln Asp Glu Val Ala Gln Pro Leu Asn Leu Ser Ala Lys Pro Lys Thr

20 25 30

Ser Asp Gly Lys Ser Pro Ala Ser Pro Thr Ser Pro His Met Pro Ala

35 40 45

Leu Arg Ile Asn Ser Gly Ala Gly Pro Leu Lys Ala Ser Val Pro Ala

50 55 60

Ala Leu Ala Ser Pro Ser Ala Arg Val Ser Thr Ile Gly Tyr Leu Asn

65 70 75 80

Asp His Asp Ala Val Thr Lys Ala Ile Gln Glu Ala Arg Gln Met Lys

85 90 95

Glu Gln Leu Arg Arg Glu Gln Gln Ala Leu Asp Gly Lys Val Ala Val

100 105 110

Val Asn Ser Ile Gly Leu Ser Asn Cys Arg Thr Glu Lys Glu Lys Thr
 115 120 125
 Thr Leu Glu Ser Leu Thr Gln Gln Leu Ala Val Lys Gln Asn Glu Glu
 130 135 140
 Gly Lys Phe Ser His Gly Met Met Asp Phe Asn Met Ser Gly Asp Ser
 145 150 155 160
 Asp Gly Ser Ala Gly Val Ser Glu Ser Arg Ile Tyr Arg Glu Ser Arg
 165 170 175
 Gly Arg Gly Ser Asn Glu Pro His Ile Lys Arg Pro Met Asn Ala Phe
 180 185 190
 Met Val Trp Ala Lys Asp Glu Arg Arg Lys Ile Leu Gln Ala Phe Pro
 195 200 205
 Asp Met His Asn Ser Asn Ile Ser Lys Ile Leu Gly Ser Arg Trp Lys
 210 215 220
 Ala Met Thr Asn Leu Glu Lys Gln Pro Tyr Tyr Glu Glu Gln Ala Arg
 225 230 235 240
 Leu Ser Lys Gln His Leu Glu Lys Tyr Pro Asp Tyr Lys Tyr Lys Pro
 245 250 255
 Arg Pro Lys Arg Thr Cys Leu Val Asp Gly Lys Lys Leu Arg Ile Gly
 260 265 270
 Glu Tyr Lys Ala Ile Met Arg Asn Arg Arg Gln Glu Met Arg Gln Tyr
 275 280 285
 Phe Asn Val Gly Gln Gln Ala Gln Ile Pro Ile Ala Thr Ala Gly Val
 290 295 300
 Val Tyr Pro Gly Ala Ile Ala Met Ala Gly Met Pro Ser Pro His Leu
 305 310 315 320
 Pro Ser Glu His Ser Ser Val Ser Ser Ser Pro Glu Pro Gly Met Pro
 325 330 335
 Val Ile Gln Ser Thr Tyr Gly Ala Lys Gly Glu Glu Pro His Ile Lys

340 345 350
 Glu Glu Ile Gln Ala Glu Asp Ile Asn Gly Glu Ile Tyr Glu Glu Tyr
 355 360 365
 Asp Glu Glu Glu Glu Asp Pro Asp Val Asp Tyr Gly Ser Asp Ser Glu
 370 375 380
 Asn His Ile Ala Gly Gln Ala Asn
 385 390

<210> 360

<211> 2117

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (239).. (1753)

<400> 360

tcggtcggag tcgtcggigt tccagctggt gggagttggc ttcactgtgt tgggcgctgg 60
 gccctagttt ctggagctgg gaagttaggc ggcgggctcc gtccctgtcc ttcagcttcc 120
 agcgttcctg ggtttccttc ggcggcgctg ggcctcgcta aggactcgcc ggccctgtgg 180
 ggcacggctt tagtggcgct tttgcgagtt cacataaata catcttaaaa ctttcaag 238
 atg gtt cta gca gat ctt gga aga aaa ata aca tca gca tta cgc tca 286
 Met Val Leu Ala Asp Leu Gly Arg Lys Ile Thr Ser Ala Leu Arg Ser
 1 5 10 15
 ttg agc aat gcc acc att atc aat gaa gag gta tta aat gct atg ctg 334
 Leu Ser Asn Ala Thr Ile Ile Asn Glu Glu Val Leu Asn Ala Met Leu
 20 25 30
 aaa gaa gta tgt aca gca tta ttg gaa gca gat gtt aat att aaa cta 382

Lys Glu Val Cys Thr Ala Leu Leu Glu Ala Asp Val Asn Ile Lys Leu
 35 40 45
 gtg aag caa ctc aga gaa aat gtt aag tct gca att gat ctt gaa gag 430
 Val Lys Gln Leu Arg Glu Asn Val Lys Ser Ala Ile Asp Leu Glu Glu
 50 55 60
 atg gca tct gga ctg aac aaa aga aaa atg att cag cat gct gta ttt 478
 Met Ala Ser Gly Leu Asn Lys Arg Lys Met Ile Gln His Ala Val Phe
 65 70 75 80
 aaa gaa ctt gta aag ctt gta gac cct gga gtt aaa gcg tgg aca ccg 526
 Lys Glu Leu Val Lys Leu Val Asp Pro Gly Val Lys Ala Trp Thr Pro
 85 90 95
 act aag gga aag caa aat gtg atc atg ttt gtt gga ttg caa ggg agt 574
 Thr Lys Gly Lys Gln Asn Val Ile Met Phe Val Gly Leu Gln Gly Ser
 100 105 110
 ggt aaa acg aca aca tgt tca aag tta gca tat tat tac cag agg aaa 622
 Gly Lys Thr Thr Thr Cys Ser Lys Leu Ala Tyr Tyr Tyr Gln Arg Lys
 115 120 125
 ggt tgg aag acc tgt ttg ata tgt gca gat aca ttc aga gca gga gcc 670
 Gly Trp Lys Thr Cys Leu Ile Cys Ala Asp Thr Phe Arg Ala Gly Ala
 130 135 140
 ttt gac cag cta aaa cag aat gcc acc aaa gca aga att ccg ttc tat 718
 Phe Asp Gln Leu Lys Gln Asn Ala Thr Lys Ala Arg Ile Pro Phe Tyr
 145 150 155 160
 ggc agc tat act gaa atg gat cct gtc atc att gct tct gaa gga gtg 766
 Gly Ser Tyr Thr Glu Met Asp Pro Val Ile Ile Ala Ser Glu Gly Val
 165 170 175
 gag aaa ttc aaa aat gaa aat ttt gaa att att att gtt gat aca agt 814
 Glu Lys Phe Lys Asn Glu Asn Phe Glu Ile Ile Ile Val Asp Thr Ser
 180 185 190

ggt cgt cac aaa caa gaa gac tct tta ttt gaa gaa agg ctt caa gtt 862
 Gly Arg His Lys Gln Glu Asp Ser Leu Phe Glu Glu Arg Leu Gln Val
 195 200 205
 tct aat gct ata caa cct gat aac att gtt tat gtg atg gat gca tcc 910
 Ser Asn Ala Ile Gln Pro Asp Asn Ile Val Tyr Val Met Asp Ala Ser
 210 215 220
 atc gga cag gct tgt gag gcc cag gcg aag gct ttt aaa gac aaa gta 958
 Ile Gly Gln Ala Cys Glu Ala Gln Ala Lys Ala Phe Lys Asp Lys Val
 225 230 235 240
 gat gta gct tca gta ata gtg aca aaa ctc gac ggt cat gcg aaa gga 1006
 Asp Val Ala Ser Val Ile Val Thr Lys Leu Asp Gly His Ala Lys Gly
 245 250 255
 ggc ggt gct ctt agt gca gtt gct gcc aca aaa agt cca att atc ttc 1054
 Gly Gly Ala Leu Ser Ala Val Ala Ala Thr Lys Ser Pro Ile Ile Phe
 260 265 270
 att ggt aca ggg gaa cat ata gat gat ttt gaa cct ttc aaa aca caa 1102
 Ile Gly Thr Gly Glu His Ile Asp Asp Phe Glu Pro Phe Lys Thr Gln
 275 280 285
 cct ttc atc agc aaa ctc ctt gga atg ggt gat att gaa gga ctg att 1150
 Pro Phe Ile Ser Lys Leu Leu Gly Met Gly Asp Ile Glu Gly Leu Ile
 290 295 300
 gat aaa gtc aat gaa ttg aag ttg gat gat aat gag gca ctt ata gag 1198
 Asp Lys Val Asn Glu Leu Lys Leu Asp Asp Asn Glu Ala Leu Ile Glu
 305 310 315 320
 aag ttg aag cac ggt cag ttt aca ttg cga gac atg tat gaa cag ttt 1246
 Lys Leu Lys His Gly Gln Phe Thr Leu Arg Asp Met Tyr Glu Gln Phe
 325 330 335
 cag aat att atg aaa atg ggc cca ttc agt cag ata ttg ggg atg att 1294
 Gln Asn Ile Met Lys Met Gly Pro Phe Ser Gln Ile Leu Gly Met Ile

340	345	350	
cct ggc ttt ggc aca gat ttt atg agc aaa ggg aat gag cag gag tca	1342		
Pro Gly Phe Gly Thr Asp Phe Met Ser Lys Gly Asn Glu Gln Glu Ser			
355	360	365	
atg gca agg ctg aag aaa ctg atg aca atc atg gac agt atg aac gat	1390		
Met Ala Arg Leu Lys Lys Leu Met Thr Ile Met Asp Ser Met Asn Asp			
370	375	380	
caa gaa ctg gac agt aca gat ggt gcc aag gtt ttc agt aag caa cca	1438		
Gln Glu Leu Asp Ser Thr Asp Gly Ala Lys Val Phe Ser Lys Gln Pro			
385	390	395	400
ggg aga atc caa aga gtt gcc cgg gga tca ggt gtg tca aca aga gat	1486		
Gly Arg Ile Gln Arg Val Ala Arg Gly Ser Gly Val Ser Thr Arg Asp			
405	410	415	
gtt caa gaa ctt ctg acc cag tat acc aag ttt gca cag atg gtc aaa	1534		
Val Gln Glu Leu Leu Thr Gln Tyr Thr Lys Phe Ala Gln Met Val Lys			
420	425	430	
aag atg gga ggt atc aaa gga ctt ttc aaa ggc ggt gat atg tct aag	1582		
Lys Met Gly Gly Ile Lys Gly Leu Phe Lys Gly Gly Asp Met Ser Lys			
435	440	445	
aat gtg agt cag tca cag atg gca aaa tta aac caa caa atg gcc aaa	1630		
Asn Val Ser Gln Ser Gln Met Ala Lys Leu Asn Gln Gln Met Ala Lys			
450	455	460	
atg atg gac cca cga gtt ctt cat cac atg ggt ggc atg gcc ggc ctt	1678		
Met Met Asp Pro Arg Val Leu His His Met Gly Gly Met Ala Gly Leu			
465	470	475	480
cag tca atg atg cgg cag ttt cag cag ggt gct gct ggc aac atg aaa	1726		
Gln Ser Met Met Arg Gln Phe Gln Gln Gly Ala Ala Gly Asn Met Lys			
485	490	495	
ggc atg atg gga ttc aat aac atg taa agacgcccc ttactaggaa	1773		

Gly Met Met Gly Phe Asn Asn Met

500

505

ctgacaaggt ggatgatgtc atctgctgag acctcacact ttctctccct cttgcaaacg 1833
 gggaagaagg atattcttgc ctgtcttgcc ttcgttcttt tgtctcaccg ttttccttgt 1893
 ctcccttccc ttctgaagtt cgggaagagt gcctggtttt tgtggaagtc atcatttctg 1953
 ctttaaactct attagttttc aacgtcctaa cacttcttaa gttaaacaaa tcatgatgta 2013
 aaattttggg atttaaaggt ttttaattgt ctcaaaggcc aagcattaca tttataaaca 2073
 gttgcgatca gtaaattaca tgatattgaa gaaagtgtcg cccg 2117

<210> 361

<211> 504

<212> PRT

<213> Mus musculus

<400> 361

Met Val Leu Ala Asp Leu Gly Arg Lys Ile Thr Ser Ala Leu Arg Ser
 1 5 10 15
 Leu Ser Asn Ala Thr Ile Ile Asn Glu Glu Val Leu Asn Ala Met Leu
 20 25 30
 Lys Glu Val Cys Thr Ala Leu Leu Glu Ala Asp Val Asn Ile Lys Leu
 35 40 45
 Val Lys Gln Leu Arg Glu Asn Val Lys Ser Ala Ile Asp Leu Glu Glu
 50 55 60
 Met Ala Ser Gly Leu Asn Lys Arg Lys Met Ile Gln His Ala Val Phe
 65 70 75 80
 Lys Glu Leu Val Lys Leu Val Asp Pro Gly Val Lys Ala Trp Thr Pro
 85 90 95
 Thr Lys Gly Lys Gln Asn Val Ile Met Phe Val Gly Leu Gln Gly Ser
 100 105 110

Gly Lys Thr Thr Thr Cys Ser Lys Leu Ala Tyr Tyr Tyr Gln Arg Lys
 115 120 125
 Gly Trp Lys Thr Cys Leu Ile Cys Ala Asp Thr Phe Arg Ala Gly Ala
 130 135 140
 Phe Asp Gln Leu Lys Gln Asn Ala Thr Lys Ala Arg Ile Pro Phe Tyr
 145 150 155 160
 Gly Ser Tyr Thr Glu Met Asp Pro Val Ile Ile Ala Ser Glu Gly Val
 165 170 175
 Glu Lys Phe Lys Asn Glu Asn Phe Glu Ile Ile Ile Val Asp Thr Ser
 180 185 190
 Gly Arg His Lys Gln Glu Asp Ser Leu Phe Glu Glu Arg Leu Gln Val
 195 200 205
 Ser Asn Ala Ile Gln Pro Asp Asn Ile Val Tyr Val Met Asp Ala Ser
 210 215 220
 Ile Gly Gln Ala Cys Glu Ala Gln Ala Lys Ala Phe Lys Asp Lys Val
 225 230 235 240
 Asp Val Ala Ser Val Ile Val Thr Lys Leu Asp Gly His Ala Lys Gly
 245 250 255
 Gly Gly Ala Leu Ser Ala Val Ala Ala Thr Lys Ser Pro Ile Ile Phe
 260 265 270
 Ile Gly Thr Gly Glu His Ile Asp Asp Phe Glu Pro Phe Lys Thr Gln
 275 280 285
 Pro Phe Ile Ser Lys Leu Leu Gly Met Gly Asp Ile Glu Gly Leu Ile
 290 295 300
 Asp Lys Val Asn Glu Leu Lys Leu Asp Asp Asn Glu Ala Leu Ile Glu
 305 310 315 320
 Lys Leu Lys His Gly Gln Phe Thr Leu Arg Asp Met Tyr Glu Gln Phe
 325 330 335
 Gln Asn Ile Met Lys Met Gly Pro Phe Ser Gln Ile Leu Gly Met Ile

340 345 350
 Pro Gly Phe Gly Thr Asp Phe Met Ser Lys Gly Asn Glu Gln Glu Ser
 355 360 365
 Met Ala Arg Leu Lys Lys Leu Met Thr Ile Met Asp Ser Met Asn Asp
 370 375 380
 Gln Glu Leu Asp Ser Thr Asp Gly Ala Lys Val Phe Ser Lys Gln Pro
 385 390 395 400
 Gly Arg Ile Gln Arg Val Ala Arg Gly Ser Gly Val Ser Thr Arg Asp
 405 410 415
 Val Gln Glu Leu Leu Thr Gln Tyr Thr Lys Phe Ala Gln Met Val Lys
 420 425 430
 Lys Met Gly Gly Ile Lys Gly Leu Phe Lys Gly Gly Asp Met Ser Lys
 435 440 445
 Asn Val Ser Gln Ser Gln Met Ala Lys Leu Asn Gln Gln Met Ala Lys
 450 455 460
 Met Met Asp Pro Arg Val Leu His His Met Gly Gly Met Ala Gly Leu
 465 470 475 480
 Gln Ser Met Met Arg Gln Phe Gln Gln Gly Ala Ala Gly Asn Met Lys
 485 490 495
 Gly Met Met Gly Phe Asn Asn Met
 500

<210> 362

<211> 689

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (94).. (354)

<400> 362

```

gcggcgctgt gggcggttgc gggagagcgg cgggccgggg cgacacggcc gtgactcgct 60
tcgcggcctt gttcctcgct gcctgaagcc acg atg cct cag ttc cag acc tgg 114
                                Met Pro Gln Phe Gln Thr Trp
                                1             5
gag gag ttc agc cgg gcg gcc gag aag ctc tac ctg gcg gac ccc atg 162
Glu Glu Phe Ser Arg Ala Ala Glu Lys Leu Tyr Leu Ala Asp Pro Met
        10             15             20
aag gta cgg gtg gtt ctc aaa tac agg cat gtt gat ggg aat ttg tgt 210
Lys Val Arg Val Val Leu Lys Tyr Arg His Val Asp Gly Asn Leu Cys
        25             30             35
atc aaa gta acg gat gat cta gtt tgt ttg gtg tac aga aca gac caa 258
Ile Lys Val Thr Asp Asp Leu Val Cys Leu Val Tyr Arg Thr Asp Gln
        40             45             50             55
gcg caa gac gta aag aag att gag aaa ttc cac agt cag tta atg cga 306
Ala Gln Asp Val Lys Lys Ile Glu Lys Phe His Ser Gln Leu Met Arg
        60             65             70
ctt atg gtg gcc aag gaa tcc cgc aat gtc act atg gaa aca gaa tga 354
Leu Met Val Ala Lys Glu Ser Arg Asn Val Thr Met Glu Thr Glu
        75             80             85
atggtttgac atgaagacga ctgttccgtt attggaagt aatcagcttt tgaaactgag 414
agtgttgga aggatatact tacgtaatgg agctgtcaaa gccgagagac cagcctgcgt 474
cctaaagttt gctttagaga gtaggaatgt cggggtttcc agttagaaaa cttttatitt 534
tgaaacgga ataaaaatct cttagaaact ttgcagata attgatgtc gggcaaatat 594
atataattat tttttctggt aaattcatgt cagtaatttg ttgaagagtt aacaagaaaa 654
ggtctttcta gattgtgtct aagatgaaat aaaaat 689

```

<210> 363

<211> 86

<212> PRT

<213> Mus musculus

<400> 363

Met Pro Gln Phe Gln Thr Trp Glu Glu Phe Ser Arg Ala Ala Glu Lys

1 5 10 15

Leu Tyr Leu Ala Asp Pro Met Lys Val Arg Val Val Leu Lys Tyr Arg

20 25 30

His Val Asp Gly Asn Leu Cys Ile Lys Val Thr Asp Asp Leu Val Cys

35 40 45

Leu Val Tyr Arg Thr Asp Gln Ala Gln Asp Val Lys Lys Ile Glu Lys

50 55 60

Phe His Ser Gln Leu Met Arg Leu Met Val Ala Lys Glu Ser Arg Asn

65 70 75 80

Val Thr Met Glu Thr Glu

85

<210> 364

<211> 950

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (28)...(891)

<400> 364

gaattccggg aaagagcgcc tgataca atg gag aag aaa cct gcg gcc aag aag 54
Met Glu Lys Lys Pro Ala Ala Lys Lys

1 5

gct ggc agt gat gct gct gcc tcc cgg ccc cgg gcc gcc aaa gta gcc 102
Ala Gly Ser Asp Ala Ala Ala Ser Arg Pro Arg Ala Ala Lys Val Ala
10 15 20 25

aaa aag gtt cac cct aag ggt aaa aag ccc aag aag gcg aag ccc cat 150
Lys Lys Val His Pro Lys Gly Lys Lys Pro Lys Lys Ala Lys Pro His
30 35 40

tgc agc cga aac cct gtc ctg gtg aga gga att ggc agg tac tcc cga 198
Cys Ser Arg Asn Pro Val Leu Val Arg Gly Ile Gly Arg Tyr Ser Arg
45 50 55

tct gct atg tac tcc agg aag gcc ttg tac aaa agg aaa tac tcg gct 246
Ser Ala Met Tyr Ser Arg Lys Ala Leu Tyr Lys Arg Lys Tyr Ser Ala
60 65 70

gcc aag acc aag gtt gag aag aag aag aaa aaa gag aag gtc ctt gct 294
Ala Lys Thr Lys Val Glu Lys Lys Lys Lys Lys Glu Lys Val Leu Ala
75 80 85

act gtc acc aaa aca gtt ggt ggg gac aag aac ggt ggc acc cgg gtg 342
Thr Val Thr Lys Thr Val Gly Gly Asp Lys Asn Gly Gly Thr Arg Val
90 95 100 105

gtg aag ctt cga aaa atg cct agg tat tat ccc acc gaa gat gtt cct 390
Val Lys Leu Arg Lys Met Pro Arg Tyr Tyr Pro Thr Glu Asp Val Pro
110 115 120

cgg aag ctg ctg agc cac ggc aag aag ccc ttc agc cag cac gtg aga 438
Arg Lys Leu Leu Ser His Gly Lys Lys Pro Phe Ser Gln His Val Arg
125 130 135

agg cta cgc tcc agc atc act ccc gga act gtc ctg atc atc ctc act 486
Arg Leu Arg Ser Ser Ile Thr Pro Gly Thr Val Leu Ile Ile Leu Thr

140	145	150	
ggg cgc cac agg ggc aag aga gtg gtt ttc ctg aag cag ctg gac agt			534
Gly Arg His Arg Gly Lys Arg Val Val Phe Leu Lys Gln Leu Asp Ser			
155	160	165	
ggc ttg ctg ctt gtg act ggg cct ctt gtc atc aac aga gtt cct ctg			582
Gly Leu Leu Leu Val Thr Gly Pro Leu Val Ile Asn Arg Val Pro Leu			
170	175	180	185
cgc aga aca cac cag aag ttt gtc att gcc acc tct aca aaa gtt gat			630
Arg Arg Thr His Gln Lys Phe Val Ile Ala Thr Ser Thr Lys Val Asp			
	190	195	200
atc agc gat gtt aaa atc ccc aaa cac ctg act gac gct tac ttc aag			678
Ile Ser Asp Val Lys Ile Pro Lys His Leu Thr Asp Ala Tyr Phe Lys			
205	210	215	
aag aag cag ctg cgc aag ccc agg cat cag gag ggc gag atc ttc gac			726
Lys Lys Gln Leu Arg Lys Pro Arg His Gln Glu Gly Glu Ile Phe Asp			
220	225	230	
aca gag aag gag aaa tac gag att aca gag cag cga aag gct gac cag			774
Thr Glu Lys Glu Lys Tyr Glu Ile Thr Glu Gln Arg Lys Ala Asp Gln			
235	240	245	
aaa gct gtg gat ttg cag att ttg cca aag att aaa gct gtt cct cag			822
Lys Ala Val Asp Leu Gln Ile Leu Pro Lys Ile Lys Ala Val Pro Gln			
250	255	260	265
ctc cag ggc tac ctg cgc tct cag ttt tcc ctg aca aac ggg atg tat			870
Leu Gln Gly Tyr Leu Arg Ser Gln Phe Ser Leu Thr Asn Gly Met Tyr			
	270	275	280
cct cac aaa ctg gtc ttc taa attgtaacc taattaaaca gcttcatagg			921
Pro His Lys Leu Val Phe			
285			
ttaaaaaaaaa aaaaaaaaaa aaccttaag			950

<210> 365

<211> 287

<212> PRT

<213> Mus musculus

<400> 365

```

Met Glu Lys Lys Pro Ala Ala Lys Lys Ala Gly Ser Asp Ala Ala Ala
  1              5              10              15
Ser Arg Pro Arg Ala Ala Lys Val Ala Lys Lys Val His Pro Lys Gly
      20              25              30
Lys Lys Pro Lys Lys Ala Lys Pro His Cys Ser Arg Asn Pro Val Leu
      35              40              45
Val Arg Gly Ile Gly Arg Tyr Ser Arg Ser Ala Met Tyr Ser Arg Lys
      50              55              60
Ala Leu Tyr Lys Arg Lys Tyr Ser Ala Ala Lys Thr Lys Val Glu Lys
      65              70              75              80
Lys Lys Lys Lys Glu Lys Val Leu Ala Thr Val Thr Lys Thr Val Gly
      85              90              95
Gly Asp Lys Asn Gly Gly Thr Arg Val Val Lys Leu Arg Lys Met Pro
      100             105             110
Arg Tyr Tyr Pro Thr Glu Asp Val Pro Arg Lys Leu Leu Ser His Gly
      115             120             125
Lys Lys Pro Phe Ser Gln His Val Arg Arg Leu Arg Ser Ser Ile Thr
      130             135             140
Pro Gly Thr Val Leu Ile Ile Leu Thr Gly Arg His Arg Gly Lys Arg
      145             150             155             160
Val Val Phe Leu Lys Gln Leu Asp Ser Gly Leu Leu Leu Val Thr Gly
      165             170             175

```

Pro Leu Val Ile Asn Arg Val Pro Leu Arg Arg Thr His Gln Lys Phe
 180 185 190
 Val Ile Ala Thr Ser Thr Lys Val Asp Ile Ser Asp Val Lys Ile Pro
 195 200 205
 Lys His Leu Thr Asp Ala Tyr Phe Lys Lys Lys Gln Leu Arg Lys Pro
 210 215 220
 Arg His Gln Glu Gly Glu Ile Phe Asp Thr Glu Lys Glu Lys Tyr Glu
 225 230 235 240
 Ile Thr Glu Gln Arg Lys Ala Asp Gln Lys Ala Val Asp Leu Gln Ile
 245 250 255
 Leu Pro Lys Ile Lys Ala Val Pro Gln Leu Gln Gly Tyr Leu Arg Ser
 260 265 270
 Gln Phe Ser Leu Thr Asn Gly Met Tyr Pro His Lys Leu Val Phe
 275 280 285

<210> 366

<211> 1836

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (89).. (1216)

<400> 366

gctgccgtcc ttcccgctc ggtggatcat gcccaggacg gcagcggtcg cgggggggaa 60
 gtgactgggc ggtgcggcgc cggagacg atg ccg ttt cca gtt aca acg cag 112

Met Pro Phe Pro Val Thr Thr Gln

1

5

gga tca caa caa acg cag cca cca cag agg cac tat ggc att acc tct	160
Gly Ser Gln Gln Thr Gln Pro Pro Gln Arg His Tyr Gly Ile Thr Ser	
10 15 20	
cct atc agc tta gcg gcc ccc aag gag act gac tgc cta ctc aca cag	208
Pro Ile Ser Leu Ala Ala Pro Lys Glu Thr Asp Cys Leu Leu Thr Gln	
25 30 35 40	
aag ctc atc gag acg ctg ttg ccc ttt ggg gtt ttt gaa gaa gaa gag	256
Lys Leu Ile Glu Thr Leu Leu Pro Phe Gly Val Phe Glu Glu Glu Glu	
45 50 55	
gaa ctg cag cgc agg att tta att ttg gga aaa tta aat aac ctg gtg	304
Glu Leu Gln Arg Arg Ile Leu Ile Leu Gly Lys Leu Asn Asn Leu Val	
60 65 70	
aaa gaa tgg att cga gaa atc agt gaa agc aag aat ctc cca caa tct	352
Lys Glu Trp Ile Arg Glu Ile Ser Glu Ser Lys Asn Leu Pro Gln Ser	
75 80 85	
gta att gaa aat gtt gga ggg aag att ttt aca ttt gga tct tac aga	400
Val Ile Glu Asn Val Gly Gly Lys Ile Phe Thr Phe Gly Ser Tyr Arg	
90 95 100	
cta gga gtc cac acg aaa ggt gct gat att gat gcg ttg tgt gtt gca	448
Leu Gly Val His Thr Lys Gly Ala Asp Ile Asp Ala Leu Cys Val Ala	
105 110 115 120	
cca aga cat gtt gat cga agt gac ttt ttc acc tca ttc tat gat aaa	496
Pro Arg His Val Asp Arg Ser Asp Phe Phe Thr Ser Phe Tyr Asp Lys	
125 130 135	
ttg aaa tta caa gaa gaa gtg aaa gat tta aga gct gtt gaa gag gca	544
Leu Lys Leu Gln Glu Glu Val Lys Asp Leu Arg Ala Val Glu Glu Ala	
140 145 150	
ttt gta cca gtt atc aaa ctc tgt ttt gat gga ata gag att gat att	592
Phe Val Pro Val Ile Lys Leu Cys Phe Asp Gly Ile Glu Ile Asp Ile	

155	160	165	
ttg ttt gca aga tta gca ctg cag act att cca gaa gat ttg gac cta			640
Leu Phe Ala Arg Leu Ala Leu Gln Thr Ile Pro Glu Asp Leu Asp Leu			
170	175	180	
cga gat gac agt ctg ctt aaa aac cta gat ata aga tgc ata aga agc			688
Arg Asp Asp Ser Leu Leu Lys Asn Leu Asp Ile Arg Cys Ile Arg Ser			
185	190	195	200
ctt aat ggt tgc agg gta acc gat gaa att tta cat cta gta cca aac			736
Leu Asn Gly Cys Arg Val Thr Asp Glu Ile Leu His Leu Val Pro Asn			
205	210	215	
att gac aac ttc agg tta act ctg aga gcc atc aaa ctg tgg gcc aaa			784
Ile Asp Asn Phe Arg Leu Thr Leu Arg Ala Ile Lys Leu Trp Ala Lys			
220	225	230	
cgg cac aac atc tat tcc aat ata tta ggt ttc ctc ggt ggt gtt tcc			832
Arg His Asn Ile Tyr Ser Asn Ile Leu Gly Phe Leu Gly Gly Val Ser			
235	240	245	
tgg gct atg cta gta gca aga act tgc cag ctt tat cca aat gca ata			880
Trp Ala Met Leu Val Ala Arg Thr Cys Gln Leu Tyr Pro Asn Ala Ile			
250	255	260	
gca tca act ctt gta cat aaa ttt ttc ttg gta ttt tct aaa tgg gaa			928
Ala Ser Thr Leu Val His Lys Phe Phe Leu Val Phe Ser Lys Trp Glu			
265	270	275	280
tgg cca aat cca gtg cta ttg aaa cag cct gaa gaa tgc aat ctt aat			976
Trp Pro Asn Pro Val Leu Leu Lys Gln Pro Glu Glu Cys Asn Leu Asn			
285	290	295	
ttg cct gtg tgg gac cca agg gta aac ccc agt gat agg tac cat ctt			1024
Leu Pro Val Trp Asp Pro Arg Val Asn Pro Ser Asp Arg Tyr His Leu			
300	305	310	
atg cct ata att aca cca gca tac cca cag cag aac tcc acg tac aat			1072

Met Pro Ile Ile Thr Pro Ala Tyr Pro Gln Gln Asn Ser Thr Tyr Asn
 315 320 325
 gtg tcc gtt tca aca cgg atg gtc atg gtt gag gag ttt aaa caa ggt 1120
 Val Ser Val Ser Thr Arg Met Val Met Val Glu Glu Phe Lys Gln Gly
 330 335 340
 ctt gct atc aca gat gaa att ttg ctg agt aag gca gag tgg tcc aaa 1168
 Leu Ala Ile Thr Asp Glu Ile Leu Leu Ser Lys Ala Glu Trp Ser Lys
 345 350 355 360
 ctt ttt gaa gct cca aac ttc ttt cag aag tac aag tat gta ttt taa 1216
 Leu Phe Glu Ala Pro Asn Phe Phe Gln Lys Tyr Lys Tyr Val Phe
 365 370 375
 ggcatgtcag ccatgttgct ctttaagtagt ggtttaacag tggcatttgt ggtatttcct 1276
 ctigccagat tcgtgaacaa gtctctctcc agtgtctgta gaattttctt tattgttaaa 1336
 aagggttag agtttttagt aaactgggtgt ttcccttcat cagtacaggg tgtagcctc 1396
 acactttagt tgcttgactt actagcagtc ctactatgtg tcagccgcct cagttcttct 1456
 aggtctgtca ctgatgacca ggatactgtc tgcacctcag caggcttggt agtgcttcaa 1516
 aagttagggt tctctctcaa gacatttcta catttaatcc tgagagcttg ctgggatagt 1576
 ttagaccatg cacagacctg gtgaaacgtc ggcgtttggc tgaatacagg ttttcaatca 1636
 ttagtagcac atttccccct tcgaaaaata tgtctgcaa tagttttcta ataatttaag 1696
 tgggtatcat ttttattaat gtcttttaat ttaatgcitt aataccttag aggtgaaaaa 1756
 gccacatgat ttgtgctgtg ttggaaatgt aagttacaat aaatcttaaa aaaagaacaa 1816
 gaaaaaaaaa aaaaaaaaaa 1836

<210> 367

<211> 375

<212> PRT

<213> Mus musculus

<400> 367

Met Pro Phe Pro Val Thr Thr Gln Gly Ser Gln Gln Thr Gln Pro Pro
 1 5 10 15
 Gln Arg His Tyr Gly Ile Thr Ser Pro Ile Ser Leu Ala Ala Pro Lys
 20 25 30
 Glu Thr Asp Cys Leu Leu Thr Gln Lys Leu Ile Glu Thr Leu Leu Pro
 35 40 45
 Phe Gly Val Phe Glu Glu Glu Glu Glu Leu Gln Arg Arg Ile Leu Ile
 50 55 60
 Leu Gly Lys Leu Asn Asn Leu Val Lys Glu Trp Ile Arg Glu Ile Ser
 65 70 75 80
 Glu Ser Lys Asn Leu Pro Gln Ser Val Ile Glu Asn Val Gly Gly Lys
 85 90 95
 Ile Phe Thr Phe Gly Ser Tyr Arg Leu Gly Val His Thr Lys Gly Ala
 100 105 110
 Asp Ile Asp Ala Leu Cys Val Ala Pro Arg His Val Asp Arg Ser Asp
 115 120 125
 Phe Phe Thr Ser Phe Tyr Asp Lys Leu Lys Leu Gln Glu Glu Val Lys
 130 135 140
 Asp Leu Arg Ala Val Glu Glu Ala Phe Val Pro Val Ile Lys Leu Cys
 145 150 155 160
 Phe Asp Gly Ile Glu Ile Asp Ile Leu Phe Ala Arg Leu Ala Leu Gln
 165 170 175
 Thr Ile Pro Glu Asp Leu Asp Leu Arg Asp Asp Ser Leu Leu Lys Asn
 180 185 190
 Leu Asp Ile Arg Cys Ile Arg Ser Leu Asn Gly Cys Arg Val Thr Asp
 195 200 205
 Glu Ile Leu His Leu Val Pro Asn Ile Asp Asn Phe Arg Leu Thr Leu
 210 215 220
 Arg Ala Ile Lys Leu Trp Ala Lys Arg His Asn Ile Tyr Ser Asn Ile

225 230 235 240
 Leu Gly Phe Leu Gly Gly Val Ser Trp Ala Met Leu Val Ala Arg Thr
 245 250 255
 Cys Gln Leu Tyr Pro Asn Ala Ile Ala Ser Thr Leu Val His Lys Phe
 260 265 270
 Phe Leu Val Phe Ser Lys Trp Glu Trp Pro Asn Pro Val Leu Leu Lys
 275 280 285
 Gln Pro Glu Glu Cys Asn Leu Asn Leu Pro Val Trp Asp Pro Arg Val
 290 295 300
 Asn Pro Ser Asp Arg Tyr His Leu Met Pro Ile Ile Thr Pro Ala Tyr
 305 310 315 320
 Pro Gln Gln Asn Ser Thr Tyr Asn Val Ser Val Ser Thr Arg Met Val
 325 330 335
 Met Val Glu Glu Phe Lys Gln Gly Leu Ala Ile Thr Asp Glu Ile Leu
 340 345 350
 Leu Ser Lys Ala Glu Trp Ser Lys Leu Phe Glu Ala Pro Asn Phe Phe
 355 360 365
 Gln Lys Tyr Lys Tyr Val Phe
 370 375

<210> 368

<211> 596

<212> DNA

<213> Mus musculus

<400> 368

ggaaacacat gcttcattgaa ctcaagcatt cagtgigtca gcaatacaca accactgaca 60
 cagtacttta tctcaggag gcatctttat gaactcaaca ggacaaatcc cattggtatg 120
 aaaggcatal ggtaaatgtt atggcgattt ggtgcaagaa ctttggagtga gaactcagaa 180

gaatgt tgcc cccttaaagc tccgggtggac catagcaaaa tatgctccca ggittaatgg 240
 attccagcaa caagactccc aagaacttct ggctttcctc ttggatggtc ttcataaga 300
 tctcaaccga gtccacgaga aaccatatgt agaactaaaa gacagtgcg gccgacccga 360
 ctgggaagta gctgcagagg cctggggaca accatctaag gagaaataga tcaatigtg 420
 tggacttggt ccatggtcag ctaagatccc aagtcaaatg caagacatgt gggcatataa 480
 gtgtccgatt cgacctttt aattttttgt ctttacactt acaatggaca gttacatgca 540
 ttttagaata cagtaattaa ttagatggta ctaccgcata cggatatggct aagctg 596

<210> 369

<211> 2898

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (183).. (2699)

<400> 369

gcggcgggcc gggcggaggc ggcgcggtc aggcgggcgg ctccacctcc gcagttccga 60
 cgccctgccc tagattttcc gatagagagt gggctctctc ctttgcttct cgcaggagtc 120
 gcagcgcccg cagtggggac ccgcagcggg acgcgggtctc cgcagcccgga gccttaagcg 180
 gg atg tgc gtg gtg ggc att gac ctc ggc ttc ctc aac tgc tac atc 227

Met Ser Val Val Gly Ile Asp Leu Gly Phe Leu Asn Cys Tyr Ile

1

5

10

15

gct gta gcg agg agc ggc ggc atc gag acc atc gcc aac gag tac agc 275

Ala Val Ala Arg Ser Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser

20

25

30

gac agg tgc acg ccg gcc tgt ata tct ttg gga tcc aga act cga gcc 323

Asp Arg Cys Thr Pro Ala Cys Ile Ser Leu Gly Ser Arg Thr Arg Ala

35	40	45	
att gga aat gca gct aag agc cag ata gtc aca aat gta aga aat aca			371
Ile Gly Asn Ala Ala Lys Ser Gln Ile Val Thr Asn Val Arg Asn Thr			
50	55	60	
att cat ggc ttc aaa aag ctt cat ggg cga tca ttt gat gac ccc att			419
Ile His Gly Phe Lys Lys Leu His Gly Arg Ser Phe Asp Asp Pro Ile			
65	70	75	
gtg caa acg gag agg atc agg ctt ccg tac gag ctg cag aag atg cct			467
Val Gln Thr Glu Arg Ile Arg Leu Pro Tyr Glu Leu Gln Lys Met Pro			
80	85	90	95
aat gga agt aca ggt gtt aag gtg cgg tac ctg gaa gaa gag cgg ccc			515
Asn Gly Ser Thr Gly Val Lys Val Arg Tyr Leu Glu Glu Glu Arg Pro			
100	105	110	
ttt gca att gag caa gtc act ggg atg ttg ctg gct aag ctt aaa gag			563
Phe Ala Ile Glu Gln Val Thr Gly Met Leu Leu Ala Lys Leu Lys Glu			
115	120	125	
acc tca gaa aat gct ctg aag aag cca gtg gct gac tgt gtg atc tcg			611
Thr Ser Glu Asn Ala Leu Lys Lys Pro Val Ala Asp Cys Val Ile Ser			
130	135	140	
atc ccg agc ttt ttc acc gac gca gag aga aga tcc gtg atg gcc gca			659
Ile Pro Ser Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Met Ala Ala			
145	150	155	
gcc cag gtt gca ggc cta aac tgt ctg agg ctg atg aat gaa acc act			707
Ala Gln Val Ala Gly Leu Asn Cys Leu Arg Leu Met Asn Glu Thr Thr			
160	165	170	175
gca gtt gca ctg gca tat gga att tat aag cag gat ctt ccc tca tta			755
Ala Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu			
180	185	190	
gat gag aaa cca agg aat gtt gtg ttt atc gac atg gga cat tct gcc			803

Asp Glu Lys Pro Arg Asn Val Val Phe Ile Asp Met Gly His Ser Ala	
195	200
205	
tac cag gtc tct gtt tgt gct ttt aac aaa gga aaa ctg aaa gtg ttg	851
Tyr Gln Val Ser Val Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu	
210	215
220	
gct act acc ttt gac cca tat ttg ggt ggc agg aac ttt gat gag gct	899
Ala Thr Thr Phe Asp Pro Tyr Leu Gly Gly Arg Asn Phe Asp Glu Ala	
225	230
235	
tta gta gac tac ttc tgc gat gaa ttc aag acc aaa tat aag ata aat	947
Leu Val Asp Tyr Phe Cys Asp Glu Phe Lys Thr Lys Tyr Lys Ile Asn	
240	245
250	255
gtc aaa gag aac tcg cgg gcc ttg ttg cgg ctg tat cag gag tgt gaa	995
Val Lys Glu Asn Ser Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu	
260	265
270	
aaa cta aag aag ctg atg agt gca aac gcg tca gac ctt ccc ctg aac	1043
Lys Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu Pro Leu Asn	
275	280
285	
atc gag tgt ttc atg aat gac ctt gat gtt tct agt aag atg aac agg	1091
Ile Glu Cys Phe Met Asn Asp Leu Asp Val Ser Ser Lys Met Asn Arg	
290	295
300	
gct caa ttt gag cag ttg tgt gct tcc ctc tta gcc agg gtt gaa cca	1139
Ala Gln Phe Glu Gln Leu Cys Ala Ser Leu Leu Ala Arg Val Glu Pro	
305	310
315	
cct tta aaa tca gta atg gat caa gct aac tta caa cgt gaa gac ata	1187
Pro Leu Lys Ser Val Met Asp Gln Ala Asn Leu Gln Arg Glu Asp Ile	
320	325
330	335
aat agc ata gag att gtg gga ggg gcc acg cgg att cct gca gtc aag	1235
Asn Ser Ile Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys	
340	345
350	

gag cag gtg act agg ttc ttt ctg aaa gac atc agt acc acc ctg aat 1283
 Glu Gln Val Thr Arg Phe Phe Leu Lys Asp Ile Ser Thr Thr Leu Asn
 355 360 365
 gct gat gaa gct gtc gcc cga gga tgt gcg ttg cag tgt gcg att ctc 1331
 Ala Asp Glu Ala Val Ala Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu
 370 375 380
 tca cca gca ttt aaa gta cgt gaa ttt tcc ata act gac ctt gtt ccc 1379
 Ser Pro Ala Phe Lys Val Arg Glu Phe Ser Ile Thr Asp Leu Val Pro
 385 390 395
 tac tca gtc aca tta agg tgg aag act tct ttt gaa gaa ggg act ggg 1427
 Tyr Ser Val Thr Leu Arg Trp Lys Thr Ser Phe Glu Glu Gly Thr Gly
 400 405 410 415
 gaa tgt gaa gtc ttc tct aag aac cac ccg gcc cca ttc tca aag gtc 1475
 Glu Cys Glu Val Phe Ser Lys Asn His Pro Ala Pro Phe Ser Lys Val
 420 425 430
 ata act ttc cac aag aag gaa cca ttt gaa cta gaa gca ttt tat act 1523
 Ile Thr Phe His Lys Lys Glu Pro Phe Glu Leu Glu Ala Phe Tyr Thr
 435 440 445
 aat ttg cat gaa gtg cct tat cct gat cca aga att gga aac ttc act 1571
 Asn Leu His Glu Val Pro Tyr Pro Asp Pro Arg Ile Gly Asn Phe Thr
 450 455 460
 att cag aat gtt ttc cca cag tct gat ggt gac agt tct aaa gta aaa 1619
 Ile Gln Asn Val Phe Pro Gln Ser Asp Gly Asp Ser Ser Lys Val Lys
 465 470 475
 gtt aaa gtt cgt att aat atc cat gga atc ttc agt gtg gcc agt gcg 1667
 Val Lys Val Arg Ile Asn Ile His Gly Ile Phe Ser Val Ala Ser Ala
 480 485 490 495
 tca gta att gag aag cag aat ctg gaa ggt gat cat aac gat gcc gct 1715
 Ser Val Ile Glu Lys Gln Asn Leu Glu Gly Asp His Asn Asp Ala Ala

500	505	510	
atg gag acg gaa gct cct aag agt gaa ggc aaa gag gat gtg gac aaa			1763
Met Glu Thr Glu Ala Pro Lys Ser Glu Gly Lys Glu Asp Val Asp Lys			
515	520	525	
atg cag gtt gac caa gaa gaa gga ggt cat cag aaa tgt cat gct gag			1811
Met Gln Val Asp Gln Glu Glu Gly Gly His Gln Lys Cys His Ala Glu			
530	535	540	
cac acc cca gaa gag gag att gac cac acc ggg gcc aaa gca aag gca			1859
His Thr Pro Glu Glu Glu Ile Asp His Thr Gly Ala Lys Ala Lys Ala			
545	550	555	
cct cct tca gat aag caa gat cgc ata aat caa act att aaa aaa ggg			1907
Pro Pro Ser Asp Lys Gln Asp Arg Ile Asn Gln Thr Ile Lys Lys Gly			
560	565	570	575
aaa atc aag agt att gat cta cct atc cag agt agc ctc tac aga cag			1955
Lys Ile Lys Ser Ile Asp Leu Pro Ile Gln Ser Ser Leu Tyr Arg Gln			
580	585	590	
ctg act caa gac ctt ctc aat agt tac att gaa aat gag ggg aag atg			2003
Leu Thr Gln Asp Leu Leu Asn Ser Tyr Ile Glu Asn Glu Gly Lys Met			
595	600	605	
ata atg cag gat aaa tta gag aaa gaa aga aat gat gct aaa aat gct			2051
Ile Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala			
610	615	620	
gtt gaa gaa tac gtc tat gat ttc aga gac aaa ttg ggc act gtc tac			2099
Val Glu Glu Tyr Val Tyr Asp Phe Arg Asp Lys Leu Gly Thr Val Tyr			
625	630	635	
gaa aag ttc atc act cca gaa gac atg aat aag ctg tct gca atg tta			2147
Glu Lys Phe Ile Thr Pro Glu Asp Met Asn Lys Leu Ser Ala Met Leu			
640	645	650	655
gaa gac aca gaa aat tgg ctg tat gaa gaa gga gaa gac cag cct aaa			2195

Glu Asp Thr Glu Asn Trp Leu Tyr Glu Glu Gly Glu Asp Gln Pro Lys
 660 665 670
 caa gtt tat gtg gat agg ctg cag gaa tta aag aaa tat ggc cag ccc 2243
 Gln Val Tyr Val Asp Arg Leu Gln Glu Leu Lys Lys Tyr Gly Gln Pro
 675 680 685
 att caa atg aag tac gtg gag cat gaa gag aga cca aaa gct tta aat 2291
 Ile Gln Met Lys Tyr Val Glu His Glu Glu Arg Pro Lys Ala Leu Asn
 690 695 700
 gac ttg ggg aaa aag att cag ctt gtc ctg aaa gtg ata gaa gca cac 2339
 Asp Leu Gly Lys Lys Ile Gln Leu Val Leu Lys Val Ile Glu Ala His
 705 710 715
 aga aac aag gat gaa aga tat gat cat ctg gat cct gct gaa atg gaa 2387
 Arg Asn Lys Asp Glu Arg Tyr Asp His Leu Asp Pro Ala Glu Met Glu
 720 725 730 735
 aga gtt gaa aag tac atc agt gac tcc atg aac tgg cta aac agt aag 2435
 Arg Val Glu Lys Tyr Ile Ser Asp Ser Met Asn Trp Leu Asn Ser Lys
 740 745 750
 atg aat gca cag aat aaa tta agt ctc act caa gat ccc gtg gta aaa 2483
 Met Asn Ala Gln Asn Lys Leu Ser Leu Thr Gln Asp Pro Val Val Lys
 755 760 765
 gtg tca gaa ata gtt aca aag tca atg gaa ctg gat aat ttc tgt aac 2531
 Val Ser Glu Ile Val Thr Lys Ser Met Glu Leu Asp Asn Phe Cys Asn
 770 775 780
 ccc atc gtt tat aag ccc aaa cca aaa gta gaa gct cct gaa gac aaa 2579
 Pro Ile Val Tyr Lys Pro Lys Pro Lys Val Glu Ala Pro Glu Asp Lys
 785 790 795
 gca aaa act ggt agt gag cac aat gga cca atg gac gga cag agt ggt 2627
 Ala Lys Thr Gly Ser Glu His Asn Gly Pro Met Asp Gly Gln Ser Gly
 800 805 810 815

tca gag acc agc cca gat cca ccc aaa gga agc tca cag cac acc gac 2675

Ser Glu Thr Ser Pro Asp Pro Pro Lys Gly Ser Ser Gln His Thr Asp

820

825

830

tcc gga gag atg gaa gtg gac taa gtgtcatgtt atccaagcag tgggitaact 2729

Ser Gly Glu Met Glu Val Asp

835

aaagggccca ttcattccttt atgcccggta cacacaacat atgttcagtt gttcttaact 2789

acttttgtca tttgtttttt ggagtagitt tgaaaagtgt ctatattgag tacactattg 2849

ctgtccattg ctgctgtgaa gccctagctg aatatagaig tacaaatca 2898

<210> 370

<211> 838

<212> PRT

<213> Mus musculus

<400> 370

Met Ser Val Val Gly Ile Asp Leu Gly Phe Leu Asn Cys Tyr Ile Ala

1

5

10

15

Val Ala Arg Ser Gly Gly Ile Glu Thr Ile Ala Asn Glu Tyr Ser Asp

20

25

30

Arg Cys Thr Pro Ala Cys Ile Ser Leu Gly Ser Arg Thr Arg Ala Ile

35

40

45

Gly Asn Ala Ala Lys Ser Gln Ile Val Thr Asn Val Arg Asn Thr Ile

50

55

60

His Gly Phe Lys Lys Leu His Gly Arg Ser Phe Asp Asp Pro Ile Val

65

70

75

80

Gln Thr Glu Arg Ile Arg Leu Pro Tyr Glu Leu Gln Lys Met Pro Asn

85

90

95

Gly Ser Thr Gly Val Lys Val Arg Tyr Leu Glu Glu Glu Arg Pro Phe

100	105	110
Ala Ile Glu Gln Val Thr Gly Met Leu Leu Ala Lys Leu Lys Glu Thr		
115	120	125
Ser Glu Asn Ala Leu Lys Lys Pro Val Ala Asp Cys Val Ile Ser Ile		
130	135	140
Pro Ser Phe Phe Thr Asp Ala Glu Arg Arg Ser Val Met Ala Ala Ala		
145	150	155
Gln Val Ala Gly Leu Asn Cys Leu Arg Leu Met Asn Glu Thr Thr Ala		
165	170	175
Val Ala Leu Ala Tyr Gly Ile Tyr Lys Gln Asp Leu Pro Ser Leu Asp		
180	185	190
Glu Lys Pro Arg Asn Val Val Phe Ile Asp Met Gly His Ser Ala Tyr		
195	200	205
Gln Val Ser Val Cys Ala Phe Asn Lys Gly Lys Leu Lys Val Leu Ala		
210	215	220
Thr Thr Phe Asp Pro Tyr Leu Gly Gly Arg Asn Phe Asp Glu Ala Leu		
225	230	235
Val Asp Tyr Phe Cys Asp Glu Phe Lys Thr Lys Tyr Lys Ile Asn Val		
245	250	255
Lys Glu Asn Ser Arg Ala Leu Leu Arg Leu Tyr Gln Glu Cys Glu Lys		
260	265	270
Leu Lys Lys Leu Met Ser Ala Asn Ala Ser Asp Leu Pro Leu Asn Ile		
275	280	285
Glu Cys Phe Met Asn Asp Leu Asp Val Ser Ser Lys Met Asn Arg Ala		
290	295	300
Gln Phe Glu Gln Leu Cys Ala Ser Leu Leu Ala Arg Val Glu Pro Pro		
305	310	315
Leu Lys Ser Val Met Asp Gln Ala Asn Leu Gln Arg Glu Asp Ile Asn		
325	330	335

Ser Ile Glu Ile Val Gly Gly Ala Thr Arg Ile Pro Ala Val Lys Glu
 340 345 350
 Gln Val Thr Arg Phe Phe Leu Lys Asp Ile Ser Thr Thr Leu Asn Ala
 355 360 365
 Asp Glu Ala Val Ala Arg Gly Cys Ala Leu Gln Cys Ala Ile Leu Ser
 370 375 380
 Pro Ala Phe Lys Val Arg Glu Phe Ser Ile Thr Asp Leu Val Pro Tyr
 385 390 395 400
 Ser Val Thr Leu Arg Trp Lys Thr Ser Phe Glu Glu Gly Thr Gly Glu
 405 410 415
 Cys Glu Val Phe Ser Lys Asn His Pro Ala Pro Phe Ser Lys Val Ile
 420 425 430
 Thr Phe His Lys Lys Glu Pro Phe Glu Leu Glu Ala Phe Tyr Thr Asn
 435 440 445
 Leu His Glu Val Pro Tyr Pro Asp Pro Arg Ile Gly Asn Phe Thr Ile
 450 455 460
 Gln Asn Val Phe Pro Gln Ser Asp Gly Asp Ser Ser Lys Val Lys Val
 465 470 475 480
 Lys Val Arg Ile Asn Ile His Gly Ile Phe Ser Val Ala Ser Ala Ser
 485 490 495
 Val Ile Glu Lys Gln Asn Leu Glu Gly Asp His Asn Asp Ala Ala Met
 500 505 510
 Glu Thr Glu Ala Pro Lys Ser Glu Gly Lys Glu Asp Val Asp Lys Met
 515 520 525
 Gln Val Asp Gln Glu Glu Gly Gly His Gln Lys Cys His Ala Glu His
 530 535 540
 Thr Pro Glu Glu Glu Ile Asp His Thr Gly Ala Lys Ala Lys Ala Pro
 545 550 555 560
 Pro Ser Asp Lys Gln Asp Arg Ile Asn Gln Thr Ile Lys Lys Gly Lys

	565		570		575
Ile Lys Ser Ile Asp Leu Pro Ile Gln Ser Ser Leu Tyr Arg Gln Leu					
	580		585		590
Thr Gln Asp Leu Leu Asn Ser Tyr Ile Glu Asn Glu Gly Lys Met Ile					
	595		600		605
Met Gln Asp Lys Leu Glu Lys Glu Arg Asn Asp Ala Lys Asn Ala Val					
	610		615		620
Glu Glu Tyr Val Tyr Asp Phe Arg Asp Lys Leu Gly Thr Val Tyr Glu					
625		630		635	640
Lys Phe Ile Thr Pro Glu Asp Met Asn Lys Leu Ser Ala Met Leu Glu					
	645		650		655
Asp Thr Glu Asn Trp Leu Tyr Glu Glu Gly Glu Asp Gln Pro Lys Gln					
	660		665		670
Val Tyr Val Asp Arg Leu Gln Glu Leu Lys Lys Tyr Gly Gln Pro Ile					
	675		680		685
Gln Met Lys Tyr Val Glu His Glu Glu Arg Pro Lys Ala Leu Asn Asp					
	690		695		700
Leu Gly Lys Lys Ile Gln Leu Val Leu Lys Val Ile Glu Ala His Arg					
705		710		715	720
Asn Lys Asp Glu Arg Tyr Asp His Leu Asp Pro Ala Glu Met Glu Arg					
	725		730		735
Val Glu Lys Tyr Ile Ser Asp Ser Met Asn Trp Leu Asn Ser Lys Met					
	740		745		750
Asn Ala Gln Asn Lys Leu Ser Leu Thr Gln Asp Pro Val Val Lys Val					
	755		760		765
Ser Glu Ile Val Thr Lys Ser Met Glu Leu Asp Asn Phe Cys Asn Pro					
	770		775		780
Ile Val Tyr Lys Pro Lys Pro Lys Val Glu Ala Pro Glu Asp Lys Ala					
785		790		795	800

Lys Thr Gly Ser Glu His Asn Gly Pro Met Asp Gly Gln Ser Gly Ser

805

810

815

Glu Thr Ser Pro Asp Pro Pro Lys Gly Ser Ser Gln His Thr Asp Ser

820

825

830

Gly Glu Met Glu Val Asp

835

<210> 371

<211> 494

<212> DNA

<213> Mus musculus

<400> 371

acccatgtac acaatggaaa atatttctgt gactttggcc gacctgttct ttgcaggaac 60
 agagaccacc agcacaactc tgacatatgg gctcctgatt ctcatggaat acccaggaat 120
 tgaagagaaa cttcatgaag gaattgacag ggttattggg ccgagccgtt gccctgcagt 180
 cccaggcagg atggatatgt cctacatgga cgctgtagtt catgagattc cgggattcag 240
 taagctcgtg tccttccaac ttggccgaag agcaaaccg gaaaccgtgg tccgagggtta 300
 tgcctcccc aaggggacag gttggaatcc cagtcaggag gccccttgat ttggcaaaca 360
 tgaggtttcg ggctcggga gagttgaacc ttgcgttttc tgagatggaa tggggagttt 420
 agttaccgga cgatttcaag gggtttctga aggaaaagcc tgtttttttg aggaagcctg 480
 ccccatggaa tggtt

494

<210> 372

<211> 184

<212> DNA

<213> Mus musculus

<400> 372

tgaagctgtt cgatagcatc tgaacaaca agtggttttac agacacgtcc atcatccttt 60
 tcctcaacaa gaaggacctc ttcgaagaaa aaataaaaaa gagccccctc acaatatgct 120
 acccagaata tgcaggctca aacacatatg aagaagcggc cgcgtatatt cagtgtcagt 180
 ttga 184

<210> 373

<211> 972

<212> DNA

<213> Mus musculus

<400> 373

aaagtggtag gactcgcgtc gcgcctgcgag actagaagga ggactccgga tccggctcgg 60
 cgctcgccct cgctcgccat ggagaagacc gagctgatcc agaaggccaa gctggcgtgc 120
 agcgagcgct acgacgacat ggccacctgc atgaaagccg tgacggagca gggcgccgag 180
 ctgtccaacg aggagcgcaa cctgctgtcg gtggcctaca aaaacgtggt agggggccgc 240
 agtccgcctg gagggctatc tcgagcattg agcagaagac cgacacctct gacaagaagt 300
 tgcagctgat caaggactat agggagaaaag tggagtcgga gctgaggctc atctgcacca 360
 cggtcctgga attgttggat aagtatttaa tagccaatgc aactaatcga gagagtaagg 420
 tcttctatct gaaaatgaag ggagattatt tccggtatct tgctgaagta gcttgtggcg 480
 atgatcgaga cagacaatan gaaattccta aggagcgtac caaagaggcg ttgatatac 540
 nangaangag atgcacctan gcaccaatca gcctgggcnt gntcntaang tgcntgtatg 600
 tcgtatgaga cgttantacc gagacatgcg tgagantgct aaacggtttt gatagcgact 660
 cagagttgat ccatgangag atcgtgangc aagcgtacta tcagtcgiaa gaagtcaata 720
 tgcactgcat anggagattg nctcaagggc ggaantacgc ctagcaacat ntcctagaca 780
 tttagctacn tctcatggnc gngngnnngg gggngngnt ttgggggagg ggcccgngng 840
 tgatgtatct caggccntgt gctcctnggc tgtatatctg taagcttcat taggcgatga 900
 tatccctagg ttcataagag cgaaatacag ctgcttcgcg cgctcatgcg agcgggagcg 960
 cgggtgttat tc 972

<210> 374

<211> 1629

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (16).. (1149)

<400> 374

```

gcggacggag gcgag atg gcg gcc acc gag ggg gtc ggg gaa tct gcg gca 51
      Met Ala Ala Thr Glu Gly Val Gly Glu Ser Ala Ala
              1              5              10
ggc ggc gag ccg gga cag ccg gag cag ccg ccg ccc ccg cct ccg ccg 99
Gly Gly Glu Pro Gly Gln Pro Glu Gln Pro Pro Pro Pro Pro Pro Pro
              15              20              25
ccg cca gca cag cag ccg cag gaa gaa gag atg gcg gct gag gcc ggg 147
Pro Pro Ala Gln Gln Pro Gln Glu Glu Glu Met Ala Ala Glu Ala Gly
              30              35              40
gaa gcg gcg gcg tcc cct atg gac gac ggg ttt ctg agc ctg gac tgc 195
Glu Ala Ala Ala Ser Pro Met Asp Asp Gly Phe Leu Ser Leu Asp Ser
              45              50              55              60
ccc acc tat gtc ttg tac agg gac aga gca gaa tgg gct gat ata gac 243
Pro Thr Tyr Val Leu Tyr Arg Asp Arg Ala Glu Trp Ala Asp Ile Asp
              65              70              75
cca gtg ccc cag aat gac ggc cct aac cca gtg gtc cag atc atc tac 291
Pro Val Pro Gln Asn Asp Gly Pro Asn Pro Val Val Gln Ile Ile Tyr
              80              85              90
agt gaa aag ttt aga gat gtt tat gat tac ttc cga gct gtt ctg cag 339

```